Acid sphingomyelinase inhibition protects mice from lung edema and lethal Staphylococcus aureus sepsis

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ABBREVIATIONS

ADAM10 A-disintegrin and metalloprotease 10

AIDS acquired immune deficiency syndrome

AJ adherens junction

ALI acute lung injury

Ami Amitriptyline

APC activated protein C

ARDS acute respiratory distress syndrome

Asm Acid sphingomyelinase

BAL bronchoalveolar lavage

CA-MRSA community acquired MRSA

CFUs colony-forming units

DAG diacylglycerol

DAMP danger-associated molecular pattern

E. coli Escherichia coli

EDVD endothelium-dependent vasodilation

ESR Electron Spin Resonance

GM-CSF granulocyte-macrophage colony stimulating factor

HA-MRSA hospital associated MRSA

HIV human immunodeficiency virus

HPLC high performance liquid chromatography

HPTLC high performance thin layer chromatography

IL interleukin

LPS lipopolysaccharide

LRs lipid rafts

Methi Methicillin

MLST Multilocus sequence typing

MMPs matrix metalloproteinases

MRSA methicillin-resistant S. aureus

MSOF multisystem organ failure

MSSA methicillin-sensitive S. aureus

NAC N-acetylcysteine

NADPH nicotinamide adenine dinucleotide phosphate

NLR NOD-like receptors

NMR nuclear magnetic resonance

Nox NADPH oxidases

P. aeruginosa Pseudomonas aeruginosa

PAF platelet-activating factor

PAMPs pathogen-associated molecular patterns

PDTC pyrrolidine dithiocarbamate

PFGE Pulsed-field gel electrophoresis

PFT Pore-forming cytotoxins

PMN polymorphonuclear

PRRs pattern-recognition receptors

ROS Reactive oxygen species

RP-HPLC reversed phase HPLC

S. aureus Staphylococcus aureus

SCCmec staphylococcal chromosomal cassette mec

SIRS systemic inflammatory response syndrome

SOD superoxide dismutase

SSTI Skin and soft tissue infection

ST sequence type

TJ tight junction

TLC Thin Layer Chromatography

TLRs Toll-like receptors

TRAIL TNF-related apoptosis-inducing ligand

UV ultraviolet

Vanco Vancomycin

1. INTRODUCTION

1.1. Staphylococcus aureus (S. aureus)

1.1.1. Overview of S. aureus

S. aureus was discovered in the 1880s (Ogston 1880, Ogston 1881, Ogston 1882a, Ogston 1882b) and is a faculative pathogenic Gram-positive bacterium. Currently, S. aureus is one of the most virulent and common pathogens inside and outside hospitals and infections with S. aureus are associated with considerable morbidity and mortality (Laupland et al 2013, Tom et al 2014, van Hal et al 2012).

Humans and other mammals are major reservoirs for *S. aureus*. Three out of ten people in the United States are asymptomatically colonized with *S. aureus* on their skin or mucous membranes, most commonly in the anterior nares (Gorwitz et al 2008). Some people are only intermittent carriers, and some carry the bacteria for longer periods. Nasal colonization with *S. aureus* increases the risk of developing serious infection by the same strain (von Eiff et al 2001, Williams et al 1959), as when the bacterium is introduced into deeper tissues by cuts in the skin, in-dwelling catheters, aspiration, or surgery. Moreover, immune-deficient patients with advanced surgery, malignant diseases, prolonged stays in intensive care units and long-term care facilities and old patients are increasing since the beginning of the 21st century, which is another reason for *S. aureus* infections.

Skin and soft tissue infection (SSTI) is the most common clinical manifestation of *S. aureus* disease (Hayward et al 2008, Lautz et al 2011), recent studies describe an increase in the incidence of SSTI in Australia and New Zealand over the past decade (O'Sullivan et al 2011, Vaska et al 2012, Williamson et al 2013, Williamson et al 2014). In addition to *S. aureus* SSTI, *S. aureus* also causes a spectrum of invasive infections, including osteomyelitis, necrotizing pneumonia, joint infections, endocarditis, sepsis, and death. In particular, *S. aureus* bacteremia is associated with considerable morbidity and mortality, with reported

global incidence rates varying between 14 and 41 per 100,000 population (El Atrouni et al 2009, Laupland et al 2013), although it should be noted that differences in case ascertainment and study methodology limit comparisons between regions.

1.1.2. Evolution of S. aureus

In the pre-antibiotic era, prior to the introduction of penicillin for the treatment of *S. aureus* infections, the mortality rate of individuals with an *S. aureus* infection was about 80% (Skinner et al 1941). In 1929, Alexander Fleming reported his observations of the bactericidal effects of a fungal contaminant that produced penicillin, which can kill *S. aureus* on culture plates and is non-toxic to animals in enormous doses (Fleming 1929). Subsequently, with mass production of penicillin, the death rates from bacterial pneumonia and meningitis in World War II dramatically dropped, comparing to World War I (Neushul 1993).

Alexander Fleming noted that the growth of E. coli and a number of other bacteria belonging to the colityphoid group was not inhibited by penicillin (Fleming 1929). Further work has been done to find the cause of the resistance of these organisms to the action of penicillin. In 1940, an enzyme, which was called "penicillinase" and capable of hydrolyzing the active β-lactam ring in penicillin, was described in *Escherichia coli* (*E. coli*) (Abraham 1940). Soon thereafter, in 1944, penicillinase was extracted from penicillin resistant *Staphylococci* (Kirby 1944). Later on, more and more penicillin-resistant *S. aureus* strains were observed in the hospital and community. Currently, 90 to 95% of all *S. aureus* strains are resistant to penicillin, with the plasmid encoded penicillinase readily transferable via transduction or conjugation.

In 1961, 2 years after the introduction of methicillin, a penicillinase-resistant penicillin, the first strain of methicillin-resistant S. aureus (MRSA) was reported in a United Kingdom hospital due to the acquisition of the mecA gene (Eriksen 1961). This gene encodes for a penicillin-binding protein (PBP2a) which is expressed in the bacterial cell wall and which has a low affinity for β -lactam antibiotics. Thus, this group of antibiotics can't disrupt the synthesis of the peptidoglycan layer of bacteria and is ineffective against bacteria expressing

this gene. As a consequence, *S. aureus* will survive. There is evidence that strains of methicillin-sensitive *S. aureus* (MSSA) became methicillin resistant through the acquisition of the SCCmec element, probably from coagulase-negative staphylococcal strains, and that this has occurred on multiple occasions (Robinson et al 2004). The gene encoding meticillin resistance, mecA, is part of a larger genetic element known as the staphylococcal chromosomal cassette mec (SCCmec) (Ito et al 2001). The SCCmec element contains the mecA gene, chromosomal cassette recombinase (ccr) genes, mec regulatory genes and a junkyard region which contains non-essential components of SCCmec (Deurenberg et al 2008).

In recent years MRSA is now reported in about 60 to 70% of all *S. aureus* isolates found worldwide. There are now almost 100,000 cases of life threatening MRSA infections in the U.S. each year, evidences from the Centers for Disease Control and Prevention suggest with about 19,000 related deaths, more than the number of deaths from acquired immune deficiency syndrome (AIDS), which is induced by human immunodeficiency virus (HIV) (Klevens et al 2007).

Glycopeptides, such as vancomycin, are the treatment of choice for infections due to MRSA. Unfortunately, up to now, three vancomycin-resistant MRSA isolates have been reported from the US since 2002 (Boyce et al 2005, Courvalin 2006, Weigel et al 2007). By far, the biggest threat in *S. aureus* is the spread of vancomycin-resistant MRSA isolates. Lack of previous or additional reports of vancomycin-resistant MRSA isolates might be because of lack of detection (several of those isolates had vancomycin intermediate susceptibility) or to lack of stability of the plasmid-mediated vancomycin-resistant determinants in *S. aureus* (Perichon et al 2004). However, a recent report indicates that a single plasmid transfer from vancomycin-resistant enterococci to MRSA may be sufficient for expression of resistance (Weigel et al 2007).

Linezolid, quinupristin-dalfopristin, tigecycline, ceftopibrole and daptomycin are all available therapeutic options for treating vancomycin-resistant MRSA infections since they are all active *in vitro* against those isolates. However, the clinical efficacy of the best antibiotic combinations remains to be determined using animal models of infection since we (fortunately) have not faced outbreaks with those isolates to this day.

1.1.3. Typing methods for S. aureus

For the first three decades after their appearance, MRSA strains typically have remained hospital associated MRSA (HA-MRSA). In addition, since the 1990s, in an unexpected epidemiological 'move', MRSA strains also began to appear in the community among people who had none of the usual risk factors for such infections. Such community acquired MRSA (CA-MRSA), characterized by the presence of the toxin Panton-Valentine leukocidin, spread worldwide, first in the community, but later on also in healthcare facilities. At this moment, the distinction between CA-MRSA and HA-MRSA is beginning to fade (Lowy 1998, Lowy 2003).

A thorough knowledge of the spread and the molecular evolution of MRSA is required to effective develop strategies to control the dissemination of MRSA. Therefore, several typing methods have been developed during the last decades. MRSA strains can be typed using both phenotypic and molecular methods. There are many phenotypic typing methods, including the use of colonial characteristics, biochemical reactions, antibiotic susceptibility pattern, susceptibility to various phages and toxin production. The most important molecular typing methods in current use comprise pulsed-field gel electrophoresis, multilocus sequence typing, SCCmec typing and spa locus typing (Aires de Sousa et al 2004).

Pulsed-field gel electrophoresis (PFGE). As one of the earlier molecular methods, PFGE remains the most popular technique to differentiate MRSA isolates. In PFGE for S. aureus, the chromosomal DNA is digested with the restriction enzyme SmaI, and the obtained DNA fragments are separated by agarose gel electrophoresis in an electric field with an alternating voltage gradient. The resulting banding patterns are analyzed using a special software package (Tenover et al 1995). The advantage of this method is that it provides great discrimination between strains and is useful in the investigation of outbreaks by allowing differentiation of

unrelated strains. Disadvantages associated with the method relate principally to difficulties with inter-laboratory comparison of results. Thus reliable comparison of strains between regions and internationally is not always possible.

Multilocus sequence typing (MLST). MLST is based on the sequence analysis of fragments of seven *S. aureus* housekeeping genes, i.e. arcC, aroE, glpF, gmk, pta, tpi and yqiL, each approximately 500-bp in length (Enright et al 2000). The DNA sequences are compared to those of previously identified alleles at each locus on the MLST online database (http://www.mlst.net). Each allele is given a number, and a string of seven numbers then represents the allelic profile designated sequence type (ST) of an isolate. The MLST scheme for *S. aureus* was developed in 2000 and the details of more than 1500 isolates are available at the *S. aureus* MLST website http://saureus.mlst.net (Enright 2006). The advantage of MLST is that the geographic source and clinical information on each isolate can be stored with its sequence online, making it useful for international and local surveillance purposes. Disadvantages associated with MLST are the economic and time-consuming costs of performing seven PCRs and 14 DNA-sequencing reactions per isolate.

SCCmec typing. Seven major SCCmec types and their subtypes, which range in size from 20 to 67 kb, are defined by combinations of different classes of mec and ccr genes (Chongtrakool et al 2006). The SCCmec gene cluster evolves rapidly and becomes another target for sequencing methods to differentiate MRSA strains. Unfortunately, a major disadvantage of such a method is that it is not feasible for routine applications, since the relative large number of PCR reactions that are needed to determine the structure of SCCmec are time consuming (Kondo et al 2007).

Spa locus typing. Typing of a single locus zone in the polymorphic region X of *S. aureus* protein A (spa) has also become increasingly popular during recent years (Frenay et al 1996, Moodley et al 2006). The diversity of the spa gene, consisting mainly of a number of repeats of 24 bp in length, is attributed to point mutations, as well as to deletions and duplications of the repeats (Kahl et al 2005, Shopsin et al 1999). Spa typing is less expensive and

time-consuming than MLST and can be used to study both the molecular evolution as well as inter-hospital comparisons since it requires sequencing of one locus.

In summary, although a lot of knowledge on the spread of MRSA clones has been gained in last decades, there are still a number of questions unanswered. Further investigations, addressing both basic research and performing epidemiological studies, are needed to understand completely the molecular evolution of *S. aureus*.

1.2. Sepsis

1.2.1. Overview of sepsis

Sepsis is a very heterogeneous clinical syndrome broadly defined as the systemic host response to an infection. Indeed, sepsis can be initiated by any microorganism, whether it is bacterial, fungal, viral, parasitic, or by microbial products and toxins, and is then propagated by a complex network of inflammatory mediators and cellular dysfunction.

In 1989, Roger Bone and colleagues proposed the term "sepsis syndrome" for the first time to define patients who have severe sepsis, by establishing a set of clinical parameters (Bone et al 1989). Sepsis syndrome was defined as hypothermia (less than 96 °F [35.5 °C]) or hyperthermia (greater than 101 °F [38.3 °C]); tachycardia (greater than 90 beat/min); tachypnea (greater than 20 breath/min); clinical evidence of an infection site; and the presence of at least one end-organ demonstrating inadequate perfusion or dysfunction expressed as poor or altered cerebral function, hypoxemia (PaO₂ less than 100 mbar on room air), elevated plasma lactate, or oliguria (urine output less than 30 mL/h or 0.5 mL/kg body weight/h without corrective therapy) (Bone et al 1989). If untreated, the patient may develop systemic inflammatory response syndrome (SIRS), septic shock and multisystem organ failure (MSOF), which are the deadly forms of the disease.

The most common sites of bacterial infection are the lungs, abdominal cavity, the skin, the urinary tract and primary infections of the blood stream. A microbiological diagnosis is made

in about half the cases; Gram-negative bacteria account for about 60% of cases, Gram-positive for the remainder (Alberti et al 2002, Angus et al 2001).

Sepsis remains a significant problem in medical management, with an annual worldwide incidence of approximately 18 million cases with an associated 30-40% mortality rate (Blanco et al 2008, Karlsson et al 2007). In the U.S. alone, approximately 750,000 patients annually are diagnosed with sepsis, with a mortality rate ranging from 30% to 50% (Angus et al 2001). Most patients with sepsis are admitted to intensive care units and are on mechanical ventilation. The U.S. Center for Disease Control and Prevention indicates that sepsis is one of the top ten leading causes of death in the U.S., and estimates the annual costs for the treatment of patients with sepsis are estimated to exceed \$17 billion (Angus et al 2001). Sepsis may be responsible for a majority of the mortality associated with significant public health concerns such as malaria, tuberculosis, HIV/AIDS and others. What's more, the incidence of sepsis increases annually probably mainly due to an increase in the number of immunocompromised patients, increase in antibiotic resistance and the aging population.

Unfortunately, very few new treatments have been introduced over the past several decades although many people are working in the field. Current management of septic patients is predominantly non-specific, relying on a range of interventions such as intravenous fluids and medications, antibiotics, mechanical ventilation, nutritional support and corticosteroid therapy. Therefore, there is an urgent need for new effective treatments for sepsis.

1.2.2. Sepsis pathogenesis

Sepsis develops when the host response to a pathogen or a microbial toxin is accelerated to an inappropriate degree. The immune system relies on a process of molecular pattern recognition to determine the appropriate immunologic response to a foreign protein. These bacterial motifs, which are recognized by the innate immune system, have been named pathogen-associated molecular patterns (PAMPs) or microorganism-associated molecular patterns (Janeway et al 1998). In Gram-negative bacteria, lipopolysaccharide (LPS; known also as endotoxin) correlates with the ability to activate host cell membranes. In Gram-

positive bacteria, identified structural components in the bacteria cell wall account for their biological activity since there is no endotoxin in these type of bacteria (Majcherczyk et al 1999, Morath et al 2001). However, Gram-positive bacteria can also produce potent exotoxins, which exhibit the properties of super antigens and cause massive T-cell activation and release of pro-inflammatory lymphokines, suggesting a plausible role for these toxins as a cause of the profound shock that is seen in patients with toxic shock (Lavoie et al 1999).

PAMP's as well as other danger-associated molecular pattern (DAMP) molecules will bind to their receptors in the host cell membrane and begin a process of intracellular signaling and cellular activation: On one hand, the mechanisms involve widespread fibrin deposition causing microvascular occlusion, the development of tissue exudates further compromising adequate oxygenation, and disorders of microvascular homeostasis resulting from the elaboration of vasoactive substances such as platelet-activating factor (PAF), histamine and prostanoids (Anderson et al 1991). On the other hand, cellular infiltrates, particularly neutrophils, damage tissue directly by releasing lysosomal enzymes and superoxide-derived free radicals. TNF- α and other cytokines increase the expression of the inducible nitric oxide synthase and increased production of nitric oxide causes further vascular instability (Azevedo et al 2006) and may also contribute to the direct myocardial depression that occurs in sepsis (Landry et al 2001). Microvascular occlusion and vascular instability results in coagulopathy, fever, vasodilation and capillary leak, ultimately sepsis and multiple organ failure (Cohen 2002) (**Figure 1.2.2.1.**).

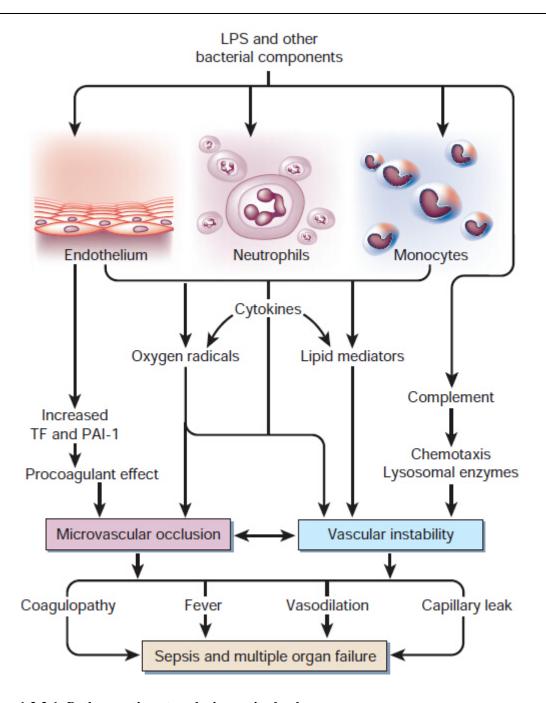


Figure 1.2.2.1. Pathogenetic networks in septic shock

Lipopolysaccharide (LPS) and other microbial components simultaneously activate multiple parallel cascades that contribute to the pathophysiology of adult respiratory distress syndrome (ARDS) and septic shock. The combination of poor myocardial contractility, impaired peripheral vascular tone and microvascular occlusion results in tissue hypoperfusion and inadequate oxygenation, and finally multiple organ failure (Cohen 2002).

During a very long time, the prevailing concept of the pathogenesis of sepsis was that mortality is the consequence of an uncontrolled hyper-inflammatory response of the host. The disappointing results of nearly 40 years of anti-inflammatory strategies and the development

of animal models that more closely mimic clinical sepsis have led to the reconsideration of the pathophysiology of sepsis. Sepsis is now considered a misbalance between pro-inflammatory reactions (designed to kill invading pathogens but at the same time responsible for tissue damage) and anti-inflammatory responses (designed to limit excessive inflammation, but at the same time making the host more vulnerable for secondary infections) (Anas et al 2010) (**Figure 1.2.2.2.**).

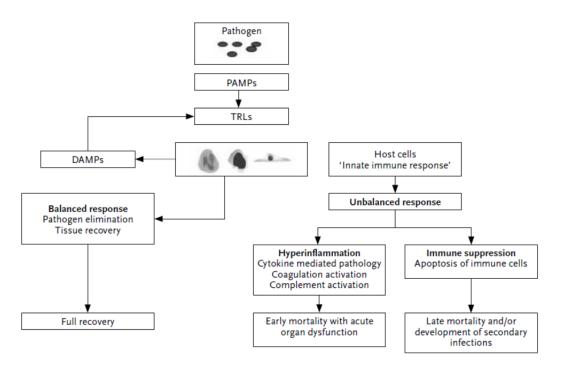


Figure 1.2.2.2. Important components of the host response to sepsis

The interaction between pathogens and the host is mediated initially via an interaction between PAMPs (pathogen associated molecular pathogens) and TLRs (Toll-like receptors). The resulting innate response of immune cells can result in a balanced reaction leading to pathogen elimination and tissue recovery or an unbalanced reaction that on the one hand can lead to exaggerated inflammation and tissue injury and on the other hand to immune suppression caused by immune cell apoptosis (Anas et al 2010).

In addition, new players have been described in the field of vascular dysfunction, such as platelet-derived microparticles, which are associated with apoptosis of vascular cells and cardiac failure (Azevedo et al 2007). However, the correlation of these pathways to outcome is so far poorly understood.

1.2.3. Mechanisms of acute lung injury (ALI) and acute respiratory distress syndrome (ARDS)

Currently, the incidence of ALI and ARDS in the USA has been reported to be 79 and 59 per 100,000 people per year, respectively (Bernard et al 1994, Herridge et al 2005, Peek et al 2006, Rubenfeld et al 2005, Wheeler et al 2007). Based on the growth of the population, the incidence will likely double in the next 25 years (Rubenfeld et al 2005).

The highest incidence of ALI is seen during sepsis, with approximately 25% of all ARDS cases stemming from severe sepsis (Brun-Buisson et al 2004) and 42.8% of sepsis was pneumonia (Blanco et al 2008). Moreover, ALI/ARDS are associated with a lethality of approximately 40%, accounting for around 75,000 deaths per year in the USA (Rubenfeld et al 2005, Wheeler et al 2007).

ALI/ARDS was first described in 1967 (Ashbaugh et al 1967) and a large body of research has been ongoing in order to understand ALI/ARDS and to improve the clinical outcomes of this entity. ALI/ARDS is a clinical syndrome, characterized by the acute onset of severe hypoxemia with diffuse bilateral infiltrates in the chest radiograph and without evidence of left atrial hypertension. The difference between both entities is the degree of hypoxemia. In ALI, the ratio of arterial oxygen tension (PaO_2) to the fraction of inspired oxygen (FiO_2) is \leq 300, while in ARDS it is \leq 200 (Bernard et al 1994).

The pathophysiology of ALI/ARDS is not completely understood. Initially, a direct pulmonary or indirect extrapulmonary insult is believed to cause a proliferation of inflammatory mediators that promote neutrophil accumulation in the microcirculation of the lung. These neutrophils activate and migrate in large numbers across the vascular endothelial and alveolar epithelial surfaces, releasing proteases, cytokines, and reactive oxygen species. This migration and mediator release lead to pathologic vascular permeability, gaps in the alveolar epithelial barrier, and necrosis of type I and II alveolar cells. This, in turn, leads to the pulmonary edema, hyaline membrane formation, and loss of surfactant that decrease pulmonary compliance and make air exchange difficult. Subsequent infiltration of fibroblasts

can result in collagen deposition, fibrosis, and further progression of the disease (Matthay et al 2003, Matthay et al 2005, Ware et al 2000).

Increased permeability of microvascular barriers, resulting in extravascular accumulation of protein-rich edema fluid, is a cardinal feature of acute inflammation and a central pathophysiologic mechanism in ALI and ARDS (**Figure 1.2.3.**) (Bachofen et al 1977, Matthay et al 2003, Ware et al 2000).

Neutrophils are proposed to have an important role in mediating ALI. When recruited to a site of infection/inflammation, they exert a variety of beneficial functions (phagocytosis, production of reactive oxygen species and nitric oxide species, and degranulation of lytic enzymes) that, when well regulated, enable clearance of the invading pathogen. However, it is also hypothesized that the recruitment of activated PMNs may be potentially harmful when these same functions are dysregulated and directed at otherwise normal host tissue, culminating in injury and organ damage.

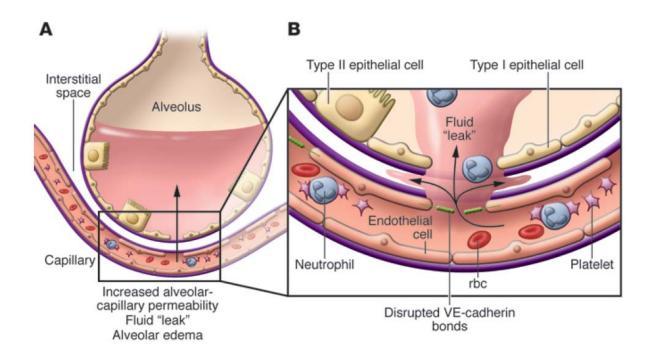


Figure 1.2.3. Mechanism of lung edema

(A) Disrupted alveolar barrier function, resulting in increased permeability to water, proteins, and other solutes, is a hallmark of clinical and experimental ALI. Intra-alveolar accumulation of neutrophils, other leukocytes, erythrocytes and inflammatory mediators is also associated with altered endothelial and epithelial barrier function. (B) Disruption of VE-cadherin bonds is a central mechanism of altered endothelial barrier function in experimental ALI and in models of sepsis and systemic vascular destabilization. Disruption of VE-cadherin bonds also facilitates transendothelial migration of leukocytes and, in some studies, is associated with accumulation of leukocytes and platelets in microvessels (Matthay 2003).

1.2.4. ALI/ARDS therapy

Despite the importance of ALI/ARDS healthcare issue, very few new treatments have been introduced over the past three decades, and the mortality and morbidity rates of ALI/ARDS -related conditions remains high. Current management of ALI/ARDS patients is predominantly non-specific, relying on a range of interventions such as intravenous fluids and medications, antibiotics, mechanical ventilation, nutritional support, corticosteroid therapy, and prevention of stress ulcers and venous thromboembolism (Adhikari et al 2004, Briel et al 2010, Dellinger et al 2008, Geerts et al 2008, Lin et al 2010, National Heart et al 2006, Peter et al 2008, Petrucci et al 2013).

Despite the large amount of research elucidating the molecular mechanisms underlying ALI/ARDS, the investigation of pharmacologic therapies has led almost exclusively to negative results, often in contrast to very promising results in animal studies. Although some animal studies support the potential efficacy of anti-inflammatory therapies for decreasing lung injury, clinical trials have not demonstrated a convincing reduction in mortality using granulocyte-macrophage colony stimulating factor (GM-CSF) or glucocorticoids, antioxidants, or anticytokine therapies that were tested in patients with sepsis (Bernard et al 1987, Bernard et al 1997, Meduri et al 1998, Meduri et al 2007, Paine et al 2012, Steinberg et al 2006). Although pulmonary hypertension and lung vascular injury are important features of ALI and ARDS, vasodilator therapies including prostaglandin E1 and nitric oxide have not reduced mortality (Abraham et al 1999, Taylor et al 2004). Treatment to accelerate the resolution of pulmonary edema with aerosolized or intravenous β-adrenergic agonists also failed to improve survival (Gao Smith et al 2012). Nutritional supplement with ω-3 fatty acid may be

harmful (Rice et al 2011).

Newer approaches, such as targeting the coagulation system, have been considered. Recombinant human activated protein C (APC) was found to reduce 28-day mortality in patients with severe sepsis (Bernard et al 2001). However, follow-up studies among patients with severe sepsis and a low risk of death and in children with severe sepsis were negative (Abraham et al 2005, Nadel et al 2007). Furthermore, a recent trial of APC has provided evidence that this anticoagulant and anti-inflammatory agent does not have efficacy for patients with severe sepsis, the most lethal cause of ALI and ARDS (Ranieri et al 2012). Strategies and rationale for anticoagulants for ALI and ARDS will now need to be reevaluated.

Explanations for these outcomes are likely multifactorial, the lack of efficacy of many of these agents does raise the question of whether or not these treatments may perform better in more homogeneous cohorts of patients. Therefore, further research is needed to recommend any of these agents. Without therapeutic product currently approved for treatment of ALI/ARDS, there is clearly an urgent need for new effective and affordable treatments.

1.3. Ceramide-enriched membrane platforms

1.3.1. Lipid interactions and domain formation

The biological membranes of eukaryotic cells are comprised mainly of sphingolipids, (glycerol-) phospholipids and cholesterol. Sphingolipids are characterized by a 1, 3-dihydroxy-2-aminoalkane backbone, also named sphingoid base (Hakomori 1983). Sphingosine, the most prevalent backbone of mammalian sphingolipids refers to (2S, 3R, 4E)-2-amino-4-octadecene-1, 3-diol. Sphingoid bases vary in length of the alkyl chain and position and number of the double bonds. Ceramide is generated from sphingosine by attachment of a fatty acid via an amide ester bond. The fatty acids in the ceramide moiety also vary in chain length and saturation. Thus, ceramide is composed of D-erythro-sphingosine and a fatty acid usually containing 2 – 32 carbon atoms in the acyl chain that are connected

via an amide ester bond. Ceramides are further modified by attachments of headgroups to form sphingomyelin, gangliosides, sulfatides, globosides or cerebrosides, for example, forming sphingomyelin by reaction with phosphorylcholine (Barenholz et al 1980, Kolesnick et al 2000). The most prevalent membrane sphingolipid is sphingomyelin, which consists of a very hydrophobic ceramide moiety (a D-erythro-sphingosine bound to a fatty acid by an amide ester) and a hydrophilic phosphorylcholine headgroup (Hakomori 1983). The acyl chain of the fatty acid may contain 2 to 32 carbon atoms.

In 1972, Singer and Nicolson described the fluid mosaic model of the cell membrane; this model suggested a random distribution of lipids and proteins in the cell membrane, which was in a liquid-disordered phase. This model predicted free movement of proteins in the lipid bilayer, which was based on biophysical experiments that determined the melting temperatures of lipids (Singer et al 1972). However, biophysical studies in the last 15 years revised this model and suggested the formation of small domains in the cell membrane that exist in a liquid-ordered phase and thus form distinct domains in the cell membrane (Brown et al 1998, Simons et al 1997).

Sphingomyelin is the most prevalent cellular sphingolipid and synthesized on the luminal side of the Golgi apparatus or the plasma membrane. Thus, it localizes predominantly to anti-cytoplasmic leaflets of the cell membrane and intracellular vesicles (Emmelot et al 1975, Futerman et al 1990, Jeckel et al 1990). This distribution pattern of sphingomyelin, which results in lipid bilayer asymmetry, is critical for the genesis of distinct membrane domains and, as discussed below, signal transduction. Sphingomyelin consists of a highly hydrophobic ceramide moiety and a hydrophilic phosphorylcholine headgroup (Barenholz et al 1980, Kolesnick et al 2000). Sphingolipids interact with each other via hydrophilic interactions between the sphingolipid headgroups (Brown et al 1998, Kolesnick et al 2000, Simons et al 1997). In addition, sphingolipids, and in particular the predominant sphingolipid sphingomyelin, interact with cholesterol via hydrogen bonds with the hydroxy group in the cholesterol molecule and via hydrophobic van der Waal interactions between the ceramide moiety and the sterol ring system. These binding forces result in a relatively tight interaction

between these lipids and in the spontaneous formation of domains that are in the liquid-ordered phase or even of gel-like domains with higher melting temperatures than other phospholipids in the cell membrane (Brown et al 1998, Kolesnick et al 2000, Simons et al 1997). These distinct sphingolipid- and cholesterol-enriched membrane domains were named rafts (Simons et al 1997). Recent microscopy studies of cell membranes using the STET technique suggest that these rafts have a diameter of less than 20 nm (Eggeling et al 2009). Cholesterol and some cholesterol precursors not only interact with sphingolipids but also seem to fill the void spaces between bulky sphingolipids and, sterically, to stabilize sphingolipid- and cholesterol-enriched domains (Megha et al 2004, Xu et al 2001). Extraction of cholesterol from rafts by interference with the cholesterol metabolism employing drugs such as filipin, nystatin or methyl-beta-cyclodextrin (Keller et al 1998) destroys rafts supporting the critical role of cholesterol for the integrity of at least some rafts.

However, at present only indirect evidence exists to support the presence of rafts in cells under in vivo conditions, for instance at physiological temperature. The concept of rafts is still somewhat controversial (Munro 2003), since the use of detergents employed in most studies characterizing rafts may change the membrane and only cause the formation of rafts (Munro 2003). Recently, Brugger and co-workers suggested the lipid composition of HIV particles released from living cells (Brugger et al 2006). This study demonstrated a high concentration of sphingolipids and cholesterol in the viral coat suggesting that viral budding occurs in distinct domains of the cell membrane that are enriched with these lipids arguing that rafts exist *in vivo*.

1.3.2. Ceramide synthesis and metabolism

Diverse stress stimuli, such as cytokines, environmental stress and chemotherapeutic or anti-cancer drugs (Hannun et al 2002, Senchenkov et al 2001, Spiegel et al 2002) (**Figure 1.3.2.A.**) induce ceramide formation, and therefore ceramide is involved in the regulation of cell growth, differentiation, cell cycle arrest and apoptosis.

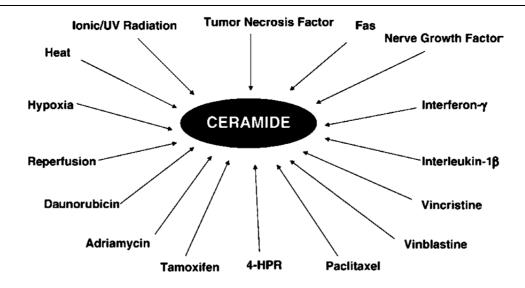


Figure 1.3.2.A. Ceramide formation in response to diverse stress stimuli

Ceramide formation is induced in response to environmental stress, ionic/ultraviolet radiation, heat, hypoxia, reperfusion, cytokines and growth factors, tumor necrosis factor, interferon-gamma and interleukin-1-beta as well as chemotherapeutic agents/anticancer drugs (Pandey et al 2007).

The hydrolysis of sphingomyelin is catalyzed by the activity of acid, neutral, or alkaline sphingomyelinase and results in the generation of ceramide (Gulbins et al 2003, Hannun et al 2008, Quintern et al 1989). Further, ceramide is generated in membranes by a de novo pathway involving the enzyme ceramide synthase (Kolesnick et al 2000) (**Figure 1.3.2.B.**). Recent studies further revealed three additional pathways for the formation of ceramide, i.e. by the reverse activity of the acid ceramidase catalyzing synthesis of ceramide from sphingosine (Okino et al 2003), by hydrolysis of complex glycosylated lipids (Ishibashi et al 2007) and by hydrolysis of ceramide-1-phosphate (Mitra et al 2007). Ceramide can also be converted into other sphingolipids, such as ceramide-1-phosphate, sphingosine, and sphingosine-1-phosphate.

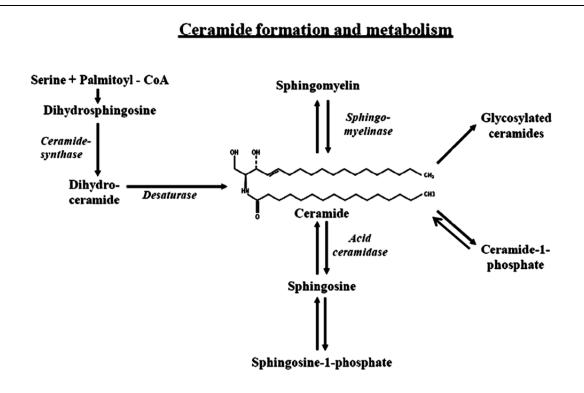


Figure 1.3.2.B. Ceramide synthesis and metabolism

Ceramide can be generated from the sphingomyelin via sphingomyelinase pathway (sphingomyelin metabolism), degradation of glycosylated sphingolipids or via the *de novo* synthesis pathway where cells synthesize ceramide from serine and palmitoyl-CoA (*de novo* synthesis). Ceramide can be further converted into other sphingolipids such as ceramide-1-phosphate, glycosylated ceramide, sphingosine and sphingosine-1-phosphate (Becker et al 2010a).

1.3.3. Acid sphingomyelinase (Asm) and ceramide-enriched membrane platforms

Acid sphingomyelinase (Asm) is the first and best-characterized sphingomyelinase and previous study already showed the enzyme critically involved in many forms of cell activation reviewed for instance by Gulbins et al. (Gulbins et al 2003). There are two forms of Asm, a lysosomal Asm and a secretory Asm that are both derived from the same gene, but differ in their glycosylation pattern and are also differentially processed at the NH2-terminus (Schissel et al 1998a). Most of Asm seems to reside in classical lysosomes, where it mediates the catabolism of sphingomyelin. Asm-deficiency leads to the accumulation of sphingomyelin and a lysosomal storage disorder named Niemann-Pick disease type A and B. Many studies suggested that the pool of Asm insecretory lysosomes seems to participate in signal transduction events (Bao et al 2010, Grassmé et al 2001a, Herz et al 2009, Schissel et al 1996, Schissel et al 1998b). Appropriate cellular activation triggers the fusion of secretory

lysosomes and the cell membrane, and this fusion results in the exposure of Asm on the outer leaflet of the cell membrane (Bao et al 2010, Herz et al 2009).

Usually, Asm hydrolyzes sphingomyelin to ceramide, preferentially at an acidic pH. However, because other lipids crucially influence the Michaelis-Menten constant (Km) of the enzyme to its substrate, the enzyme seems to be able to hydrolyze sphingomyelin also under almost neutral PH conditions (Schissel et al 1996, Schissel et al 1998a). Since Asm is predominantly present in the outer leaflet of the cell membrane (Calderon et al 1997, Grassmé et al 2001a, Grassmé et al 2001b), the hydrolysis of sphingomyelin results in ceramide-enriched membrane domains that are primarily in the outer leaflet of the cell membrane, or in general in anti-cytoplasmic leaflets of cellular membranes.

Changes in the glycosylation pattern of Asm result in the expression of a secretory form of Asm that is released upon stimulation, for instance via interleukin-1 receptors (Schissel et al 1996, Schissel et al 1998b). Further, several studies demonstrated that stimuli such as CD95, DR5 and CD40 or infection with some pathogenic bacteria and viruses mobilize intracellular vesicles/secretory lysosomes, a process that results in exposure of Asm on the outer leaflet of the cell membrane (Cremesti et al 2001, Dumitru et al 2006, Grassmé et al 2001a, Grassmé et al 2002b, Grassmé et al 2003a, Grassmé et al 2003b, Grassmé et al 2005).

Lysosomal Asm and secretory Asm hydrolyze sphingomyelin from the plasma membrane and generate ceramide within cell membranes. The release of ceramide within the cell membrane alters the biophysical characteristics of membranes, because they spontaneously self-associate to small, highly hydrophobic, and ordered ceramide-enriched membrane microdomains (Holopainen et al 1998, Kolesnick et al 2000, Nurminen et al 2002). These microdomains spontaneously fuse to larger ceramide-enriched membrane domains, also named membrane platforms, that can reach a width of up to 5 μm (Gulbins et al 2003). Ceramide-enriched membrane platforms seem to be very hydrophobic and stable, since ceramide molecules are highly packed and ordered. Furthermore, the presence of ceramide excludes cholesterol molecules from membrane domains, at least in artificial membranes, suggesting that ceramide

also changes the composition of rafts (Megha et al 2004, Megha et al 2006) with an increased concentration of ceramide and a decreased concentration of cholesterol, respectively.

1.3.4. Visualization of ceramide-enriched membrane domains

The formation of ceramide-enriched membrane platforms in the plasma membrane upon generation of ceramide might be critical for the signaling function of ceramide, which were demonstrated by several methods *in vivo* and *in vitro*.

First, activation of several receptors, such as CD95, DR5, CD40, and the platelet-activating factor receptor, but also some bacterial and viral infections or stress stimuli, trigger the surface exposure of Asm and the formation of ceramide-enriched membrane platforms by fluorescence and electron microscopy (Cremesti et al 2001, Dumitru et al 2006, Grassmé et al 2001a, Grassmé et al 2002b, Grassmé et al 2003a, Grassmé et al 2003b, Grassmé et al 2005) **1.3.4.**). Secondly. studies on phosphatidylcholine/sphingomyelin-composed unilamellar vesicle that were treated with sphingomyelinase immobilized onto a microbead confirmed the formation of ceramide-enriched membrane macrodomains (Holopainen et al 1998, Nurminen et al 2002). Furthermore, in vitro studies also indicated the formation of distinct membrane domains by magnetic resonance spectroscopy and atomic force microscopy studies, which revealed laminar phase separation of long chain ceramides in glycerol-phospholipid/cholesterol bilayers and formation of stable, distinct domains that correspond with a transition of fluid phospholipid bilayers into a gel-like phase (Huang et al 1999, ten Grotenhuis et al 1996, Veiga et al 1999). Finally, Ira and Johnston used a combination of atomic force microscopy and total internal reflection fluorescence to directly visualize clustering of small membrane domains into larger domains in artificial membranes composed of 1, 2-dioleoyl-sn-glycero-3-phosphocholine/sphingomyelin/cholesterol mixtures upon treatment with Bacillus cereus sphingomyelinase to generate ceramide or incubation with C₁₆-ceramide. The studies revealed that enzymatic hydrolysis of sphingomyelin to ceramide in model membranes resulted in very rapid reorganization of the membrane, clustering of domains and the formation of larger distinct domains that presumably correspond to ceramide-enriched membrane domains. The addition of C₁₆-ceramide also

resulted in the formation of larger domains in these bilayers, albeit with different kinetics and less impact on membrane organization (Ira et al 2008).

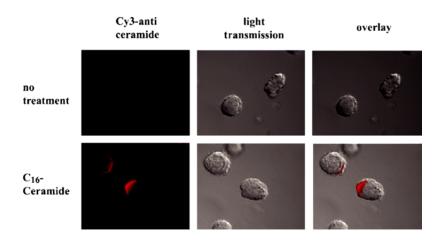


Figure 1.3.4. Ceramide forms ceramide-enriched membrane platforms in the cell membrane

Jurkat T cells $(0.5 \text{ x} \cdot 10^6 \text{ cells/sample})$ were centrifuged for 5 min at 1400 rpm, resuspended in 90 µl PBS. Cells were rested for 8 min at 37 °C, shaked at 400 rpm, and treated with 1 µM C₁₆ ceramide for 5 min. Cells were fixed in 1% PFA for 20 min, washed once, unspecific binding sites were blocked with 2% fetal calf serum (FCS) and stained with anti-ceramide antibody clone 15B4 (1:20 dilution). Cells were incubated on ice for 45 min, washed once and incubated for 45 min on ice with 100 µl of a Cy3 F (ab) 2 fragment of a donkey anti-mouse IgM (1:300). Cells were washed once and analyzed on a fluorescence microscope (Grassmé et al 2007).

1.3.5. Function of ceramide-enriched membrane platforms

Ceramide-enriched membrane domains may have several biological functions. First, the composition and fluidity of ceramide-enriched membrane domains differ from the surrounding areas in biological membranes, which are perfect structures to sort proteins in cells and to provide a mean for the spatial re-organization of receptors and/or intracellular signaling molecules within these membrane domains. Trapping and clustering of activated receptors in ceramide-enriched membrane domains was demonstrated for CD95, DR5, or CD40 (Dumitru et al 2006, Grassmé et al 2001a, Grassmé et al 2002a, Grassmé et al 2002b), but many more receptors may use the mechanism of clustering to reach a very high density in circumscribed areas of the cell membrane. The reorganization of receptors within a relatively small area of the cell membrane, which is required for the transmission of signals

via many receptor molecules. Receptor aggregation and trapping in ceramide-enriched membrane domains may limit lateral diffusion and, thus, stabilize the interaction of a ligand with its receptor, in particular if the ligand is also trapped in distinct membrane domains. The interaction of ligand-bound receptors with the very hydrophobic ceramide-enriched membrane platform and/or individual ceramide molecules may in addition stabilize conformational changes that may occur upon activation of a receptor by its ligand. Furthermore, ceramide-enriched membrane domains may sort intracellular signalling molecules, for instance via farnesyl or geranyl-moieties, which may result in the spatial association of activated receptors with signalling molecules that transmit the signal from the receptor into the cell, while at the same time inhibitory molecules are excluded from this area of the cells. Thus, in general, ceramide-enriched membrane platforms may primarily function to re-organize receptor and signaling molecules in and at the cell membrane to facilitate and amplify signaling processes via a specific receptor.

Second, in addition to its function in membrane platforms, ceramide was also shown to directly interact and regulate several molecules including cathepsin D (Heinrich et al 1999), phospholipase A2 (Huwiler et al 2001), kinase suppressor of Ras (identical to ceramide-activated protein kinase) (Zhang et al 1997), ceramide-activated protein serine-threonine phosphatases(CAPP) (Dobrowsky et al 1993), protein kinase C isoforms (Muller et al 1995) and c-Raf-1 (Yao et al 1995). A direct binding of ceramide was demonstrated for cathepsin D (Heinrich et al 1999), phospholipase A2 (Huwiler et al 2001) and CAPP (Chalfant et al 2004, Dobrowsky et al 1993), although at present the details and the specificity of ceramide-protein interactions are still unknown except for cathepsin D. Cathepsin D binds ceramide within a short domain of the cathepsin D molecule, which triggers the autocatalytic cleavage of cathepsin D to its active form and promotes, via still unknown mechanisms, the translocation of active cathepsin D from lysosomes into the cytoplasm where cathepsin D triggers cell death via Bid, Bax and Bak (Heinrich et al 1999, Schneider-Brachert et al 2004). Ceramide might facilitate the transport of cathepsin D over the double membrane by forming a hydrophobic coat around the protein, the formation of ceramide channels (Siskind et al 2000) or by a very short disruption of the membrane bilayer.

Third, ceramide has been shown to regulate several ion channels. Ceramide inhibits the potassium channel Kv1.3 and the calcium release activated calcium channel in lymphocytes (Bock et al 2003, Gulbins et al 1997, Lepple-Wienhues et al 1999, Szabo et al 1996). This is also consistent with the finding that Kv1.3 localizes to ceramide-enriched membrane domains after stimulation via CD95 (Bock et al 2003, Lepple-Wienhues et al 1999). However, these studies do not exclude that ceramide also affects ion channels by a direct interference or by the change of the lipid composition in ceramide-enriched membrane platforms. The calcium release activated calcium channels that are central in the regulation of cellular Ca²⁺ concentrations and, thus, involved in multiple cellular pathways (Lee et al 2004), are also inactivated upon stimulation of cells via CD95 (Hannun et al 2000) or the TNF-receptor (Zemann et al 2007) or upon treatment with synthetic ceramides, C2, C6 and C16-ceramides, respectively. Genetic deficiency of the Asm abrogated the inhibition of the calcium release activated calcium channels by CD95 and TNF-receptor stimulation. Finally, ceramide-molecules seem to form channels or pores, at least in the outer mitochondrial membrane (Siskind et al 2000, Siskind et al 2006). These channels might be important for the induction of apoptosis, although it is unknown whether ceramide pores are also formed in vivo. The regulation of ion channels by ceramide is a poorly investigated field, although its potential for many physiological and pathophysiological processes appears immense.

In summary, ceramide-enriched membrane domains serve the temporal and spatial organization of signaling molecules to regulate multiple cell functions. However, the mechanisms responsible for the action of ceramide on these downstream targets are not fully understood.

1.3.6. Asm/ceramide in bacterial infections

Asm/ceramide in internalization of bacteria. Numerous studies, using either genetic deficiency of pharmacological inhibition of Asm, demonstrated that the activation of Asm and the concomitant release of ceramide upon the infection of human epithelial and myeloid cells with *Neisseria gonorrhoeae* (Grassmé et al 1997, Hauck et al 2000), the infection of

endothelial cells with *S. aureus (Esen et al 2001)*, the infection of pulmonary epithelial cells and fibroblasts with *Pseudomonas aeruginosa (P. aeruginosa)* (Grassmé et al 2003b), the infection of immature dendritic cells with *Escherichia coli* (Falcone et al 2004), the infection of macrophages with *Listeria monocytogenes* (Utermohlen et al 2003) or *Salmonella typhimurium (McCollister et al 2007)*, and the infection of mononuclear cells with *Mycobateria avium (Utermohlen et al 2008)*, resulted in uptake of the bacteria (**Figure 1.3.6.A.**). The bacteria very rapidly activate the enzyme, induce a rapid surface translocation of the Asm and trigger the release of ceramide and, thus, the formation of ceramide-enriched membrane platforms, which seem to be central for the uptake of pathogens.

Asm/ceramide in bacterial killing. Infection of macrophages with Listeria monocytogenes (Utermohlen et al 2008) or Salmonella typhimurium (McCollister et al 2007) results in intracellular killing of the bacteria. In wild-type macrophages, the phagosome rapidly fuses with the lysosome to form a phago-lysosome and to kill and digest the bacteria. In contrast, Asm-deficient macrophages were unable to kill the bacteria. Studies with Listeria monocytogenes also demonstrated that Asm deficient macrophages impaired the maturation and fusion of intracellular phagosomes with lysosomes and led to development of sepsis and greatly increased mortality of Asm deficient mice (Schramm et al 2008, Utermohlen et al 2003). Moreover, Yang and colleagues showed that the Asm is also required to produce ROS upon infection, which also kills the pathogens. Deficiency of the Asm prevents ROS release and reduces bacterial killing (Zhang et al 2008) (Figure 1.3.6.B.).

Asm/ceramide in cell death induced by bacterial infection. In addition to mediating the internalization of pathogens and fusion of intracellular vesicles, Asm and ceramide have been shown to be also crucial for the induction of cell death on infection of endothelial cells with *S. aureus* (Esen et al 2001), on infection of immature dendritic cells with *E. coli* (Falcone et al 2004), on infection of pulmonary epithelial cells and fibroblasts with *P. aeruginosa* (Grassmé et al 2003b, Kannan et al 2008). The molecular mechanisms by which Asm and ceramide are involved in induction of cell death are still not well-known. Below is a summary of possible mechanisms: a. Ceramide-enriched membrane platforms cluster CD95 and induce cell death

on infection of epithelial cells with *P. aeruginosa* (Becker et al 2012, Grassmé et al 2000). b. Ceramide-enriched membrane platforms are required to internalize *P. aeruginosa*, induce apoptosis and regulate the cytokine response in infected cells. Impaired bacterial killing in Asm-deficient mice induced overwhelming inflammation and cell death (Grassmé et al 2003b, Kannan et al 2006) (**Figure 1.3.6.C.**).

Asm/ceramide in cytokine release induced by bacterial infection. The release of cytokines, which is moderately increased in the lungs of wild-type mice upon infection, is uncontrolled and exaggerated in Asm-deficient mice infected with *P. aeruginosa*, resulting in a cytokine storm and the death of the mice (Grassmé et al 2003b). This finding is confirmed by Kannan and co-workers' work (Kannan et al 2006). However, the mechanisms that mediate the activation of Asm and cytokines release by *P. aeruginosa* require definition.

Asm/ceramide in host survival. Our group revealed that Asm/ceramide are critical for the internalization of *P. aeruginosa* into epithelial cells and fibroblasts, the induction of death of infected cells, and controlled release of cytokines critical, finally facilitating the mice survival *P. aeruginosa* infection (Grassmé et al 2003b). Schramm and colleagues ascertained the role of Asm/ceramide in *Listeria monocytogenes* infection by demonstrating that Asm-deficient macrophages showed impaired phagolysosome fusion and maturation correlated with severe sepsis and increased mortality of Asm-deficient mice (Schramm et al 2008). Moreover, recent studies showed that Asm-deficienct mice controlled the bacteria in small granulomas to protect the mice from uncontrolled inflammation upon *Mycobacteria avium* infection, but not wild-type mice (Utermohlen et al 2008).

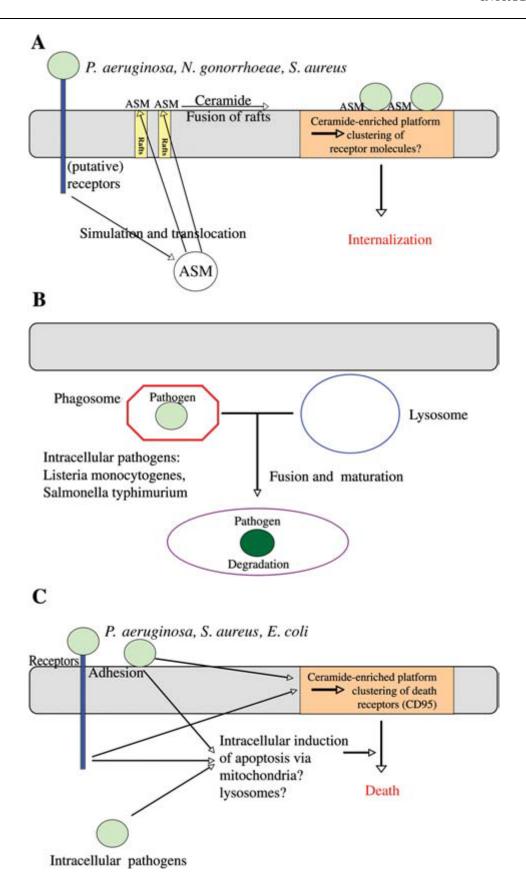


Figure 1.3.6. Functions of Asm and ceramide during bacterial infections

Asm functions in the outer leaflet of the cell membrane to mediate internalization of pathogens (A) and in lysosomes to mediate fusion of phagosomes with lysosomes (B). Asm also seems to be

involved in maturation of phagolysosomes (B). Finally, surface and intracellular ceramide generated by Asm activity is important for induction of cell death upon infection with some pathogens (C) (Grassmé et al 2008).

1.4. Redox signaling

1.4.1. Overview of Reactive oxygen species (ROS)

ROS are chemically reactive molecules containing oxygen. Examples include oxygen ions and peroxides. ROS are formed as a natural byproduct of the normal metabolism of oxygen and have important roles in cell signaling and homeostasis (Devasagayam et al 2004). Various ROS (Figure 1.4.1.), including O₂-, H₂O₂, OH, and ONOO-, participate in cell signaling under certain physiological or pathological conditions. The most important of these ROS is O₂-, which is unstable and short-lived because it has an unpaired electron, and it is highly reactive with a variety of cellular molecules, including proteins and DNA. O2⁻ is reduced to H₂O₂ by superoxide dismutase (SOD), an enzyme which catalyzes the dismutation of superoxide radicals $(O_2^- + O_2^- + 2H^+ - O_2 + H_2O_2)$ (McCord et al 1969). Both O_2^- and H_2O_2 can diffuse from their sites of generation to other cellular locations. H₂O₂ is further reduced to generate the highly reactive 'OH through the Haber-Weiss or Fenton reaction under pathological conditions. In contrast to O₂ and H₂O₂, OH is highly reactive and, therefore, causes primarily local damage. In addition, O2 can also interact with NO to form another reactive oxygen free radical, ONOO. Under physiological conditions, O2. preferably produces H₂O₂ via the dismutation reaction. However, when excess O₂. is produced, a substantial amount of O₂ reacts with NO to produce ONOO (Figure 1.4.1.).

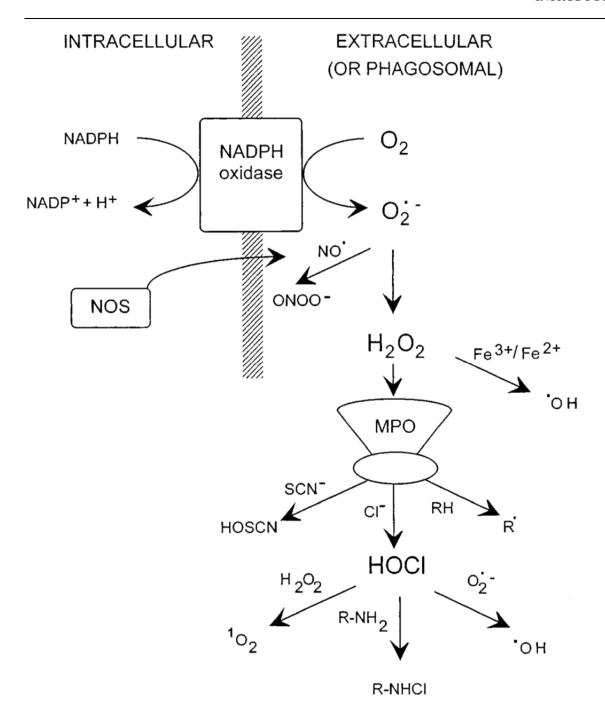


Figure 1.4.1. Possible oxidant generating reactions with stimulated neutrophils. NOS, nitric oxide synthase; MPO, myeloperoxidase (Hampton et al 1998)

1.4.2. ROS production and regulation

O₂ is the progenitor of other ROS. In mammalian cells, many pathways are involved in the production of O₂, including nicotinamide adenine dinucleotide phosphate (NADPH) oxidase, xanthine oxidase, mitochondrial respiration chain, and NO synthase-uncoupling. NADPH oxidase has been detected in nearly every tissue, and in many cells, such as those in phagocytes and vascular cells, it is the primary source of ROS. Recent studies suggest that

NADPH oxidase localizes to specific subcellular compartments, including lamellipodial focal complexes and focal adhesions, membrane ruffles, caveolae and lipid rafts, endosomes, sarcoplasmic reticulum, and the nucleus. NO synthases normally localize in caveolae and function as homodimers to synthesize NO. When exposed to oxidative or nitrosative stress, NOS becomes structurally unstable ("uncoupling state") and exhibits NADPH oxidase activity resulting in O_2 — formation. Given that ROS are short-lived and diffusible, the localization of ROS signals in specific subcellular compartments suggests that mammalian cells contain temporally and spatially organized redox signaling pathways that regulate various cellular functions.

An antioxidant is a molecule that inhibits the oxidation of other molecules. Oxidation is a chemical reaction that transfers electrons or hydrogen from a substance to an oxidizing agent. Oxidation reactions can produce free radicals. In turn, these radicals can start chain reactions. When the chain reaction occurs in a cell, it can cause damage or death to the cell. Antioxidants terminate these chain reactions by removing free radical intermediates, and inhibit other oxidation reactions. They do this by being oxidized themselves, so antioxidants are often reducing agents such as thiols, ascorbic acid, or polyphenols (Sies 1997).

ROS formation and redox signaling are well known to play a major role in physiology as well as in a variety of pathologies. For instance, in the heart, cardiomyocyte differentiation, and excitation-contraction coupling are under tight redox control (Burgoyne et al 2012, Steinberg 2013). On the other hand, cardiac pathologies, such as ischemia/reperfusion injury, heart failure, and arrhythmias can be prevented or blocked by inhibiting specific processes that result in ROS generation in several experimental models (Anderson et al 2014, Kaludercic et al 2014, Takimoto et al 2007, Youn et al 2013). Thus, it appears that pro-oxidant generation and antioxidant defense need to be tightly regulated (Chance et al 1979). Indeed, disruption of redox signaling and control, and imbalance in favor of pro-oxidant species is defined oxidative stress, term first coined in 1985 (Jones 2006, Sies et al 1985). Conversely from pathological modifications (Chance et al 1979, Powers et al 2008), it appears that

physiological redox signaling is characterized by reversible oxido-reductive modifications, confined both spatially and temporally in subcellular compartments and microdomains.

1.5. Endothelial Barrier

1.5.1. Overview of Endothelial Barrier

The vascular endothelium lining the inner surface of blood vessels serves as the first interface for circulating blood components to interact with cells of the vascular wall and surrounding extravascular tissues. In addition to regulating blood delivery and perfusion, a major function of vascular endothelia, especially those in exchange microvessels (capillaries and postcapillary venules), is to provide a semipermeable barrier that controls blood-tissue exchange of fluids, nutrients, and metabolic wastes while preventing pathogens or harmful materials in the circulation from entering into tissues.

Blood fluid, solutes, and even circulating cells can cross the endothelium via two routes: through the cell body (transcellular), or between the cells (paracellular, or intercellular)(Mehta et al 2006) (Figure 1.5.1.). The transcellular pathway, which contributes very little to the leakage of events in pathophysiological conditions, includes vesicle-mediated endocytosis, vacuole-vesicular organelles (VVOs) and regulated water channels (aquaporins). On the other hand, the paracellular pathway, which is responsible for the majority of leakage of blood fluid and proteins across the microvascular endothelium under pathophysiological conditions, is mainly mediated by junctional proteins (Figure 1.5.1.).

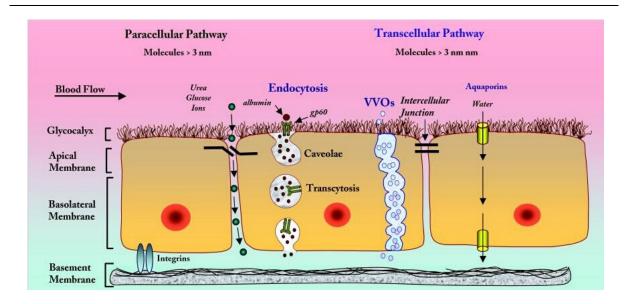


Figure 1.5.1. Transcellular and paracellular permeability pathways across the microvascular endothelium

Barrier function of the microvasculature is provided by closely apposed endothelial cells of themicrovessel walls. The thin layer of endothelium is attached to the microvascular basement membrane via endothelial membrane-bound integrins. Endothelial cells are joined together by intercellular junction proteins that allow the selective passage of solutes and fluids across the endothelium. Intercellular junctions can become more porous, or even form large-sized gaps under pathophysiological conditions. The glycocalyx forms a selective filter across the endothelial luminal surface, forming an additional permeability barrier. Solutes can also traverse the cell interior via receptor-mediated vesicle endocytosis originating at caveolae, or via vacuole-vesicular organelles (VVOs) that can fuse with trafficking vesicles and form open transcellular pores. Transcellular water transport can occur in parallel with other fluxes, through regulated water channels (aquaporins) in the endothelial cell membrane (Yuan et al 2010).

Two types of intercellular junctions have been characterized as the cell–cell adhesive barrier structures in the microvascular endothelium: the adherens junction (AJ) and tight junction (TJ) (Komarova et al 2010, Mehta et al 2006). The former has been identified in nearly all types of vascular beds, especially in the peripheral microvasculature. Vascular endothelial (VE)–cadherin is believed to be the most important protein in forming the molecular basis, as well as regulating the function of AJs. Intracellularly, VE–cadherin is connected to the actin cytoskeleton via a family of catenins (α -, β -, γ -, and p120-catenins) (Mehta et al 2006). Thus, the stability of the VE–cadherin–catenin–cytoskeleton complex is essential to the maintenance of endothelial barrier function (Alcaide et al 2008, Sallee et al 2006, Vincent et al 2004).

Endothelial tight junctions are composed of interactions of tight junction proteins: occludin, claudins, and JAM-A (Abbott et al 2010, Hawkins et al 2005, Mehta et al 2006), which are connected to the actin cytoskeleton via zona occludens proteins (ZO-1, ZO-2) and α -catenin. ZO proteins play both structural and signaling roles in tight junctions (Hawkins et al 2005, Shen et al 2009).

During host defense against infection or tissue injury, endothelial barrier dysfunction occurs as a consequence as well as cause of inflammatory responses. Endothelial barrier dysfunction is characterized by leakage of fluid, proteins, or small molecules, measured as excessive flux of these molecules across the endothelium (termed hyper-permeability), and clinically manifests as accumulation of plasma-like, protein-rich fluid in the extravascular space leading to tissue swelling (termed edema) (Yuan et al 2010).

1.1.1. Leukocytes and Endothelial Barriers

Endothelial hyper-permeability occurs following trauma, pathogen infection, or chronic disease states, which is a generalized response to inflammation (Kumar et al 2009, Lush et al 2000). A hallmark of inflammation is extravasation of leukocytes from the blood to the tissue across the microvascular endothelium (Cavanagh et al 1998, Lewis et al 1986, Nathan 2006). Leukocytes, which are white blood cells circulating in the blood, include lymphocytes (T-cells, B-cells, and natural killer cells), monocytes, and polymorphonuclear (PMN) granulocytes (neutrophils, eosinophils, and basophils) (Moser et al 2010).

Neutrophil extravasation is a multi-stage process: rolling, activation, adhesion, and transmigration, requiring complex interactions of PMNs or other leukocytes with the microvascular endothelium (**Figure 1.5.2.**) (Butcher 1991, Kubes 2002). Leukocyte trans-endothelial migration occurs in response to endothelial hyper-permeability caused by bacterial invasion or tissue inflammatory injury. In the presence of a compromised microvascular endothelial barrier, leukocytes can become immobilized by firm adhesion to the micro-vessel luminal surface and cross the endothelium into the tissues step by step.

Generally, PMNs are the first leukocyte cell type to arrive at the site of barrier dysfunction (Nathan 2006). After and/or during transmigration across the micro-vessel wall, PMNs will become activated and undergo a respiratory burst, characterized by release of granule secretions of numerous compounds (Lewis et al 1986), which can attack and liquify tissue surrounding the compromised vasculature (pus formation) (Nathan 2006). PMNs also secrete chemokines or induce endothelial expression of chemokines (Middleton et al 1997) to attract other leukocytes (macrophages, monocytes, and immune cells) to the site of inflammation. Hence, leukocyte activation and migration across the endothelium are both cause and consequence of endothelial hyper-permeability and barrier dysfunction (Nathan 2006).

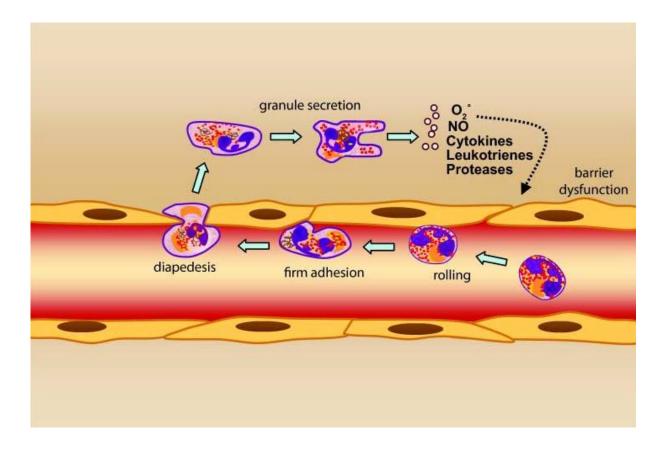


Figure 1.5.2. The stages of neutrophil extravasation

Neutrophil transmigration is a sequential process of (1) rolling along the microvessel wall, (2) firm adhesion to the endothelium (via interactions with cell surface adhesion molecules), (3) diapedesis (transmigration) coordinated by interactions between cell surface glycoproteins, followed by migration into the extravascular space, and (4) neutrophil activation, characterized by granule secretions of

hyper-permeability-inducing agents (oxygen free radicals (O₂-), NO, cytokines, and arachidonic acid metabolites: leukotriences and prostaglandins), further contributing to barrier dysfunction (Yuan et al 2010).

1.6. Aims of the study

Sepsis is a devastating and complex syndrome and continues to be a major cause of morbidity and mortality among critically ill patients at the surgical intensive care unit setting in the United States (Angus et al 2001, Dombrovskiy et al 2007, Kung et al 2008, Martin et al 2003, Melamed et al 2009, Russell 2006). Antibiotics alone are often insufficient to cure patients with *S. aureus*—induced sepsis. Although treatment with effective doses of bactericidal antibiotics indeed prevents the bacterial burden, antibiotics often fail to prevent fatal lung edema after septic infection with *S.*

aureus.

Our group has demonstrated that Asm/ceramide system activates several receptors, mediates entry of several microorganisms into cells and participates in signal transduction events. Particularly, we discovered *S. aureus* infection activates the Asm/ceramide system, and finally induces apoptosis of human endothelial cells (Esen et al 2001). However, it is unknown whether the Asm/ceramide system also plays an important role in endothelial cells injury and lethal lung edema induced by systemic *S. aureus* infection. The endothelium is a highly dynamic cell layer that is involved in a multitude of physiological functions, thus, it is very important to emphasize the potential value of the endothelium as a target for lethal lung edema therapy in sepsis.

The present thesis first defines the role of Asm in regulating lung edema induced by systemic *S. aureus* infections. Because ceramide is an important signaling molecule that regulates redox signaling (Zhang et al 2007), the present study further investigated whether lung edema induced by *S. aureus* infections is prevented by Asm deficiency. The importance of Asm for lung injury was tested in Asm-deficient mice.

Furthermore, the mechanism of Asm activation inducing lung edema was addressed. It was investigated whether *S. aureus* infections induces activation of Asm, subsequent ceramide release and activation of ROS, leading to degradation of tight junctions, neutrophils trafficking and lung edema.

The last part of the study focused on the clinical significance of the Asm/ceramic system in a *S. aureus* sepsis. It was tested whether treatment of already septic mice with Asm inhibitor amitriptyline prevents the development of lung edema and whether the combination of amitriptyline and antibiotic prevents sepsis.

Our results will increase the understanding of the signaling mechanism that Asm deficiency protects lung edema induced by *S. aureus* infections. Moreover, the study will announce a novel approach to treat severe systemic and often lethal infections and to prevent lung injury in patients with incipient sepsis.

2. MATERIALS

2.1. Chemicals

Aqua ad Injectabilia DeltaSelect GmbH, Dreieich

Acetic acid (C₂H₄O₂) Merck, Darmstadt

Acetone Sigma-Aldrich Chemie GmbH, Steinheim

Adenosine Tri-Phosphate (ATP) Sigma-Aldrich Chemie GmbH, Steinheim

Amitriptyline Sigma-Aldrich Chemie GmbH, Steinheim

β-mercaptoethanol Sigma-Aldrich Chemie GmbH, Steinheim

Bromphenol blue Sigma-Aldrich Chemie GmbH, Steinheim

C₁₆-Ceramide Biomol, PA, USA

Calcium chloride (CaCl₂) Sigma-Aldrich Chemie GmbH, Steinheim

Cardiolipin Sigma-Aldrich Chemie GmbH, Steinheim

Chloroform (CHCl₃) Ridel-de Haen, Seelze

CDP-STAR with Nitro-Block II enhancer PerkinElmer, Boston, USA

DABCO (1,4-Diazabicyclo(2,2,2)octane) Sigma-Aldrich Chemie GmbH, Steinheim

Deoxycholic acid (C24H40O4) Sigma-Aldrich Chemie GmbH, Steinheim

Dithiothreitol (DTT) Carl-Roth GmbH & Co, Karlsruhe

Dimethylsulfoxid (DMSO)Sigma-Aldrich Chemie GmbH, Steinheim

Eosin (gelblich) E.Merk, Darmstadt

Ethidium bromide Sigma-Aldrich Chemie GmbH, Steinheim

Ethanol (C2H5OH) Sigma-Aldrich Chemie GmbH, Steinheim

Ethylenediamine Tetraacetic Acid Serva Electrophoresis GmbH, Heidelberg

(EDTA)

Evan's Blue Dye Sigma-Aldrich Chemie GmbH, Steinheim

Eukitt® quick-hardening mounting Sigma-Aldrich Chemie GmbH, Riedstrasse

medium Sigma-Aldrich Chemie GmbH, Steinheim

Formamide

Glucose Sigma-Aldrich Chemie GmbH, Steinheim

Glycerol Fluka Chemie GmbH, Buchs

H₂DCFDA Molecular Probes, Eugene, OR

HEPES Carl-Roth GmbH & Co, Karlsruhe

Hydrochloric acid (HCl) Sigma-Aldrich Chemie GmbH, Steinheim

Hematoxylin Carl-Roth GmbH & Co, Karlsruhe

Imidazole (C₃H₄N₂) Sigma-Aldrich Chemie GmbH, Steinheim

Isopropanol Sigma-Aldrich Chemie GmbH, Steinheim

Ketamine Ceva Tiergesundheit GmbH, Duesseldorf

Magnesium chloride (MgCl₂) Sigma-Aldrich Chemie GmbH, Steinheim

Magnesium sulphate (MgSO₄) Sigma-Aldrich Chemie GmbH, Steinheim

Methanol (CH₃OH) Fluka Chemie GmbH, Buchs

Methicillin Sigma-Aldrich Chemie GmbH, Steinheim

Mowiol Kuraray Specialities Europe GmbH,

Frankfurt

N-acetylcysteine Sigma-Aldrich Chemie GmbH, Steinheim

N-octylglucopyranoside Sigma-Aldrich Chemie GmbH, Steinheim

Paraformaldehyde (PFA) Sigma-Aldrich Chemie GmbH, Steinheim

Paraplast plus Tissue Embedding Medium Leica Microsystems GmbH, Netherlands

Pepsin Invitrogen, Frederick, USA

Phosphatase inhibitor Sigma-Aldrich Chemie GmbH, Steinheim

Potassium chloride (KCl) Sigma-Aldrich Chemie GmbH, Steinheim

Potassium dihydrogenphosphate Sigma-Aldrich Chemie GmbH, Steinheim

(KH₂PO₄)

Protease inhibitor Carl-Roth GmbH & Co, Karlsruhe

RPMI-1640 Gibco/Invitrogen, Karlsruhe, Germany

Saponin Serva Electrophoresis GmbH, Heidelberg

Sodium acetate (CH₃COONa) Sigma-Aldrich Chemie GmbH, Steinheim

Sodium chloride (NaCl) Carl-Roth GmbH & Co, Karlsruhe

Sodium dodecyl sulphate (SDS)

Serva Electrophoresis GmbH, Heidelberg

Sodium fluoride (NaF) Sigma-Aldrich Chemie GmbH, Steinheim

Sodium hydroxide (NaOH) Sigma-Aldrich Chemie GmbH, Steinheim

Sodium phosphate (Na₂HPO₄) Merck, Darmstadt

Sodium pyrophosphate (Na₄P₂O₇) Sigma-Aldrich Chemie GmbH, Steinheim

Surgipath Paraplast Leica Microsystems GmbH, Netherlands

Taq Polymerase Invitrogen, Karlsruhe, Germany

Tiron Fluka Chemie GmbH, Buchs

Tryptic soy broth (TSB)

BD Biosciences, Heidelberg, Germany

Tris-HCl and Tris-Base Carl-Roth GmbH & Co, Karlsruhe

Triton X-100 Sigma-Aldrich Chemie GmbH, Steinheim

Tween-20 Sigma-Aldrich Chemie GmbH, Steinheim

Vancomycin Sigma-Aldrich Chemie GmbH, Steinheim

Xylazin Ceva Tiergesundheit GmbH, Duesseldorf

Xylene Applichem GmbH, Darmstadt, Germany

2.2. Tissue culture materials

Cell dissociation buffer enzyme-free Gibco/Invitrogen, Karlsruhe

DMEM (EAGLE) Gibco/Invitrogen, Karlsruhe

Fetal Calf Serum (FCS) Gibco/Invitrogen, Karlsruhe

L-Glutamine Gibco/Invitrogen, Karlsruhe

MEM non-essential aminoacids Gibco/Invitrogen, Karlsruhe

Penicilin/Streptomycin Gibco/Invitrogen, Karlsruhe

Sodium pyruvate Gibco/Invitrogen, Karlsruhe

Tissue culture flasks 75 cm² TPP, Trasadingen, Switzerland

Tissue culture flasks 25 cm² TPP, Trasadingen, Switzerland

Tissue culture test plates TPP, Trasadingen, Switzerland

Trypsin Gibco/Invitrogen, Karlsruhe

2.3. Antibodies

Alkaline phosphatase-coupled secondary Santa Cruz Biotechnology, CA, USA

antibodies

Anti-E-cadherin(H-108) rabbit IgG Santa Cruz Biotechnology, CA, USA

Anti- Ly-6G and Ly-6C (GR1) rat IgG BD Biosciences, Heidelberg, Germany

Anti-Occludin rabbit IgG Invitrogen, CA, USA

Anti-ZO1 rabbit IgG Invitrogen, CA, USA

Anti-ZO2 (H-110) rabbit IgG Santa Cruz Biotechnology, CA, USA

Cy3-donkey-anti-rabbit IgG Jackson Immunoresearch, West Grove, PA,

USA

Cy3-donkey anti-rat IgG Jackson Immunoresearch, West Grove, PA,

USA

FITC-labled Isolectin B4 Vector Laboratories, CA, USA

2.4. PCR primers

Asm-PA 1-2 Hermann GbR, Freiburg

5'-CGA GAC TGT TGC CAG ACA TC-3'

Asm-PA 2-2 Hermann GbR, Freiburg

5'-GGC TAC CCG TGA TAT TGC TG-3'

Asm-PS-2 Hermann GbR, Freiburg

5'-AGC CGT GTC CTC TTC CTT AC-3'

Myco P1 Hölle & Hüttner AG, Germany

5'-GTG CCA GCA GCC GCG GTA ATA

C-3'

Myco P4 Hölle & Hüttner AG, Germany

5'-TAC CTT GTT ACG ACT TCA CCC

CA-3′

MATERIALS

2.5. Cell lines

EOMA CRL-2586

established murine endothelial cell line

The cell line was tested monthly by PCR to exclude mycoplasma contamination.

2.6. Animals

Asm-deficient mice were kindly provided by Dr. R. Kolesnick (Memorial Sloan-Kettering

Cancer Center, NY, USA) and backcrossed for more than 10 generations on a C57BL/6

background. Syngenic wild-type littermates from the same heterozygous breeding were used

as control.

The mice used in the present study show the earliest clinical manifestation of Niemann-Pick

disease type A at approximately 12 weeks of age; therefore, all the Asm-deficient mice used

in our experiments were younger than 10 weeks of age, before any biochemical, histological

or clinical manifestations of Niemann-Pick disease type A were apparent. This excluded that

the effects observed in the Asm-deficient cells were due to altered cellular processes but

instead, were dependent on the lack of Asm. Wild-type and Asm-deficient mice were

propagated in the Animal Facility of the Uniklinikum Essen. The genotype was verified by

PCR analysis.

Mice were housed in pathogen-free conditions under diurnal lighting alternated with a dark

phase between 18:00-6:00, allowed daily food "Zuchthaltungsfutter Maus-Ratte 10 H 10"

(Eggersmann) and water ad libitum. All mice were repeatedly tested for the presence of

pathogens and were free of any pathogens according to the criteria of the Federation of

Laboratory Animal Science Associations.

2.7. Radioactive substances

[³²P] gamma-ATP

Hartmann Analytic, Braunschweig

[14C] Sphingomyelin

Perkin Elmer, Boston, MA, USA

- 40 -

2.8. Other materials

Coverslips 12 mm diameter Carl-Roth GmbH & Co, Karlsruhe

Cryo 1C Freezing container Nalgene, USA

Cryovials Carl-Roth GmbH & Co, Karlsruhe

Cuvettes 10 x 4 x 45 mm Sarstedt, Nümbrecht, Germany

Leica Confocal software (Leica)

Leica Microsystems, Germany

Microscopy glass slides 76 x 26 mm Engelbrecht, Edermunde, Germany

Minisart syringe filters Vivascience AG, Hannover, Germany

Neubauer chamber 0.1 mm Marienfeld, Germany

Parafilm Peckiney, Chicago, IL, USA

PCR Tubes Sarstedt, Nümbrecht, Germany

Polyethylene vials 20 ml Packard, USA

Silica G60 TLC plates Merck, Darmstadt

sn-1,2-Diacylglycerol (DAG) Biotrak Assay Amersham Biosciences, Freiburg

Reagents System

Steritop Vacuum-driven disposable top Millipore, Billerica, MA, USA

filters

Tryptic soy agar plates with 5% sheep BD Biosciences, Heidelberg, Germany

blood

Whatman filter paper Whatman, Maidstone, UK

X-Ray films Amersham Biosciences, Buckinghamshire,

UK

2.9. Special laboratory equipment

Fluorescence Microplate Reader BMG Labtech, Offenburg, Germany

Leica TCS SP confocal microscopeLeica Microsystems, Wetzlar, Germany

equipped with a 100× oil objective

Microtome Techno-Med, GmbH, Bielefelt, Germany

Paraffin-Embedding-System Techno-Med, GmbH, Bielefelt, Germany

Portable Datalogging Spectrophotometer Bachofer, Reutlingen, Germany

Sonorex bath sonicator Bandelin electronic, Berlin, Germany

SpeedVac (Vacuum Concentrator)Bachofer, Reutlingen, Germany

TriCarb Liquid scintillation Perkin Elmer, USA

2.10. Buffer and Solutions

Anesthesia cocktail 10% Ketamin 2 ml

2% Xylazin 0.5 ml

ddH2O 10 ml

ASM lysis buffer 0.1% Triton X-100

50 mM sodium acetate pH 5.0

Complete DMEM (Gibco) medium 500 ml DMEM (Gibco)

10% FCS

10 mM HEPES, pH 7.4

2 mM L-Glutamine

1 mM Sodium pyruvate

100 µM non-essential amino acids

100 units/ml Penicillin

100 μg/ml Streptomycin

DAG-assay Buffered Saline Solution 135 mM NaCl

1.5 mM CaCl₂

0.5 mM MgCl₂

5.6 mM Glucose

10 mM HEPES, pH 7.2

DAG-assay detergent solution 7.5% N-octylglucopyranoside

5 mM cardiolipin

1 mM DETAPAC

DAG-kinase diluent 1 mM DETAPAC, pH 6.6

0.01 M imidazole/HCl **DAG-kinase reaction buffer** 100 mM imidazole/HCl pH 6.6 100 mM NaCl 25 mM MgCl₂ 2 mM EDTA 2.8 mM DTT 5 μM ATP 10 μCi [32P] gamma-ATP Freezing medium 1 ml DMSO 2 ml FCS 7 ml complete DMEM **HEPES** buffer 132 mM NaCl 20 mM Hepes pH 7.4 5 mM KCl 1 mM CaCl₂ 0.7 mM MgCl₂ 0.8 mM MgSO₄ **HEPES/Saline** 132 mM NaCl 20 mM HEPES, pH 7.4 5 mM KCl 1 mM CaCl₂ 0.7 mM MgCl₂ 0.8 mM MgSO₄ Mowiol 6 g Glycerol 2.4 g Mowiol 6 ml ddH2O 12 ml 0.2 M Tris-Base, pH 8.5

2.5 ml PFA stock solution

0.1% DABCO

PFA 2%

7.5 ml PBS

PFA stock solution 8 g PFA

100 ml PBS

SA medium 500 ml DMEM

1 mM HEPES, pH 7.4

Trypsin 0.25% Trypsin

5 mM Glucose

1.3 mM EDTA

3. METHODS

3.1. Tissue culture techniques

3.1.1. Culture and passage of established cell lines

EOMA cells were maintained in complete DMEM medium (see Materials) at 37°C in a 10% CO₂ atmosphere. Because EOMA cells grow adherent, passage of cells was achieved by incubation with trypsin solution to dislodge the cells from the flask wall. Prior to that, the cultures were examined using a light microscope, to assess the degree of confluence. Medium, PBS and trypsin were pre-warmed at 37°C. The cell monolayer was washed with PBS for two times and trypsin was added. Detachment of cells was assessed by light microscope. The digestion was stopped by addition of medium and the cells were centrifuged at 1500 rpm for 5 minutes to pellet the cells. Cells were then re-suspended in medium, transferred to fresh flasks and kept incubated at 37°C.

3.1.2. Freezing and thawing of cells

The basic principle of successful cryo-preservation is a slow freeze and a quick thaw of cells. For the freezing step, DMSO was used to protect cells from ice crystal formation, which causes cell rupture. The freezing medium (see Materials) was prepared in advance and kept at 4°C. Cells were collected, counted with a Neubauer chamber and re-suspended at a concentration of 1x10⁶ cells/ml in freezing medium. The cell suspension was transferred in cryo-protective vials, which were placed at -80°C in a Cryo 1C Freezing Container overnight. For long-term storage, cells were placed in a liquid nitrogen storage vessel. To thaw the cells, the vials from liquid nitrogen storage were transferred to a water bath at 37°C. The vials were moved back and forth to ensure a quick thaw. After thawing, cells were washed with medium to remove the DMSO, re-suspended in fresh medium, transferred to culture flasks and incubated at 37°C.

3.2. Infection experiments

3.2.1. Preparation of Staphylococus aureus (S. aureus)

S. aureus was stored at -80°C and plated with plastic swaps on Trypticase Soy Agar plates with 5% sheep blood (Becton Dickinson #254053). The plates were incubated for 16 hrs at 37°C. Bacteria were then transferred into 40 ml 37°C pre-warmed Trypticase Soy Broth (TSB, Becton Dickinson #221093) in Erlenmeyer flasks at an optical density at 550 nm of 0.2/ml (equals to 1.85 x 10⁸ colony forming units (CFU)/ml). The bacteria were incubated for 70 min at 37°C with shaking at 125 rpm and collected during the early logarithmic growth phase by centrifuging at 3000 rpm for 10 min. The bacterial pellet was washed twice in pre-warmed DMEM supplemented with 10 mM HEPES or phosphate buffered saline (PBS, 137 mM NaCl, 2.7 mM KCL, 7 mM CaCl2, 0.8 mM MgSO4, 1.4 mM KH2PO4, and 6.5 mM Na2HPO4) and then resuspended in DMEM supplemented with 10 mM HEPES for infection of EOMA cells or at 5×10⁶ CFU per 100 μL in PBS for infection of mice. Cells or mice were then infected within the next 10 min.

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3.2.2. Infection cells with S. aureus

To evaluate the role of *S. aureus* on EOMA cells, EOMA cells were plated in 24 well plates with cover slip at 5×10^4 per well with 1 ml complete DMEM or 6 well plate at 8×10^5 per well with 4 ml complete DMEM, grown for 2 days. Prior to infection, the cells were washed with pre-warmed PBS for 2 times and maintained in buffered DMEM medium supplemented with 10 mM HEPES during infection and were inoculated with *S. aureus* at bacteria-to-host cell ratio of 200:1 or 10:1 (Multiplicity of infection (MOI) 200:1 or 10:1). Synchronous infection conditions and an enhanced bacterium-host cell interaction were achieved by a 2-min centrifugation (1000 rpm) of the bacteria onto the cells. The end of the centrifugation was defined as the starting point of infection. If required for the experiment, we added the anti-oxidant Tiron or N-acetylcysteine (NAC) or the Asm inhibitor amitriptyline 20 minutes prior to infection as follows.

3.2.3. Infection mice with S. aureus

The littermates of 8 weeks old Asm wild-type or Asm-deficient mice were infected intravenously with $5x10^6$ CFU *S. aureus*. Between the first and the last mouse infected, we allowed a time interval of maximally 10 min, to exclude a change in viable counts of the bacteria.

For pretreatment with inhibitors before infection, wt mice were injected intraperitoneally with 10 mg/kg amitriptyline, 100 mg/kg Tiron or 100 mg/kg NAC twice daily for 2.5 days. The last dose was given 1 h before infection. For treatment with amitriptyline post infection, wt mice were injected i.p. 1 h or 2 hrs after infection with 16 mg/kg amitriptyline. Antibiotics were also injected i.p. 1 h after infection with 100 mg/kg methicillin (Sigma) or 100 mg/kg vancomycin (Sigma). The injection of methicillin or vancomycin was repeated 9 hrs after infection. For mortality experiment, 10 mg/kg amitriptyline, 100 mg/kg methicillin or 100 mg/kg vancomycin were treated twice daily in indicated group until 11 days.

The mice were sacrificed at indicated infection times by cervical dislocation. The lungs were removed and used for CFU counting and histology as described below.

3.3. Determination colony-forming units (CFUs) of *S. aureus* in the liver and spleen

To quantify *S. aureus* colony forming units (CFUs) in mouse livers and spleens, the organs were removed after 12 hrs infection and homogenised in a loose Dounce homogenizor. The homogenates were lysed for 10 min in 5 mg/ml saponin (SERVA) at 37 °C to release intracellular bacteria. The samples were centrifuged at 3200 rpm for 10 min, resuspended in PBS, and plated on normal LB plates in duplicates. Bacterial CFUs were counted after the plates had been incubated overnight at 37 °C.

3.4. Immunocytochemistry

EOMA cells were grown on coverslips, infected or uninfected for indicated time and with designed treatment as above. They were fixed in 2% PFA/PBS for 10 min. For intracellular staining, cells were permeabilized with 0.1% Triton X-100/PBS for 5 min at room temperature. Cells were washed again with PBS and incubated for 60 min in PBS supplemented with 5% FCS for all antibodies to block nonspecific binding sites. Cells were washed and incubated for 45 min with either anti-ZO1 IgG, anti-ZO2 IgG, anti-E-cadherin IgG, or an anti-Occludin IgG(see Materials). Cells were then washed three times in PBS with 0.05% Tween-20 and incubated for an additional 45 min with Cy3-labeled donkey anti-rabbit antibodies. Cells were then washed again in PBS with 0.05% Tween-20. After a final PBS wash, cells were mounted on glass coverslips with moviol. Control experiments were performed with irrelevant rabbit antibodies and secondary antibodies. Control antibodies did not significantly bind to the cells. Cells were examined on a Leica TCS SP confocal microscope equipped with a 100x oil objective and images were analyzed using Leica Confocal software (Leica).

3.5. Histology

3.5.1. Preparation of the lung sample

Mice were sacrificed and the lungs were subsequently removed. The left lungs were fixed in 4% PFA for 38 hours, serially dehydrated and embedded in paraffin for sectioning at a thickness of $6~\mu m$.

3.5.2. Hematoxylin and eosin staining

Lung tissue (6-mm paraffin embedded sections) were dewaxed, rehydrated and stained for 2 min with hematoxylin and washed with water for 5 min prior to being stained with eosin for 1 min. After a final short wash with water the sections were mounted in Mowiol and evaluated using a Leica TCS-SP2 microscope.

3.5.3. Fluorescence staining for the lungs

The sections were then dewaxed, rehydrated and incubated in pepsin (see Materials) for 30 min at 37°C incubator. The sections were washed and incubated for 10 min in PBS supplemented with 5% FCS to block nonspecific binding sites. The sections were washed again and incubated overnight at 4 °C with either anti-ZO1 IgG, anti-ZO2 IgG, , anti-E-cadherin IgG, anti-Occludin IgG, or anti-Ly-6G and Ly-6C (GR1) or FITC-labeled anti-Lectin antibodies, respectively. The sections were washed in PBS with 0.05% Tween-20 and incubated for an additional 45 min with Cy3-labeled donkey anti-rabbit or anti-rat antibodies. The sections were then washed again in PBS with 0.05% Tween-20, once in PBS wash, and mounted in moviol. Control experiments were performed with irrelevant rabbit or goat antibodies and secondary antibodies. Control antibodies did not significantly bind to the lungs. The sections were examined on a Leica TCS SP confocal microscope equipped with a 40x oil objective and images were analyzed using Leica Confocal software (Leica).

3.6. Electron Spin Resonance Detection of Endothelial O2

ROS production was measured by electron spin resonance (ESR), as we described previously (Abais et al 2014, Li et al 2013b). 2x10⁵ endothelial Cells were infected with *S.aureus* for the indicated time, the medium removed, the cells scraped into 20 mM HEPES (PH 7.5), 1 mM EDTA, and 255 mM sucrose and shock frozen in liquid nitrogen. Proteins were isolated and resuspended with modified Krebs-HEPES buffer containing deferoximine (100 µM, Sigma) and diethyldithiocarbamate (5 μM, Sigma). A spin trap, 1-hydroxy-3-methoxycarbonyl-2,2,5,5-tetramethylpyrrolidine (CMH, Noxygen, Elzach, Germany) (1 mM final concentration), was then added to the mixture in the presence or absence of manganese-dependent superoxide dismutase (SOD, 200 U/mL; Sigma, St. Louis, MO). The mixture was loaded into glass capillaries and immediately kinetically analyzed for O₂ production for 10 min. The SOD-inhibited fraction of the signal was used to calibrate the system. The ESR settings were as follows: biofield, 3,350; field sweep, 60 G; microwave frequency, 9.78 GHz; microwave power, 20 mW; modulation amplitude, 3 G; points of resolution, 4,096; receiver gain, 100; and kinetic time, 10 min. The ESR signal strength was

recorded in arbitrary units and the final results were expressed as the fold changes compared to the control as described (Xu et al 2013).

3.7. Asm activity assay

The activity of Asm was measured as the consumption of radioactive [14C]-sphingomyelin to ceramide and [14C]-phophorylcholine. To this end, 8x10⁵ EOMA cells were infected with *S. aureus* for indicated times, washed, lysed in 300 μl/sample ice-cold ASM-lysis buffer (see Materials). The cells were removed from the plate, transferred into eppendorf tubes and immediately sonicated three times (3x10 s). Since [14C]-sphingomyelin is insoluble in water, it was first dried by SpeedVac centrifugation and solubilized into micelles in ASM-lysis buffer, using a bath sonicator for 10 min. Cell lysates were incubated with 0.05 μCi per sample [14C]-labeled sphingomyelin (2 GBq/mmol) for 30 min at 37°C on a thermomixer. Lipids were extracted by addition of 1 ml/sample of CHCl3:CH3OH (2:1, v/v), followed by vigorous vortexing for 30 sec and centrifugation at 14000 rpm for 5 min. An aliquot (300 μl) of the aqueous phase was applied for liquid scintillation counting. Hydrolysis of [14C]-sphingomyelin by Asm results in release of [14C]-choline chloride into the aqueous phase, whereas ceramide and unreacted [14C]-sphingomyelin remain in the organic phase. Therefore, the release of [14C]-choline chloride (pmol/10⁵ cells/h) serves to determine the activity of the Asm.

3.8. Ceramide measurement by DAG kinase assay

3.8.1. Lipid extraction and enzymatic reaction

Cellular ceramide was measured by DAG kinase assay, in which ceramide is converted to a quantifiable product (ceramide-1-phosphate) by transfer of [³²P]-phosphate from [³²P]-gamma ATP to ceramide. To this end, cells were infected as above, first extracted in CHCl₃:CH₃OH:1N HCl (100:100:1, v/v/v). The resulting biphasic mixture is composed of a lower lipid-containing organic phase, and an upper aqueous phase. An aliquot of the lower organic phase was collected and dried by evaporation of the chloroform in a SpeedVac. The dried lipids were solubilized in 20 µl of DAG-assay detergent solution (see Materials) and

sonicated for 10 min in a bath sonicator, and 50 μ l of DAG-kinase reaction buffer (see Materials), and 10 μ l of diluted enzyme (dilution 1:1, v/v in DAG-kinase diluent) (see Materials) were added. The kinase reaction was performed for 30 min at room temperature on a thermomixer. The samples were re-extracted in 1 ml/sample CHCl₃:CH₃OH:1N HCl (100:100:1, v/v/v), 170 μ l/sample DAG-assay Buffered Saline Solution (see Materials) and 30 μ l of a 100 mM EDTA solution, followed by vortexing. The resulting upper phase was removed, and the lower organic phase was again concentrated by SpeedVac centrifugation. The dried lipids were dissolved in 20 μ l/sample CHCl₃:CH₃OH (1:1, v/v).

3.8.2. Separation of lipids by Thin Layer Chromatography (TLC)

Lipids were separated on a Silica G60 TLC plate. A solvent system of CHCl₃:CH₃COCH₃:CH₃COCH₃:CH₃COOH:H₂O (10:4:3:2:1, v/v/v v/v) was added to the TLC chamber, and was allowed to saturate the atmosphere for 1 h by using a sheet of Whatman filter paper. The silica plates were loaded with the solubilized lipids, placed into the TLC chamber and the solvent front was allowed to migrate to the top of the plate. The plate was then removed, air dried for 45 min and exposed to X-ray films for 24 hours. Ceramide-spots were identified by comigration with a C₁₆-ceramide standard, and incorporation of 32 P into ceramide was quantified by liquid scintillation counting. Comparison with a standard curve using C₁₆-ceramide permitted the determination of ceramide amounts.

3.9. Evans blue microvascular permeability analysis of lung edema

To assess vascular leakage, 4% Evans blue dye (20 mg/kg) was injected into the external jugular vein 30 min before the termination of the experiment as described (Moitra et al 2007). Evans blue dye has a very high binding affinity for serum albumin. When the vascular barrier in the lung is compromised, albumin-bound Evans blue moves into the lung parenchyma. The lungs were perfused free of blood with phosphate-buffered saline via right heart, removed, dried, weighed, and was homogenized in PBS (1 ml/100 µg tissue), incubated with 2 volumes of formamide to extract the dye (18 h, 60°C), and centrifuged at 5,000 × g for 30 minutes, and the optical density of the supernatant was determined at 620 nm and 740 nm with a

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fluorescence microplate reader (BMG Labtech, Offenburg, Germany). The extravasated EB

concentration in lung homogenate was calculated against a standard curve and was expressed

as micrograms of Evans blue dye per gram of lung.

3.10.DNA techniques

3.10.1. DNA isolation

3.10.1.1 DNA isolation from mouse tails

For genotyping of wt and Asm-deficient mice, app. 1-2 mm of mouse tail was cut and placed

into 80 µl Tissue Lysis Buffer (TLB) (see Materials). The samples were incubated at 56°C

overnight and diluted with 800 µl autoclaved ddH2O.

3.10.1.2 DNA isolation from cell lines

To test cultured cell lines for the presence of Mycoplasma, 5 x10⁵ cells/sample were pelleted

and re-suspended into 50 µl TLB. The samples were incubated at 56°C for 3 h and boiled at

95°C for 10 min. The volumes were then raised to 100 µl with autoclaved ddH₂O.

3.10.2. Polymerase Chain Reaction (PCR)

3.10.2.1 Asm PCR

For the detection of Asm by PCR, 1 µl of overnight tail digest (see 3.10.1.1.) was added to 1.2

μl 10 x PCR Buffer, 2.5 mM MgCl₂, 1μl dNTP mix 5 units/ml Taq Polymerase and 0.1 μl

each of primers Asm-PA1-2, Asm-PA2-2 an Asm-PS-2 in 0.2 ml PCR tubes. The temperature

of the lid of the PCR machine was raised to 104°C and the temperature of the PCR block was

raised to 96°C for 17 min, after which the following cycle was carried out 35 times:

Denaturation: 95°C for 1 min

Annealing: 58°C for 1 min

Elongation: 72°C for 1 min 45 sec

After the last cycle, the PCR block remained at 72°C for 5 min, after which the samples were

placed at 4°C.

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3.10.2.2 Mycoplasma PCR

For the identification of mycoplasma by PCR, 1 µl of cell digest (see 3.10.1.2.) was added to

2.5 µl 10 x PCR Buffer, 4.1 mM MgCl₂, 0.5 µl dNTP mix 1.25 units/ml Taq Polymerase and

0.25 each of primers P1 and P4 in 0.2 ml PCR tubes. The temperature of the lid of the PCR

machine was raised to 104°C and the temperature of the PCR block was raised to 96°C for 17

min, after which the following cycle was carried out 25 times:

Denaturation: 95°C for 1 min

Annealing: 60°C for 1 min

Elongation: 72°C for 1 min 30 sec

After the last cycle, the PCR block remained at 72°C for 7 min, after which the samples were

placed at 4°C.

3.10.3. Agarose gel electrophoresis

PCR products were analysed on 1% agarose gels. Agarose was poured in TBE buffer (see

Materials) that contained 0.01 µg/ml ethidium bromide. The samples (15 µl) were loaded on

the gel along with 0.1 µg/µl of a 100-bp-standard. The gel was run under 5 V/cm current.

Visualization of the DNA fragments was performed under UV-light.

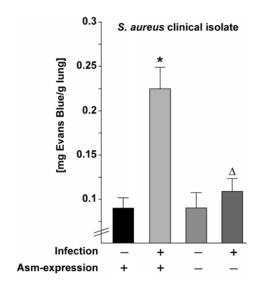
4. RESULTS

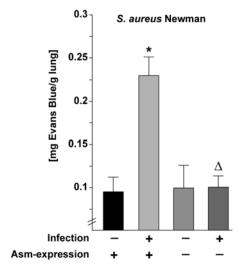
4.1. Asm deficiency prevent S. aureus-induced lung edema

4.1.1. Asm deficiency mitigates pulmonary edema upon S. aureus infection

To investigate whether activation of Asm is required in the *in vivo* development of lung edema upon *S. aureus* infection, we systemically infected C57BL/6 wild type (wt) and Asm-deficient mice with *S. aureus* for various time periods. To date, a large amount of studies indicated that degradation of tight junctional proteins leads to microvascular leakage and finally pulmonary edema (Corada et al 1999, Jang et al 2011). To determine pulmonary edema, we injected Evans blue dye into the mice 30 min before sacrificing the mice to analyze lung edema. The studies revealed massive leakage of Evans blue dye into the lungs of wt mice but almost no leakage into the lungs of Asm-deficient mice upon systemic infection with a clinical *S. aureus* strain (Figure 4.1.1.A-1.) or the *S. aureus* Newman strain (Figure 4.1.1.A-2.). Moreover, hematoxylin and eosin (H&A) staining of the lungs demonstrated that the clinical *S. aureus* infection induced massive lung edema in a time-dependent manner in wt mice, a finding that was absent or much less pronounced in Asm-deficient mice (Figure 4.1.1.B.).

A-1 A-2





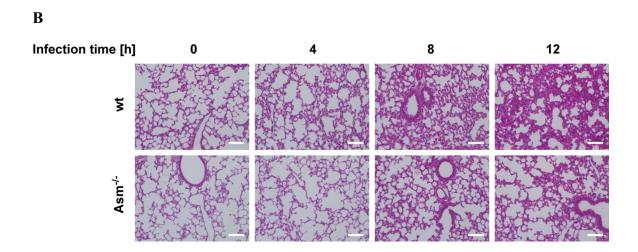


Figure 4.1.1. Effect of Asm deficiency on pulmonary edema upon S. aureus infection

- (A) Wild-type (wt) and Asm-deficient mice were infected with a clinical *S. aureus* strain (A-1) or the *S. aureus* Newman strain (A-2) for the indicated time periods. Evans blue dye was injected 30 min before sacrificing the mice, flushing the lung via the right heart to remove intravascular Evans Blue and removal of the lungs. The amount of dye leaking into the lung tissue was quantified. Shown is the number (mean \pm SD) of the concentration of Evans blue dye in the lungs from each 5 wildtype and Asm-deficient mice. *, significant differences between uninfected mice and infected mice; Δ , significant differences between infected wild-type mice and Asm-deficient mice (all P<0.05; t-test).
- (B) Wild-type and Asm-deficient mice were infected with *S. aureus* for the indicated time periods. They were sacrificed and lung sections were stained with H&E and analyzed by light microscopy for the detection of lung edema. Scale bar is $100 \, \mu M$ (magnification, $63 \times$). Representative images from three independent experiments are shown.

4.1.2. Asm deficiency prevents neutrophil trafficking to the lung

Neutrophils have a pivotal role in the defense against bacterial infections. However, overwhelming activation of neutrophils is known to elicit tissue damage and contribute to severe sepsis (Adams et al 2001, Guo et al 2002, Windsor et al 1993).

This led us to examine whether Asm expression is also required for pulmonary neutrophil trafficking during systemic *S. aureus* infection. To this end, we stained lung sections from infected wt and Asm-deficient mice with anti-GR1 antibodies, a neutrophil marker. Confocal fluorescence microscopy studies reveal that *S. aureus* infection induced excessive neutrophil trafficking to the lung in a time-dependent manner in wild type mice (**Figure 4.1.2.A.**). However, neutrophil trafficking into the lung tissue was reduced markedly in Asm-deficient mice after infection (**Figure 4.1.2.A.**). Quantitative analysis of neutrophils demonstrates that

Asm is an important regulator for *S. aureus*—induced neutrophil trafficking to the lung during *S. aureus* sepsis (**Figure 4.1.2.B.**).

A

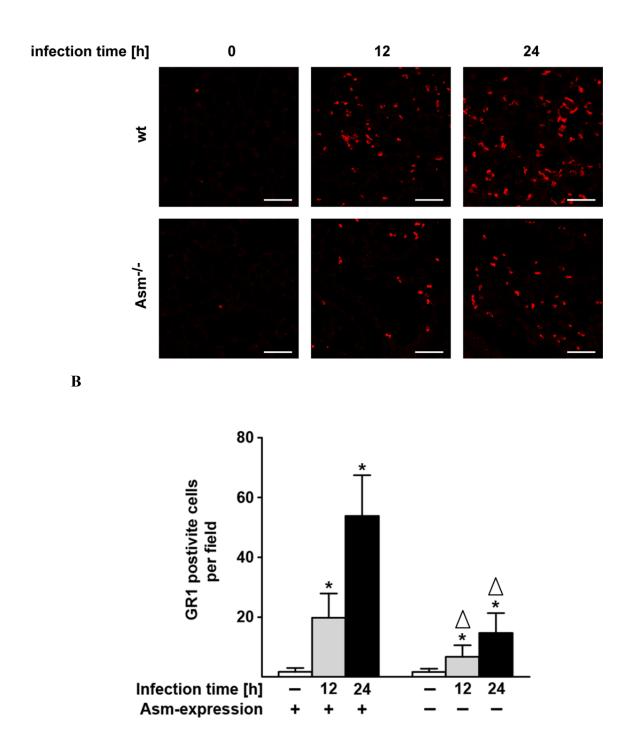


Figure 4.1.2. Effect of Asm deficiency on neutrophil trafficking induced by S. aureus infection

(A and B) For determination of neutrophil trafficking, wt and Asm-deficient mice were left uninfected or were infected with a clinical *S. aureus* strain for different time points. Lung sections were stained with Cy3-labeled anti-GR1 antibodies and analyzed by fluorescence microscopy. Scale bar is 50 μM. Shown are representative images from three independent experiments. Cells staining positive for GR1,

a neutrophil marker, were quantified by analysis of 50 fields per group. Shown is the number (mean \pm SD) of GR1-positive cells per field of 63x magnification. *, significant differences between uninfected mice and infected mice; Δ , significant differences between infected wild-type mice and Asm-deficient mice (all P<0.05; t-test).

Taken together, these findings indicate that Asm plays a key role in the development of pulmonary edema induced by systemic infection with *S. aureus*. Asm deficiency prevents the development of lung injury during infection.

4.2. Infection of endothelial cells with S. aureus activates

Asm and leads to the production of ROS in a positive feedback loop

4.2.1. S. aureus infection rapidly activates the Asm

To test whether systemic *S. aureus* infections activates Asm, we infected murine endothelial (EOMA) cells with a clinical *S. aureus* strain (MOI 200:1) and measured Asm activity. *S. aureus* infection induced a marked activation of the Asm (**Figure 4.2.1.A.**). Additionally, the well-characterized *S. aureus* sepsis strain Newman was tested to determine whether systemic *S. aureus* infections induced Asm activation is a general phenomenon. Following infection with *S. aureus* sepsis strain Newman (MOI 200:1), the kinetics of Asm activation showed a similar pattern in EOMA cells than after infection with the clinical *S. aureus* strain (**Figure 4.2.1.B.**).

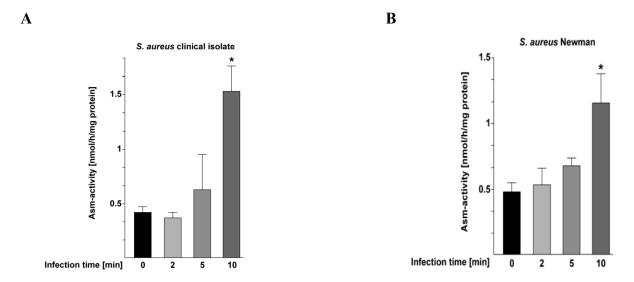


Figure 4.2.1. S. aureus infection activates Asm

Asm activity were measured in EOMA cells after infection with a clinical *S. aureus* strain (MOI 200:1) (A) or the *S. aureus* Newman strain (MOI 200:1) (B) for 0, 2, 5, or 10 min. Results show the mean \pm SD of three independent experiments. *, significant differences compared to uninfected control mice (P<0.05, t-test).

4.2.2. S. aureus infection also induces a marked formation of the ceramide

As we know Asm is one of the most important sphingomyelinase which hydrolyzes sphingomyelin to ceramide and phosphorylcholine. To further define whether systemic *S. aureus* infections induces the formation of ceramide, which is the product of Asm activity, we infected EOMA cells with a clinical *S. aureus* strain or the *S. aureus* Newman stain (MOI 200:1) and measured ceramide production. The results showed a rapid release of ceramide upon these two *S. aureus* strains infection (**Figure 4.2.2.A. and B.**).

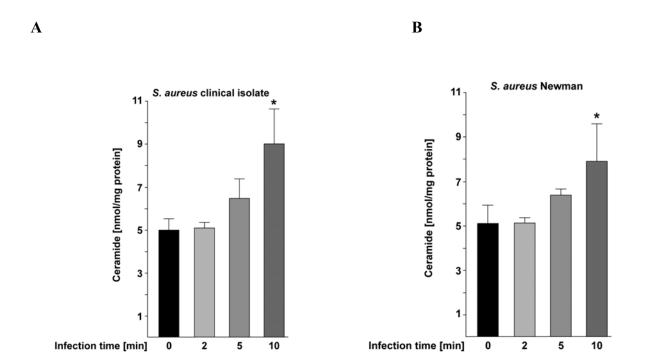


Figure 4.2.2. S. aureus infection induced ceramide release

Ceramide concentrations were measured in EOMA cells after infection with a clinical *S. aureus* strain (MOI 200:1) (A) or the *S. aureus* Newman strain (MOI 200:1) (B) for 0, 2, 5, or 10 min. Results show the mean \pm SD of three independent experiments. *, significant differences compared to uninfected control mice (P<0.05, t-test).

4.2.3. S. aureus infection induces a rapid production of the ROS

Amitriptyline is a tricyclic antidepressant (TCA). It is the most widely used TCA and is efficacious for the treatment of depression (Barbui et al 2001, Garattini et al 1998). Several publications indicated that amitriptyline works as a functional Asm inhibitor and for instance reduces the pulmonary accumulation of ceramide in cystic fibrosis (Becker et al 2010b, Grassmé et al 1997, Kornhuber et al 2008, Kornhuber et al 2010, Kornhuber et al 2011, Teichgraber et al 2008).

ROS have been shown for a long time to play a critical role in host-pathogen interactions (Djaldetti et al 2002, Karupiah et al 2000, Moore et al 2012, Pai et al 2012, Wyllie et al 2011). Previous studies showed a critical role of the Asm in ROS production in macrophages and hepatocytes (Hatanaka et al 1998, Pai et al 2012, Reinehr et al 2005, Zhang et al 2007). To investigate whether *S. aureus* infection induces ROS production and whether *S. aureus*-induced ROS production depends on Asm, we infected EOMA cells with two different strains (MOI 200:1) and analyzed the production of oxygen radicals. The results showed that *S. aureus* infection induced a rapid production of ROS in EOMA cells (**Figure 4.2.3.A. and B.**), which was prevented by pre-incubation with the functional Asm inhibitor amitriptyline (Ami) (**Figure 4.2.3.A. and B.**) indicating that the production of ROS after infection with *S. aureus* requires the activation of Asm.

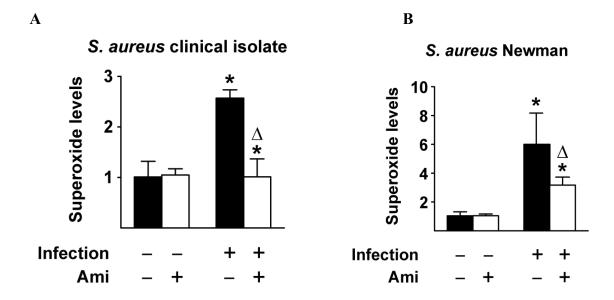


Figure 4.2.3. S. aureus-induced ROS, a process that depends on the Asm

EOMA cells were preincubated with amitriptyline (20 μ M) for 20 min and then infected with a clinical *S. aureus* strain (MOI 200:1) (A) or the *S. aureus* Newman strain (MOI 200:1) (B) for 7.5 min. The production of ROS was quantified by electron spin resonance. Relative O_2^- levels were used to indicate ROS accumulation. Data for panels A and B are mean \pm SD of four independent experiments. Significant differences between infected and non-infected controls were determined by t-test and are indicated by asterisk (* P<0.05). Significant differences between untreated samples and amitriptyline-treated samples were determined by t-test and are indicated by delta ($^{\Delta}$ P<0.05).

4.2.4. Infection of endothelial cells with *S. aureus* activates Asm and leads to the production of ROS in a positive feedback loop

To further define the interaction of *S. aureus*-induced Asm activation and ROS production, we pre-incubated of EOMA cells with the functional Asm inhibitor amitriptyline (Ami) or with antioxidant Tiron or NAC for 20 min, and infected EOMA cells with a clinical *S. aureus* strain at a lower multiplicity of infection (MOI= 10:1) for another 20 min and determined Asm activity and ROS production. The results revealed a similar but slightly delayed time course of Asm activation (**Figure 4.2.4.A.**) and ROS release (**Figure 4.2.4.B.**). Pre-incubation of EOMA cells with the antioxidants Tiron or N-acetylcysteine (NAC) reduced Asm activation by *S. aureus* (**Figure 4.2.4.A.**). Pre-incubation of EOMA cells with the functional Asm inhibitor amitriptyline (Ami) or with Tiron or NAC also inhibited ROS release (**Figure 4.2.4.B.**) suggesting a positive feedback loop of *S. aureus*—induced Asm activation and ROS release.

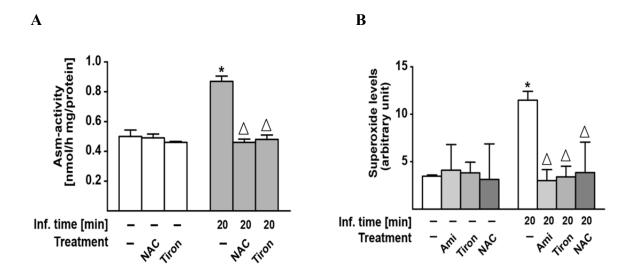


Figure 4.2.4. S. aureus-induced Asm activation and ROS production form a positive feedback loop

EOMA cells were pre-incubated with Ami or NAC or Tiron (20 μ M) for 20 min and then infected with a clinical *S. aureus* strain (MOI 10:1) for 20 min. Ceramide concentrations (A) and ROS production (B) were measured. Data for panels A and B are mean \pm SD of four independent experiments. Significant differences between infected and non-infected controls were determined by t-test and are indicated by asterisk (* P<0.05). Significant differences between untreated samples and amitriptyline-treated samples were determined by t-test and are indicated by delta ($^{\Delta}$ P<0.05).

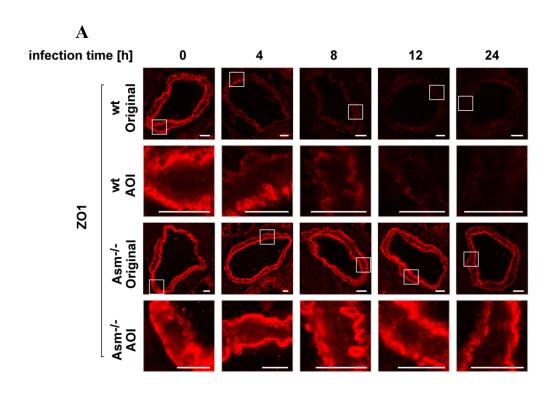
4.3. S. aureus induces degradation of junctional proteins via the Asm/ceramide system

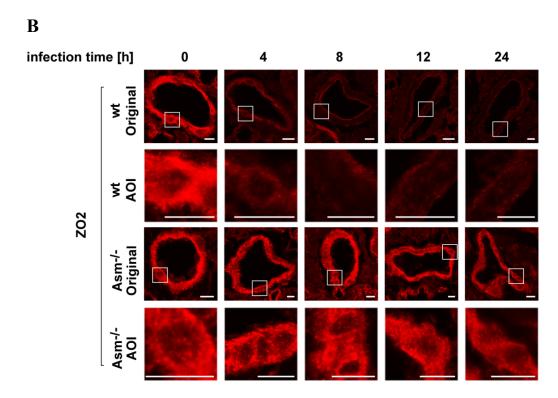
4.3.1. Asm deficiency prevents degradation of junctional proteins upon S. aureus infection in vivo

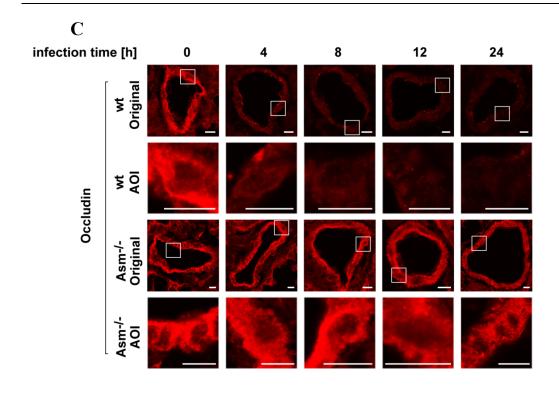
During a severe *S. aureus* infection, the bacteria and their toxins may spread in the bloodstream and affect the integrity of endothelial cells, thereby resulting in increased vascular permeability (Hocke et al 2006, Seeger et al 1990). It is well documented that endothelial activation plays a major role in the cellular immune response to sepsis (Aird 2003, Ait-Oufella et al 2010, Boos et al 2006).

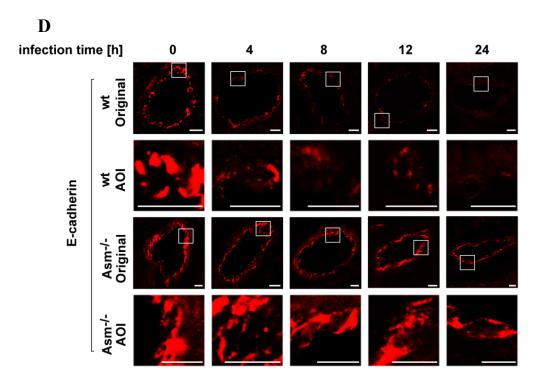
To gain insight into the mechanism by which Asm and ceramide mediate endothelial dysfunction and lung edema after *S. aureus* infection, we determined whether systemic infection with *S. aureus* induces the breakdown of junctional proteins in pulmonary endothelial cells *in vivo*, and, if so, whether this process depends on the Asm/ceramide system. To this end, we systemically infected wt and Asm-deficient mice with 5x10⁶ a clinical *S. aureus* strain. We then obtained lung sections and stained them with Cy3-labeled antibodies against ZO1, ZO2, Occludin, or E-cadherin. Confocal microscopy showed that infection with *S. aureus* induces dramatic degradation of ZO1, ZO2, Occludin, and E-cadherin junctional proteins in a time-dependent manner in endothelial cells from blood vessels in wt lungs but not in endothelial cells from the lungs of Asm-deficient mice (**Figure 4.3.1.A-D.**). Thus, the disruption of junctional proteins, which is caused by *S. aureus* infection *in vivo*, requires functional Asm.

Co-stainings of lung sections with Cy3-coupled antibodies against junctional proteins and FITC isolectin B4, which is a marker for endothelial cells, confirmed that junctional proteins are only degraded in lung endothelial cells of wt mice upon infection with S. aureus, but not in Asm-deficient endothelial cells (**Figure 4.3.1.E-H.**).

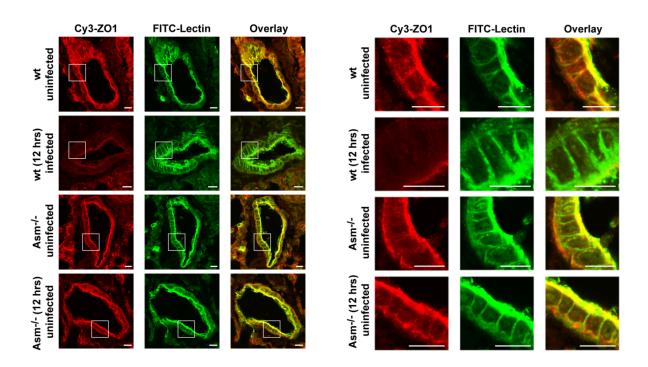




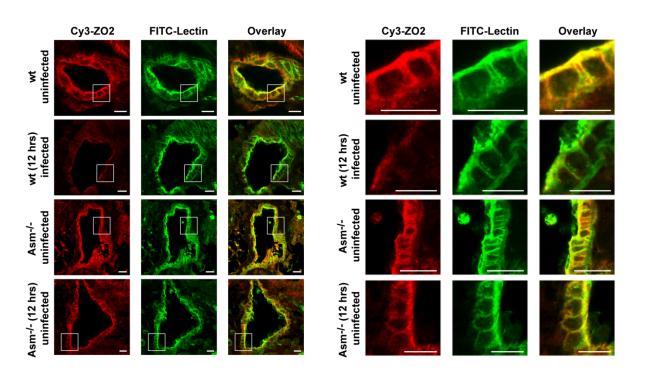




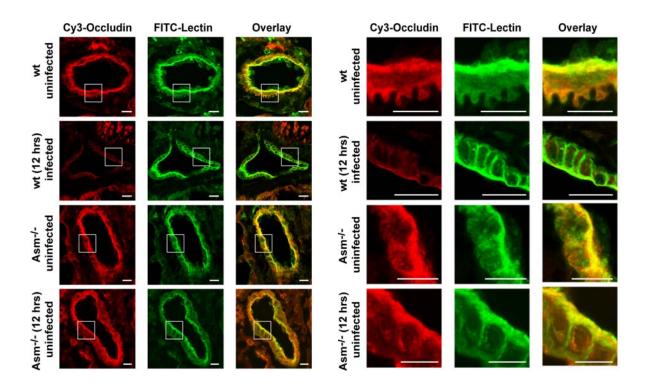
E-1 E-2



F-1 F-2



G-1 G-2



H-1 H-2

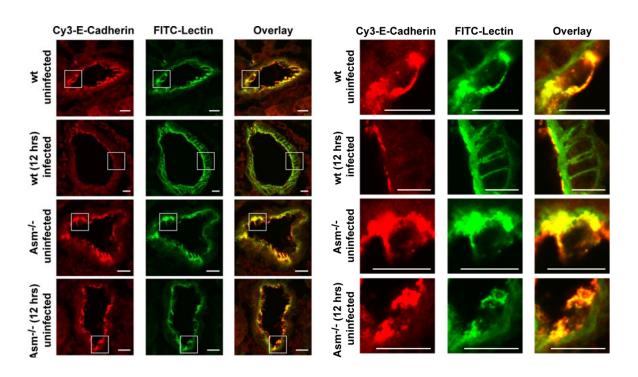


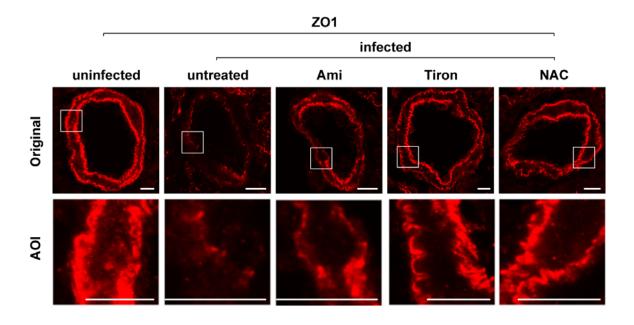
Figure 4.3.1. Effect of Asm deficiency on degradation of junctional proteins upon S. aureus infection in vivo

Wild-type and Asm-deficient mice were left uninfected or were infected with *S. aureus* for different time points. The lungs were removed, fixed, dehydrated and embedded in paraffin for sectioning at a thickness of 6 μ m. The lung sections were stained with Cy3-labeled anti-ZO1 (A and E), anti-ZO2 (B and F), anti-Occludin (C and G) or anti-E-cadherin (D and H) antibodies (magnification, 40×). Representative fluorescence images from three independent experiments are shown (original image and an area of interest [AOI]). Scale bar is 10 μ M.

4.3.2. Asm and ROS are necessary to degradation of junctional proteins induced by S. aureus infection in vivo

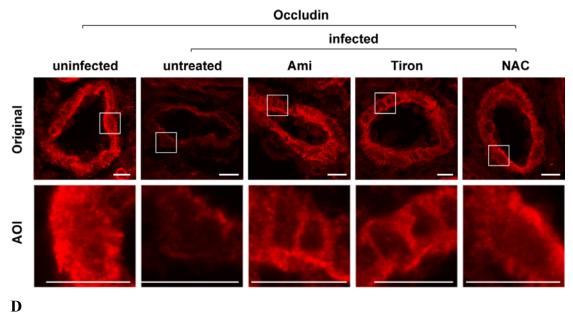
In order to further confirm that Asm is involved in regulating junctional proteins degradation upon *S. aureus* infection *in vivo* and whether junctional proteins degradation presupposes the production of ROS, we pretreated wt mice with intraperitoneal injections of amitriptyline or Tiron and then infected them with a clinical *S. aureus* strain. Confocal microscopy analysis demonstrated that the inhibition of Asm or ROS also protects junctional proteins in lung endothelial cells from degradation after systemic *S. aureus* infection *in vivo* (**Figure 4.3.2.A-D.**).

A



B





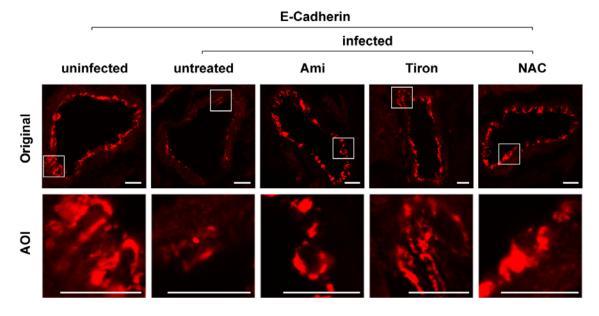


Figure 4.3.2. Inhibition of Asm and ROS prevents *S. aureus*-induced degradation of junctional proteins *in vivo*

Wild type C57BL/6J mice were pretreated with 10 mg/kg amitriptyline, 100 mg/kg Tiron or 100 mg/kg NAC by intraperitoneal injection, twice daily for 2.5 days, and then infected with *S. aureus* for 12 hrs. The lungs were removed, fixed, dehydrated and embedded in paraffin for sectioning at a thickness of 6 μ m. The lung sections were stained with Cy3-labeled anti-ZO1 (A), anti-ZO2 (B), anti-Occludin (C) or anti-E-cadherin (D) antibodies (magnification, 40×). Representative fluorescence images from three independent experiments are shown (original image and an area of interest [AOI]). Scale bar is 10 μ M.

4.3.3. Asm and ROS are necessary to degradation of junctional proteins induced by S. aureus infection in vitro

To further confirm the degradation of junctional proteins is a consequence of Asm activation and ROS production, we pre-incubated EOMA cells with 20 µM amitriptyline, 10 mM Tiron or 10 mM NAC before infection with a clinical *S. aureus* strain (MOI 10:1). We found that inhibition of Asm or ROS protects junctional proteins from degradation after *S. aureus* infection in the EOMA cells (**Figure 4.3.3.**).

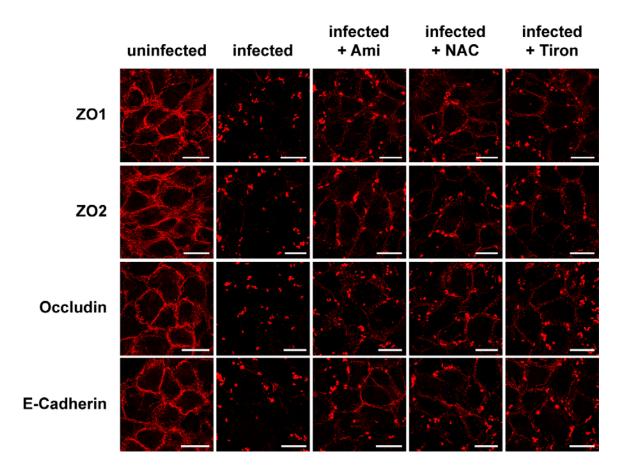


Figure 4.3.3. Inhibition of Asm and ROS prevents *S. aureus*-induced degradation of junctional proteins *in vitro*

EOMA cells were pretreated for 20 min with amitriptyline (20 μ M), Tiron (10 mM) or NAC (10 mM) before being infected with a clinical *S. aureus* strain (MOI 10:1) for 2hrs. Immunoflourescence stainings were performed with antibodies against ZO1, ZO2, Occludin, or E-cadherin for determination of the degradation of these junctional proteins. The presented pictures are representative of the results of at least three independent experiments (magnification, $40\times$). Scale bar is 25 μ M.

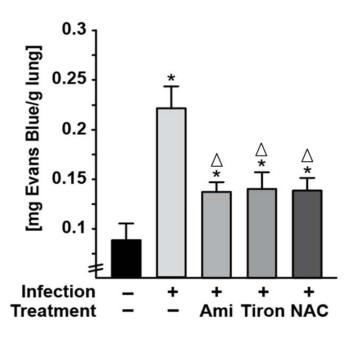
The data presented above demonstrate that *S. aureus* infection leads to the degradation of tight junctional proteins *in vitro* and *in vivo*. Genetic deficiency or pharmacological inhibition of Asm prevents *S. aureus*-induced degradation of junctional proteins. Moreover, inhibition of ROS also protects junctional proteins from degradation. Collectively, these findings indicate that Asm mediates the *S. aureus*-induced breakdown of junctional proteins by ROS.

4.4. Pharmacologic inhibition of Asm or ROS before systemic infection with *S. aureus* prevents lung edema

4.4.1. Pretreatment with amitriptyline, Tiron or NAC alleviates pulmonary edema upon S. aureus infection

To test the significance of the pathway from the Asm via ROS to the degradation of junctional proteins for the development of lung edema, we treated wt mice with intraperitoneal injections of amitriptyline, Tiron or NAC before systemic infection with a clinical *S. aureus* strain and then measured lung edema. *S. aureus* infection induced severe lung edema (**Figure 4.4.1.A. and B.**), events that were prevented by pretreatment with amitriptyline, Tiron or NAC (**Figure 4.4.1.A. and B.**). These findings show that lung edema induced by *S. aureus* via the pathway through Asm and ROS can be prevented by pretreatment with pharmacologic inhibitors of this pathway.

A



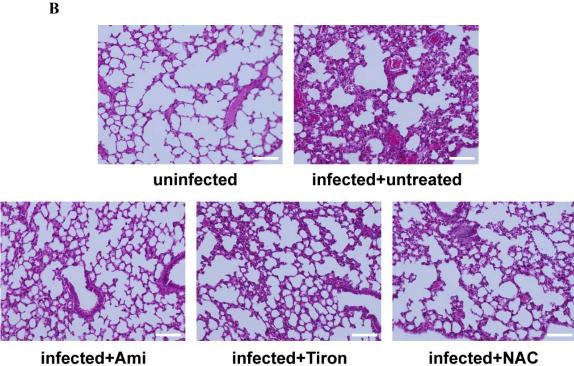


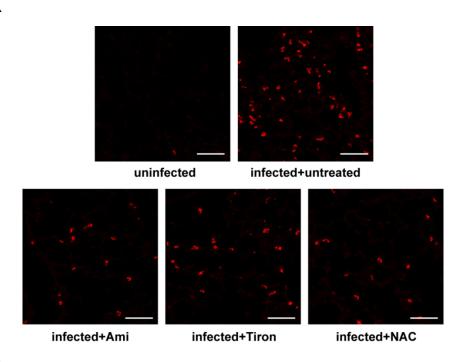
Figure 4.4.1. Effect of pharmacological Asm inhibition and neutralization of ROS on pulmonary edema upon *S. aureus* infection

Wild-type mice were pretreated by intraperitoneal injection of 10 mg/kg amitriptyline, 100 mg/kg Tiron or 100 mg/kg NAC, twice daily for 2.5 days. Mice were infected with *S. aureus* for 12 hrs. Lung edema was determined by extravasation of Evans Blue (A) and by staining with H&E (scale bar is 100 μ M, magnification, 20×) (B). Representative images from three independent experiments are shown. *, significant differences between uninfected and infected samples; Δ , significant differences between treated and untreated samples (all P<0.05, t-test).

4.4.2. Pretreatment with amitriptyline, Tiron or NAC decreases neutrophil trafficking into the lung

Next, we tested whether Asm and ROS play an important role on neutrophil trafficking to the lung induced by *S. aureus* infection as suggested by their marked effect on the integrity of junctional proteins and lung edema. To this end, we treated wt mice with intraperitoneal injections of amitriptyline, Tiron or NAC before systemic infection with a clinical *S. aureus* strain and then measured neutrophil influx. The results revealed that pretreatment with amitriptyline, Tiron or NAC prevented influx of neutrophils into the lung (**Figure 4.4.2.A. and B.**). This data indicates that Asm and ROS facilitate neutrophil trafficking following into lung tissue upon *S. aureus* infection.

A



B

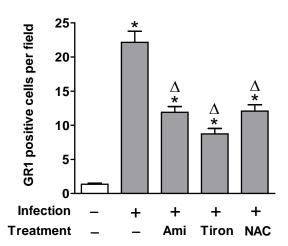


Figure 4.4.2. Effect of amitriptyline, Tiron or NAC on neutrophil trafficking into lung tissue induced by *S. aureus* infection

Wild-type mice were pretreated by intraperitoneal injection of 10 mg/kg amitriptyline, or 100 mg/kg Tiron or 100 mg/kg NAC twice daily for 2.5 days. Mice were infected with *S. aureus* for 12 hrs. Neutrophil emigration was determined by staining of lung sections with Cy3-labeled anti-GR1 antibody (scale bar is 50 μ M) followed by fluorescence microscopy (A). Shown are representative images from three independent experiments. Neutrophil trafficking was quantified by analysis of 50 fields per group (B). Displayed is the average of GR1-positive cells per field of 63x magnification. *, significant differences between uninfected and infected samples; Δ , significant differences between treated and untreated samples (all P<0.05, t-test).

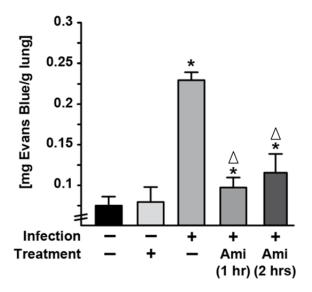
The results from **4.4.1** and **4.4.2** indicate pharmacologic inhibition of Asm or ROS before systemic infection with *S. aureus* prevents lung edema and influx of neutrophils into the lung.

4.5. Treatment of already septic mice with amitriptyline prevents the development of lung edema

4.5.1. Treatment with amitriptyline 1 hr or 2 hrs post *S. aureus*-infection reduces pulmonary edema

The finding that both Asm-deficiency and pre-incubation with the Asm inhibitor amitriptyline protect mice from lung edema induced by *S. aureus* infection led us question whether the administration of amitriptyline reduces the severity of pulmonary edema in mice that were already infected with *S. aureus*. If so, amitriptyline administration might be a clinically relevant therapeutic option for the treatment of *S. aureus*—induced pulmonary edema. To this end, we infected wt mice with a clinical *S. aureus* strain and treated them with amitriptyline 1 or 2 hrs later. Twelve hours after infection, the mice were sacrificed and Evans Blue extravasation was determined or lung sections were stained with H&E. As shown in **Figure 4.5.1.A. and B.,** treatment with amitriptyline reduced the severity of pulmonary edema even after the onset of systemic infection with *S. aureus*.

A



B

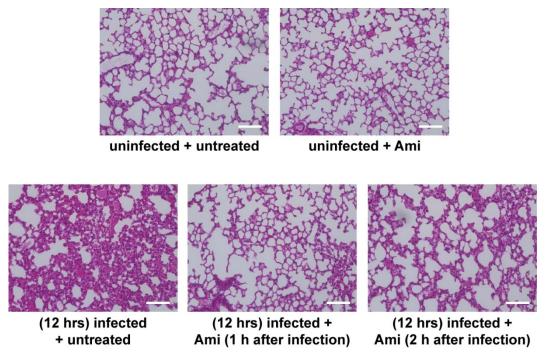


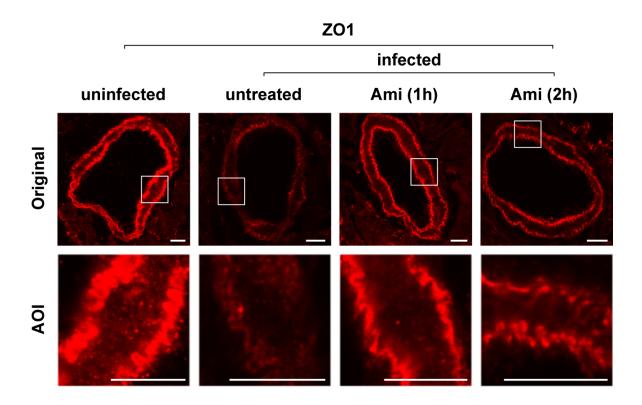
Figure 4.5.1. Amitriptyline treatment prevents lung edema in *S. aureus*-infected mice even after onset of the systemic infection

Wild-type mice were infected with *S. aureus*. 1 h or 2 hrs later they were i.p. injected with 16 mg/kg amitriptyline. The mice were sacrificed 12 hrs after infection. Lung edema was determined by extravasation of Evans Blue (A) and by staining with H&E (scale bar is 100 μ M, magnification, 20×) (B). Panel A shows the mean \pm SD from 4 mice. Images in B are representative from three independent experiments. *, significant differences between uninfected and infected samples; Δ , significant differences between treated and untreated samples (all P<0.05, t-test).

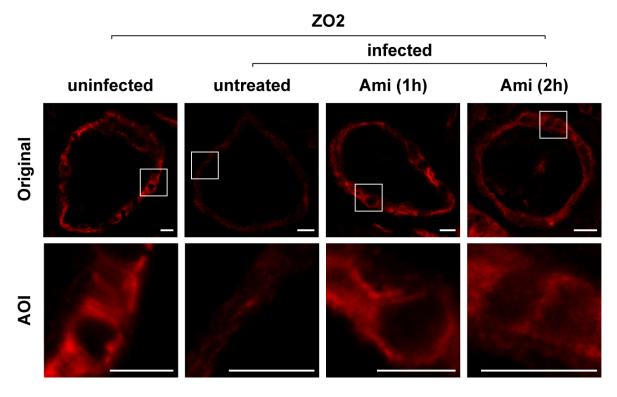
4.5.2. Treatment with amitriptyline 1 hr or 2 hrs after *S. aureus*-infection prevents degradation of junctional proteins

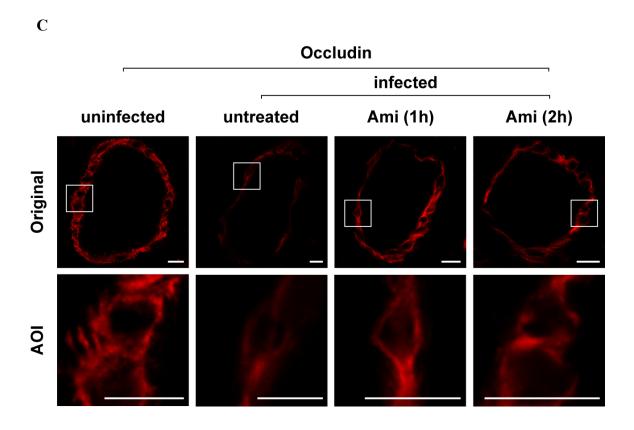
To determine whether pharmaceutical blockade of Asm by amitriptyline even after infection with *S. aureus* also protects the mice from degradation of junctional proteins *in vivo*, wild-type C57BL/6J mice were infected with a clinical *S. aureus* strain. The mice were treated with i.p. injection of 16 mg/kg amitriptyline 1 hr or 2 hrs after infection, respectively. The mice were sacrificed 12 hrs after infection and the lung sections were stained with anti-ZO1, anti-ZO2, anti-Occludin or anti-E-cadherin antibodies and analyzed by confocal fluorescence microscopy. The results showed amitriptyline-treatment reduced the degradation of junctional proteins even when the drug was applied 1 hr or 2 hrs post infection with *S. aureus* (Figure 4.5.2. A-D.).

A



B





D

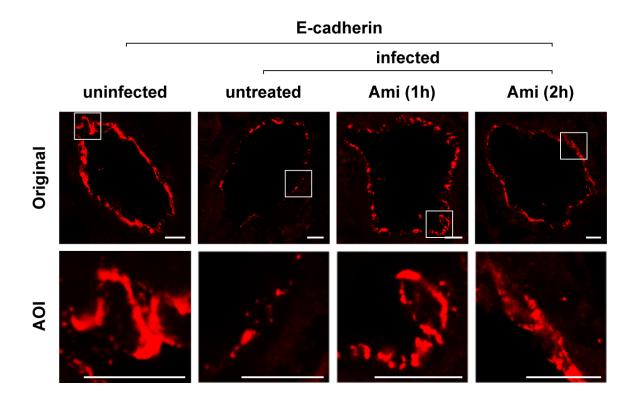


Figure 4.5.2. Amitriptyline treatment prevents degradation of junctional proteins even if administered after *S. aureus* infection

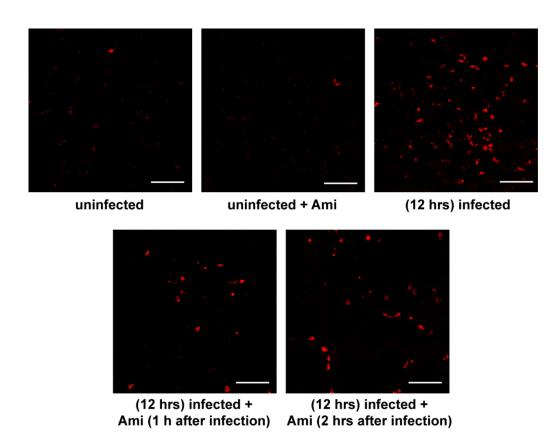
Wild-type mice were infected with *S. aureus* and were treated 1 h or 2 hrs after infection with i.p. amitriptyline. Twelve hours after infection, the mice were sacrificed. Lung sections were stained with Cy3-labeled antibodies against ZO1 (A), ZO2 (B), Occludin (C) or E-cadherin (D). Images were obtained by confocal microscopy and are representative of three independent experiments (magnification, $40\times$). The original image and an area of interest (AO1) are shown. Scale bar is $10 \mu M$.

4.5.3. Treatment with amitriptyline 1hr or 2 hrs after infection prevents neutrophil trafficking into the lung tissue

To determine whether pharmacological inhibition of Asm with amitriptyline also reduces neutrophil trafficking after infection of mice with *S. aureus*, wild-type C57BL/6J mice were infected with *S. aureus*. Again, the mice received 16 mg/kg amitriptyline by i.p. injected 1 hr or 2 hrs after infection. The mice were sacrificed 12 hrs after infection and the lung sections were stained with anti-GR1 antibody. The results demonstrated that amitriptyline treatment reduced pulmonary influx of neutrophils even if injected 1 hr or 2 hrs after infection, which

confirms that Asm play an important role in *S. aureus*-induced neutrophil trafficking (**Figure 4.5.3. A. and B.**).

A



B

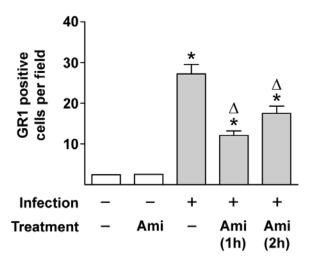


Figure 4.5.3. Amitriptyline treatment reduces S. aureus-induced neutrophil trafficking

Wild-type mice were infected with *S. aureus* for 1 hr or 2 hrs, and then treated with i.p. injection of 16 mg/kg amitriptyline. The mice were sacrificed 12 hrs after infection and the lungs were removed, fixed, dehydrated and embedded. The lung sections were stained with Cy3-labeled anti-GR1 antibody (scale bar is 50 μ M, magnification, 63×) (A). Representative images from three independent experiments are shown. The average number of GR1-positive cells per field of 63x magnification was quantified by analysis of 50 fields per group (B). Data are shown as mean \pm SD, n = 3. *, significant differences between uninfected and infected samples; Δ , significant differences between treated and untreated samples (all P<0.05, t-test).

This indicates that amitriptyline treatment after systemic infection with *S. aureus* protects junctional proteins degradation and reduces pulmonary influx of neutrophils, finally preventing pulmonary edema. Thus, amitriptyline might be a novel therapy to *S. aureus*-induced sepsis.

4.6. The combination of amitriptyline and antibiotics in the very early time can be a novel therapy to *S. aureus*-induced sepsis

4.6.1. The combination of amitriptyline and antibiotics contributes to bacteria killing

Sepsis remains a challenge for intensive care physicians and is one of the leading causes of death nowadays. Although improvements in supportive care of patients with sepsis (eg, more effective and less damaging mechanical ventilation, improved fluid resuscitation, and broad-spectrum antibiotic coverage) have improved survival rates, sepsis remains a condition with high mortality ranging from 20% to 50% of severely affected patients (Creamer et al 2012, Kanafani et al 2009, Moore et al 2011).

Clinically, treating *S. aureus* sepsis with antibiotics often achieves only limited success, and severe lung edema often still develops even with appropriate antibiotic treatment (Kanafani et al 2009, Moore et al 2011, Moore et al 2012). Thus, with the aim of developing novel efficient therapeutic approaches to the treatment of *S. aureus*—induced sepsis and lung edema, we examined the effect of a combination of amitriptyline and antibiotics on bacterial killing and lung edema after systemic *S. aureus* infection. To this end, we infected wt mice with a

clinical *S. aureus* strain or the *S. aureus* Newman strain. One hour after infection with the incidence of first clinical symptoms, amitriptyline (Ami) or methicillin (Methi) or vancomycin (Vanco) or a combination of amitriptyline and either methicillin or vancomycin were injected. The injection of methicillin or vancomycin was repeated after 9 hrs. Control mice were left uninfected. The mice were sacrificed 12 hrs after infection, and bacterial numbers were determined in liver and spleen. Only antibiotics alone or in combination with amitriptyline kill bacteria in liver and spleen (**Figure 4.6.1. A-B.**). Treatment with amitriptyline alone can't kill bacteria and even shows more bacterial numbers in liver and spleen compared to untreated wt mice after infection (**Figure 4.6.1. A-B.**).

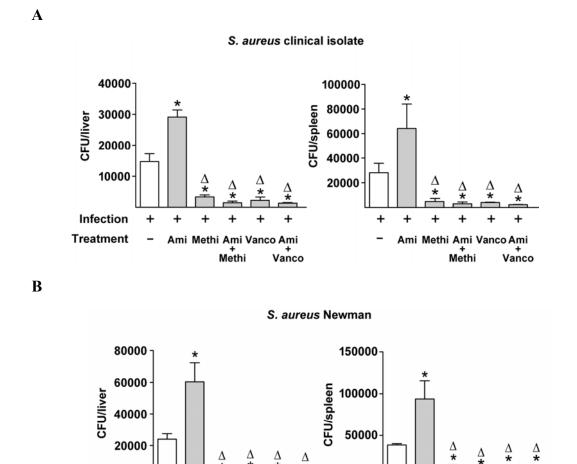


Figure 4.6.1. Effect of the combination of amitriptyline and antibiotics on bacteria killing

+ Vanco

Ami Methi Ami Vanco Ami

+ Methi

Infection Treatment

Wild-type mice were infected with a clinical *S. aureus* strain (A) or the *S. aureus* Newman strain (B). They were then left untreated; treated with an i.p. injection of amitriptyline (16 mg/kg) 1 h after

Ami Methi Ami Vanco Ami

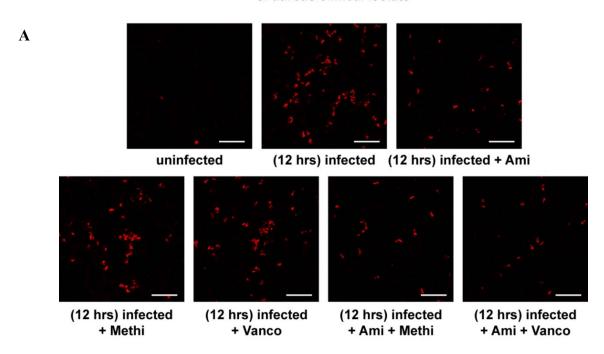
+ Methi Vanco

infection; treated with either methicillin or vancomycin (both 100 mg/kg) 1 h and 9 hrs after infection; or treated with the combination of amitriptyline and methicillin or vancomycin. The mice were sacrificed 12 hrs after infection. The liver and spleen were removed, homogenized, and lysed in saponin for the quantification of intracellular and extracellular bacteria (CFU) on lysogeny broth (LB) plates. Data shown are mean \pm SD of three independent experiments. *, significant differences between uninfected and infected samples; Δ , significant differences between treated and untreated samples (P<0.05, t-test).

4.6.2. The combination of amitriptyline and antibiotics inhibits neutrophil trafficking into the lung

To define the effect of the combination of amitriptyline with antibiotics on neutrophil trafficking into the lung upon *S. aureus* infection, we infected wt mice with a clinical *S. aureus* strain or the *S. aureus* Newman strain. One hour after infection with the incidence of first clinical symptoms, amitriptyline or methicillin or vancomycin or a combination of amitriptyline and either methicillin or vancomycin were injected. The injection of methicillin or vancomycin was repeated after 9 hrs. Control mice were left uninfected. The mice were sacrificed 12 hrs after infection and the left lungs were removed. Obtained lung sections were stained with anti-GR1 antibody and analysed by confocal fluorescence microscopy. The results showed *S. aureus*-induced neutrophil trafficking into the lung is abrogated by treatment with amitriptyline alone or combining with antibiotics, but not treatment with methicillin or vancomycin alone (Figure 4.6.2. A-B.).

S. aureus clinical isolate



B

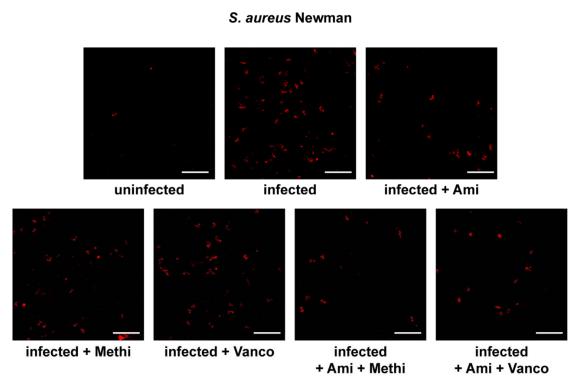


Figure 4.6.2. The combination of amitriptyline and antibiotics abrogates *S. aureus*-induced neutrophil trafficking into the lung

Wild-type mice were infected with a clinical *S. aureus* strain (A) or the *S. aureus* Newman strain (B). They were then left untreated; treated with an i.p. injection of amitriptyline (16 mg/kg) 1 h after infection; treated with either methicillin or vancomycin (both 100 mg/kg) 1 h and 9 hrs after infection; or treated with the combination of amitriptyline and methicillin or vancomycin. 12 hrs after infection, four mice per group were sacrificed and the left lungs were removed, fixed, dehydrated and embedded in paraffin for sectioning at a thickness of 6 μ m. The lung sections were stained with Cy3-labeled anti-GR1 antibody (scale bar is 50 μ M, magnification, 63×). Representative fluorescence images from three independent experiments are shown.

4.6.3. The combination of amitriptyline and antibiotics protects mice from tight junctional proteins degradation after S. aureus infection

To determine the effect of the combination of amitriptyline with antibiotics on degradation of pulmonary junctional proteins upon *S. aureus* infection, we infected wt mice with a clinical *S. aureus* strain or the *S. aureus* Newman. One hour after infection with the incidence of first clinical symptoms, amitriptyline or methicillin or vancomycin or a combination of amitriptyline and either methicillin or vancomycin were injected. The injection of methicillin or vancomycin was repeated after 9 hrs. Control mice were left uninfected. The mice were sacrificed 12 hrs after infection and the left lungs were removed. Lung sections were stained

with anti-ZO1, anti-ZO2, anti-Occludin or anti-E-cadherin antibodies. The stainings were analysed by confocal fluorescence microscopy. The results showed that only treatment with amitriptyline alone or combining with antibiotics, but not treatment with methicillin or vancomycin alone, prevented breakdown of TJ proteins *in vivo* after infection of mice with *S. aureus* (**Figure 4.6.3. A-D.**).

S. aureus clinical isolate

A-1

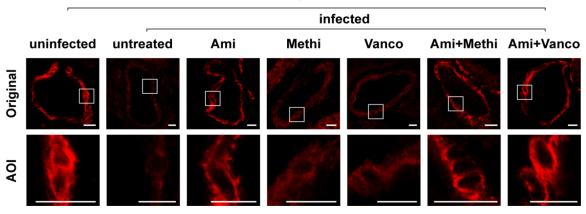
A-2

S. aureus Newman

B-1

S. aureus clinical isolate

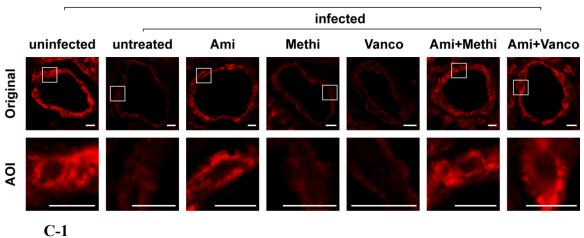
ZO2



B-2

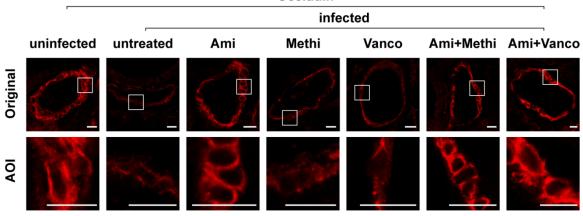
S. aureus Newman

ZO2



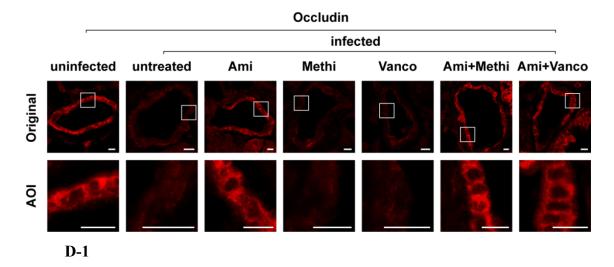
S. aureus clinical isolate

Occludin

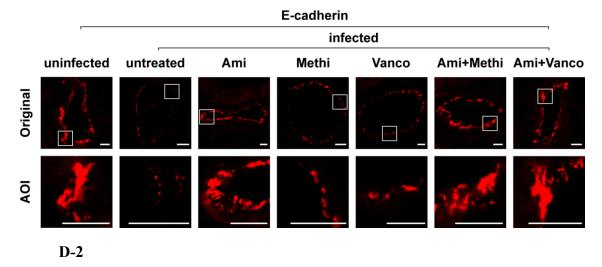


C-2

S. aureus Newman



S. aureus clinical isolate



S. aureus Newman

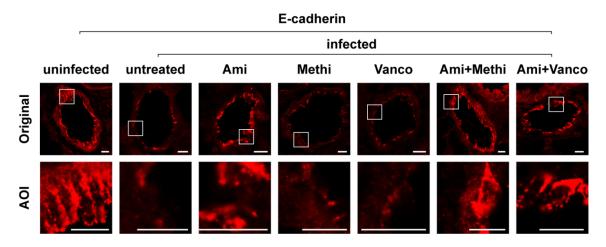


Figure 4.6.3. The combination of amitriptyline and antibiotics inhibits degradation of pulmonary tight junctional proteins upon *S. aureus* infection

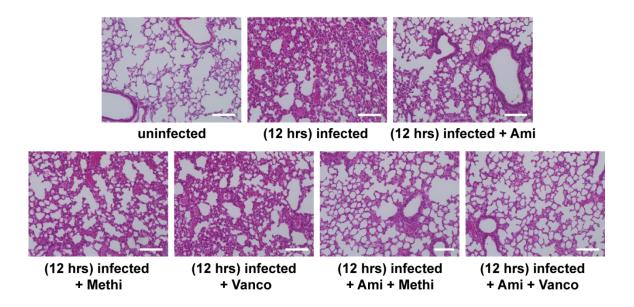
Wild-type mice were infected with a clinical *S. aureus* strain (A-D-1) or the *S. aureus* Newman strain (A-D-2). They were then left untreated; treated with an i.p. injection of amitriptyline (16 mg/kg) 1 h after infection; treated with either methicillin or vancomycin (both 100 mg/kg) 1 h and 9 hrs after infection; or treated with the combination of amitriptyline and methicillin or vancomycin. After 12 hrs infection, four mice per group were sacrificed and the left lungs were removed, fixed, dehydrated and embedded in paraffin for sectioning at a thickness of 6 μ m. The lung sections were stained with Cy3-labeled anti-ZO1 (A), anti-ZO2 (B), anti-Occludin (C) or anti-E-cadherin (D) antibodies (scale bar is 10 μ M, magnification, 40×). Representative fluorescence images from three independent experiments are shown.

4.6.4. The combination of amitriptyline and antibiotics rescues mice form S. aureus-induced lung edema

To determine the effect of the combination of amitriptyline with antibiotics on pulmonary edema upon *S. aureus* infection, we infected wt mice with a clinical *S. aureus* strain or the *S. aureus* Newman strain. One hour after infection, amitriptyline or methicillin or vancomycin or a combination of amitriptyline and either methicillin or vancomycin were injected. The injection of methicillin or vancomycin was repeated after 9 hrs. Control mice were left uninfected. The mice were sacrificed 12 hrs after infection and the left lungs were removed. Lung sections were stained with Hematoxylin-Eosin and analysed by confocal fluorescence microscopy. The results showed that only treatment with amitriptyline alone or combining with antibiotics, but not treatment with methicillin or vancomycin alone, prevented lung edema *in vivo* after infection of mice with *S. aureus* (Figure 4.6.4.A. and B.).

A

S. aureus clinical isolate



В

S. aureus Newman

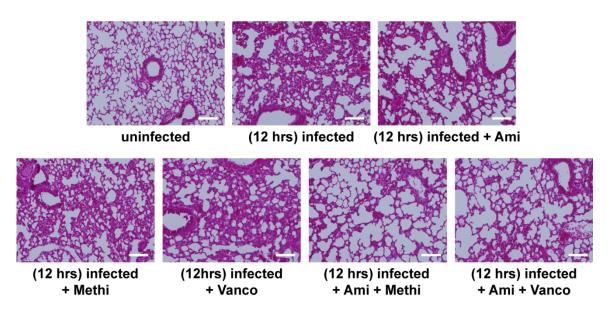


Figure 4.6.4. The combination of amitriptyline and antibiotics inhibits lung edema upon S. aureus infection

Wild-type mice were infected with a clinical *S. aureus* strain (A) or the *S. aureus* Newman strain (B). They were then left untreated; treated with an i.p. injection of amitriptyline (16 mg/kg) 1 h after infection; treated with either methicillin or vancomycin (both 100 mg/kg) 1 h and 9 hrs after infection; or treated with the combination of amitriptyline and methicillin or vancomycin. After 12 hrs infection, four mice per group were sacrificed and the left lungs were removed, fixed, dehydrated and embedded

in paraffin for sectioning at a thickness of 6 μ m. The lung sections were stained with Hematoxylin-Eosin (scale bar is 100 μ M, magnification, 20×). Representative fluorescence images from three independent experiments are shown.

4.7. The pharmacological treatment of lung edema and bacterial burden protects from lethality of *S. aureus* sepsis

To investigate the link between bacterial burden and sepsis-induced lethality, we performed mortality experiments with untreated and pharmacologically treated wt and Asm-deficient mice after infecting them intravenously with 5×10⁶ CFU *S. aureus*. Wt mice died between 26 and 52 h after infection. Treatment of wt mice with amitriptyline delayed the death of the mice and the mice died between 50 and 85 h after infection. A very similar time course was observed for Asm-deficient mice that died between 50 and 80 h of infection. Treatment of wt mice with methicillin or vancomycin (1 and 9 h after infection and then twice daily) alone only rescued 50 % mice (11-day observation period). In contrast, the treatment of wt mice with a combination of amitriptyline and antibiotics rescued 100 % of infected wt mice, and no deaths were observed. Likewise, Asm-deficient mice under antibiotic intervention were also completely protected from sepsis-induced lethality (**Figure 4.7.**).

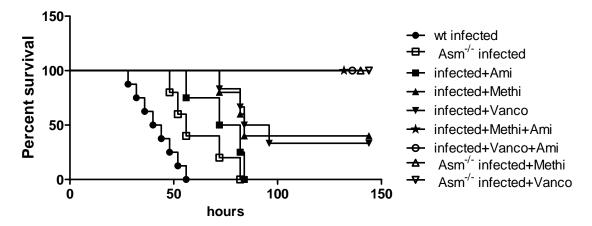


Figure 4.7. The pharmacological treatment of lung edema and bacterial burden protects from lethality of *S. aureus* sepsis

Wild-type (wt) and Asm-deficient (Asm^{-/-}) mice were infected intravenously with 5×10^6 CFU S. aureus. Mice were then left untreated or were pharmacologically treated with amitriptyline (Ami) (1 h after infection, then twice daily), methicillin (Methi), or vancomycin (Vanco) (1 and 9 h after infection

and then twice daily) or with a combination of amitriptyline and antibiotics. Survival was observed for up to 11 days. Data are shown in percent survival. Significance was determined by log-rank (Mantel—Cox) test.

In summary, these data indicate that the inhibition of lung edema in Asm-deficient or amitriptyline-treated mice together with a sufficient antibiotic treatment, which reduces the number of bacteria, is able to completely protect from lethality of *S. aureus* sepsis.

4.8. Control studies

4.8.1. Amitriptyline, Tiron or NAC has no effect on EOMA cells

To eliminate the effect of the amitriptyline, Tiron or NAC on junctional proteins degradation in EOMA cells, we treated endothelial cells with 20 μ M amitriptyline, 10 mM Tiron or 10 mM NAC for 140 min and stained the cells with the antibodies against ZO1, ZO2, Occludin, and E-cadherin. We found that amitriptyline, Tiron or NAC alone is without effect on TJs degradation in EOMA cells (**Figure 4.8.1.**).

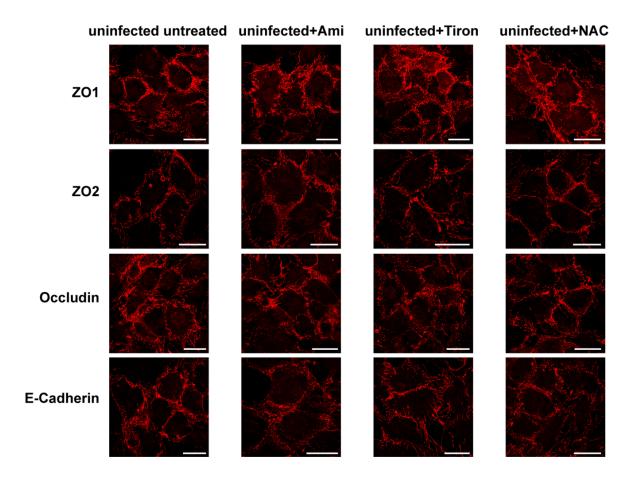


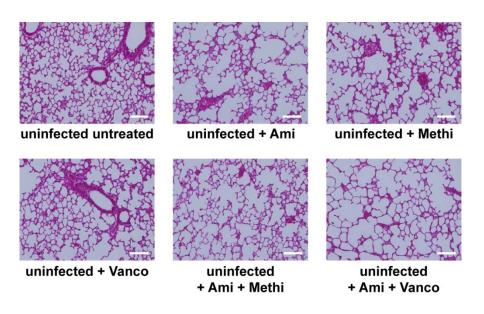
Figure 4.8.1. Effect of amitriptyline, Tiron or NAC on the distribution of ZO1, ZO2, Occludin and E-cadherin in EOMA cells

EOMA cells were treated for 140 min with amitriptyline (20 μ M), Tiron (10 mM) or NAC (10 mM). Immunoflourescence stainings were performed with antibodies against ZO1, ZO2, Occludin, or E-cadherin for determination of the degradation of these tight junction proteins. The presented pictures are representative of the results of at least three independent experiments (magnification, 40×). Scale bar is 25 μ M.

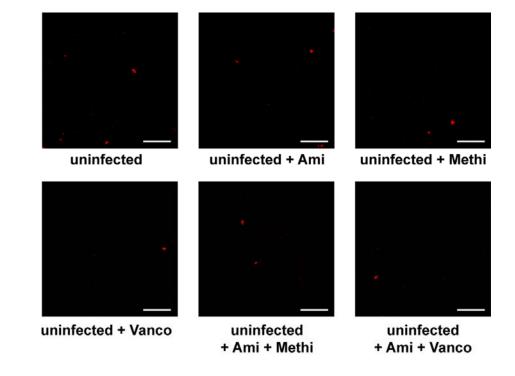
4.8.2. The drugs have no effect on lung parameters

To eliminate the effect of the drugs on lung parameters in uninfected mice, amitriptyline or methicillin or vancomycin or a combination of amitriptyline and either methicillin or vancomycin were injected. The injection of methicillin or vancomycin was repeated after 8 hrs. Control mice were left untreated. The mice were sacrificed 11 hrs after treatments. Lung sections were stained with Hematoxylin-Eosin (**Figure 4.8.2.A.**), anti-GR1 antibody (**Figure 4.8.2.B.**) and anti-ZO1 (**Figure 4.8.2.C.**), anti-ZO2 (**Figure 4.8.2.D.**), anti-Occludin (**Figure 4.8.2.E.**) or anti-E-cadherin (**Figure 4.8.2.F.**) antibodies. The stainings were analysed by confocal fluorescence microscopy. The studies confirmed that the drugs were without effect on lung parameters.

A

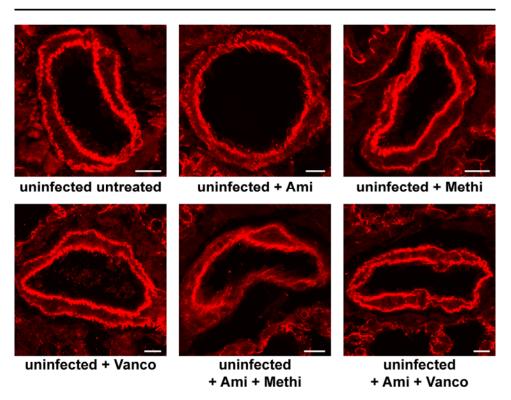


B



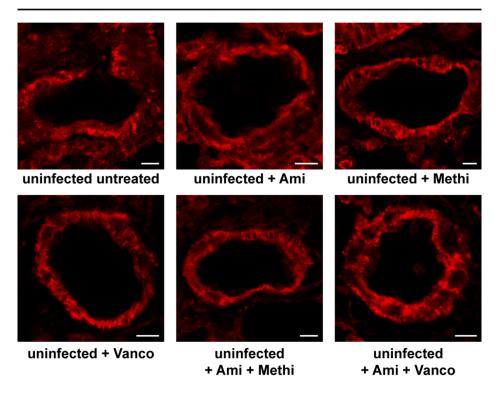
 \mathbf{C}

Z01



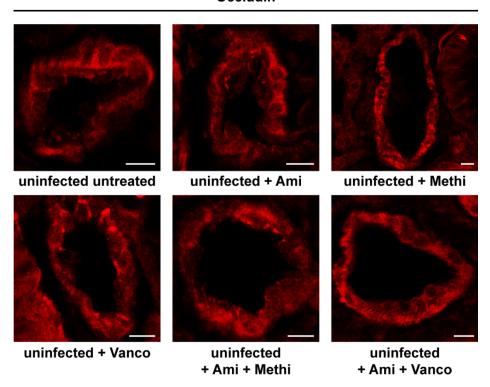
D

ZO2



E

Occludin



F

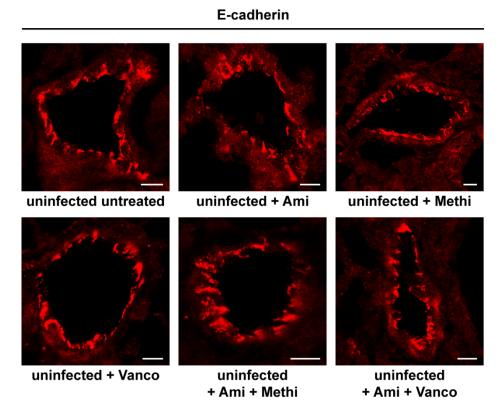


Figure 4.8.2. Effect of the drugs on lung parameters

Wild-type mice were treated with an i.p. injection of amitriptyline (16 mg/kg), either methicillin or vancomycin (both 100 mg/kg) or with a combination of amitriptyline and Methicillin or vancomycin. Injection of the antibiotics was repeated after 8 hrs. After 11 hrs treatments, four mice per group were sacrificed and the left lungs were removed, fixed, dehydrated and embedded in paraffin for sectioning at a thickness of 6 μ m. The lung sections were stained with Hematoxylin-Eosin (A) (scale bar is 100 μ M, magnification, 20×), Cy3-labeled anti-GR1 antibody (B) (scale bar is 50 μ M, magnification, 63×), or Cy3-labeled anti-ZO1 (C), anti-ZO2 (D), anti-Occludin (E) or anti-E-cadherin (F) antibodies (scale bar is 10 μ M, magnification, 40×). Representative fluorescence images from three independent experiments are shown.

5. DISCUSSION

5.1. Discussion of the Methods

5.1.1. Determination of Asm activity in cell lysates

Different methods are used to determine sphingomyelinase enzymatic activity, such as assays of pure enzyme and assays of cell extracts. In these assays the enzymatic activity of sphingomyelinase can be assayed by determining the conversion of sphingomyelin to ceramide and phosphorylcholine.

For assaying purified sphingomyelinase, natural or synthetic sphingomyelin is prepared, pure or mixed with other lipids, in the form of extruded large unilamellar vesicles (LUVs) approximately 100 nm in diameter (Richards et al 1986). When LUVs are assayed with sphingomyelinase, ceramide production in the bilayers leads to vesicle aggregation, which in turn produces an increase in turbidity or light scattering in the suspension. Thus the reaction can be followed in real time just by measuring the increase in turbidity (absorbance at 500 nm) or in light scattering (e.g. with a fluorometer with both the excitation and emission monochromators adjusted at 500nm).

For assaying sphingomyelinase activity in cell lysates, sphingomyelin need to be labeled, radioactively, fluorescently or otherwise. In the present study, the enzymatic activity was measured as the degradation of radioactive [14C]-sphingomyelin to ceramide and [14C]-phosphorylcholine. Because [14C]-phosphorylcholine is soluble in water, it is easily separated from the substrate [14C]-sphingomyelin and ceramide, which remains in the organic phase following extraction. Sphingomyelin can serve as substrate for three forms of sphingomyelinases that manifest acid, neutral or basic pH optima for maximal enzyme activity (Hannun 1996). In the present study Asm activity was discriminated from the neutral or basic sphingomyelinase activity by performing the assay at pH 5.0. Because of the difficulty in bringing together the enzyme and substrate molecules in the presence of cell homogenates, a suitable detergent, such as Triton X-100 was used. It should be noted that,

apart from emulsifying the substrate, the detergents bind and modify the enzyme activity, thus detergent concentration and initial detergent:substrate ratio was kept constant for reproducibility of assays. Finally, it has been suggested that the Asm may be located in detergent-resistant/insoluble fractions; thus, for determination of Asm activity in whole-cell lysates, no centrifugation step was performed after lysis and sonication of the cells to prevent pelleting and loss of the Asm.

5.1.2. Ceramide measurement by diacylglycerol (DAG) kinase assay

The crucial role of ceramide in numerous cellular processes and particularly stress responses, has led to the necessity of developing rapid and quantitative assays for ceramide determination. In the literature, there are several methods reported for quantifying ceramide such as normal phase high performance liquid chromatography (HPLC) analysis after derivatization with a fluorescent tag (Couch et al 1997, Iwamori et al 1979, Previati et al 1996, Yano et al 1998), evaporative lightscattering detection (McNabb et al 1999), high performance thin layer chromatography (HPTLC) analysis (Motta et al 1994), or using cells labeled with radioactive precursors (Tepper et al 2000). Ceramide molecular species can be determined following hydrolysis and analysis of the liberated and derivatized sphingoid bases by means of HPLC (Nishimura et al 1985, Smith et al 1995) and fatty acids by means of GC/MS (Samuelsson et al 1969). New methods for quantitative analysis of ceramide molecular species have been developed and are based on HPLC or reversed phase HPLC (RP-HPLC) separation of their fluorescent analogs prepared after derivatization with anthroyl cyanide (Yano et al 1998), benzoyl chloride (Couch et al 1997), or benzoic anhydride (Iwamori et al 1979). Moreover, mass spectrometry methodologies have been developed for the detection of molecular species of ceramide (Couch et al 1997, Gu et al 1997, Kalhorn et al 1999, Karlsson et al 1998, Liebisch et al 1999, Mano et al 1997, Watts et al 1999). However, most of these methods require long periods of processing and/or analysis.

The DAG kinase assay is a widely used method for the rapid quantification of ceramide. The primary advantages of the DAG kinase assay are the measurement of total mass levels of ceramide; the use of crude lipid extracts in the assay; and the ability of process a large number

of samples in a rapid manner. DAG kinase activity was originally reported by Hokin and Hokin (Hokin et al 1959). The enzyme was validated as an analytical tool in measuring diglyceride levels by the demonstration of a linear relationship between the amount of diglyceride added to an *in vitro* assay and the amount of product (phosphatidic acid) formed. Ceramides share structural similarities with diglycerides, and Schneider and Kennedy reported that bacterial DAG kinase can utilize ceramide as a substrate with a K_m nearly five times greater than that for diglyceride (Schneider et al 1973). Early attempts to use DAG kinase to quantify ceramide revealed a linear but non-quantitative relationship between substrate added and product formed. Further modification of the assay demonstrated that DAG kinase could also be used for quantitative conversion of ceramide to ceramide-1-phosphate over a range of 25 pmol to 2 nmol (Van Veldhoven et al 1995). These refinements have required special emphasis on the protocol of lipid extraction, purity of the reagents used for the preparation of the mixed micelles and on the development of high levels of recombinant DAG kinase.

The nonpolar properties of ceramide require that it be extracted from cells in organic solvents. Thus, the cells are lysed in a solution containing chloroform and methanol. Acidification of lysates with hydrochloric acid helps extraction of shorter acyl chain ceramide-1-phosphates or hydroxylated ceramides, thus being important to gain optimal usage of the exogenously added ceramides or internal standards. In the DAG kinase reaction, it is critical that the substrate is in a soluble form for optimal conversion to product by the enzyme. Mixed micelles containing a non-ionic detergent, such as n-octyl- β -glucopyranoside, and a phosholipid, such as cardiolipin, are utilized for this purpose. Of particular importance is the level of ceramide conversion to ceramide-1-phosphate. For the DAG kinase assay to yield reliable quantitative results, the reaction must go to completion with total conversion of DAG and ceramide. Otherwise, the results become sensitive to the effects of the efficiency of the reaction (K_m and V_{max} consideration of the DAG kinase) and to possible 'competition' between DAG and ceramide as substrates. In the present study, an excess of enzyme and ATP was used which

allowed linear and quantitative conversion and was sufficient for the phosphorylation of cellular ceramides as well as exogenously added ceramide.

5.1.3. Detection of lung edema by Evans Blue Dye

Evans Blue dye is widely used to study *in vitro* cellular permeability (Patterson et al 1992) and *in vivo* vascular leakage (Ferrero 2004). Historically, the dye was introduced for its utility in blood volume determinations by the dye dilution technique (Gibson et al 1937). Eventually, because the very high affinity of the dye for albumin was discovered (Freedman et al 1969, Rawson 1943), it began to be used as a surrogate marker for serum albumin flux across the luminal barrier in many *in vivo* experimental situations. Although subsequent investigations have revealed that the dye-albumin conjugate is not covalent in nature (Le et al 1947), it continues to be used today in situations where use of radioactively labeled albumin is not feasible or for histological examinations of injured tissue (Finck et al 1989, Moitra et al 2007, Saria et al 1983).

In the present study, pulmonary vascular permeability was estimated by using the Evans blue method. Evans blue dye, which strongly binds to albumin, is a well-known marker of protein extravasation in models of acute lung injury (Turnage et al 1995). A critical point to detect lung edema is to allow Evans blue dye to circulate for some time, which can ensure that albumin-bound Evans blue moves into the lung parenchyma through compromised vascular barrier in the lung. The major problem in detection of vascular leakage is the possibility of intravascular Evans blue dye residual. This would lead to an amplification of the optical density signal a false-positive result. To avoid this artifact, the lungs were perfused free of blood with phosphate-buffered saline via the pulmonary artery. Another crucial point is that total amount of dye should be calculated by means of a standard calibration curve. In the present study, results were expressed as µg/g of wet tissue.

5.1.4. Measurement of production of ROS by Electron Spin Resonance (ESR)

ROS formation and signaling are of major importance and regulate a number of processes in physiological conditions, which has led to the necessity of developing specific and sensitive assays for ROS determination. In the literature, there are several methods reported to allow measurement of generation and accumulation of different ROS, particularly H₂O₂, O₂⁻, and NO, in cells and/or organisms, such as fluorescent ROS dye technologies (Chen et al 2010, Zielonka et al 2010), genetically encoded ROS reporters (Ostergaard et al 2001, Schwarzlander et al 2011), nanoparticle delivery systems (Koo et al 2007, Lee et al 2009), and nanotube ROS probes (Kim et al 2011, Leeuw et al 2007). However, there are two major problems associated with even the most recently developed ROS fluorescent probes that still persist: reversibility and reaction rate.

ESR was first observed in Kazan State University by Soviet physicist Yevgeny Zavoisky in 1944, and was developed independently at the same time by Brebis Bleaney at the University of Oxford. ESR spectroscopy is a technique for studying materials with unpaired electrons. The basic concepts of ESR are analogous to those of nuclear magnetic resonance (NMR), but it is electron spins that are excited instead of the spins of atomic nuclei. ESR is the most direct technique and an effective and unique way to detect free radicals in biological samples. ESR spectroscopy is particularly useful for studying organic radicals.

Although unpaired electrons of species such as NO, ·OH, or O_2 · are too low in concentration and short-lived to be directly detected by ESR in biological systems, this dilemma can be circumvented by ESR measurement of more stable secondary radical species formed by adding exogenous spin-traps—molecules that react with primary radical species to give longer-lasting radical adducts with characteristic ESR signatures that can accumulate to levels permitting detection (Blodig et al 1999, Chen 2008). As we known, the concentration of ROS is very low and this would lead to the difficulty for detecting by ESR. To avoid this artifact, enough cells need to be prepared. Finally, since superoxide dismutase (SOD) catalyzes the dismutation of superoxide radicals (O_2 · + O_2 · + O_2 +

5.1.5. Asm-deficient animals

To determine the crucial role of Asm in the present study, Asm-deficient mice were used. The Asm knock-out mouse was originally generated in the laboratory of Dr. E. Schuchman (Horinouchi et al 1995) and has been proven to be a valuable tool in investigating the role of Asm in different cellular processes. Unfortunately, a study from Nix and Stoffel (2000) reported marked biochemical alterations and membrane dysfunction in cells derived from their line of Asm knock-out mice such as: increase of sphingomyelin and gycosphingolipids in the plasma membrane of hepatocytes, reduction of caveolin levels in embryonic fibroblasts, reduced signalling through tyrosine kinases in T lymphocytes, lymphopenia, the absence of proliferation of T cells in response to anti-CD3, reduced expression of the anti-apoptotic adapter FLIP, and a paradoxical increase in apoptosis of anti-CD3 pre-treated splenocytes upon activation of CD95 (Nix et al 2000). Therefore, the authors concluded that the previously reported apoptotic abnormalities in Asm-deficient cells and tissues (Cifone et al 1995, Lin et al 2000, Morita et al 2000, Pena et al 2000, Perez et al 1997, Santana et al 1996, Zundel et al 1998, Zundel et al 2000) did not result merely from Asm deficiency, but rather were impacted by disruption of membrane microdomains in response to altered sphingolipid metabolism (Nix et al 2000).

However, Lozano and co-workers pointed out that the phenotype of the Asm-deficient mouse line used in the study of Nix and Stoffel was different from the mouse line generated in the laboratory of Dr. Schuchman, which displayed, up to a certain age (12-16 weeks), only a minimal increase in sphingomyelin content, unchanged levels of caveolin-1, normal MAP-kinase signalling and tyrosine phosphorylation patterns, no lymphopenia, normal T cells proliferation and no decrease in FLIP levels (Lozano et al 2001). Furthermore, the life expectancy of around 9-10 months (Pena et al 2000, Santana et al 1996) was in contrast with that of the mice generated by Stoffel and co-workers, who reported that the life span of their Asm-deficient mice was maximally 4 months, with mice succumbing to advanced Niemann-Pick disease type A(Otterbach et al 1995). The mice used in the present study show

the earliest clinical manifestation of Niemann-Pick disease type A between 12-16 weeks of age; therefore, all the Asm-deficient mice involving in our experiments were carried out with animals younger than 10 weeks of age, before any biochemical, histological or clinical manifestations of Niemann-Pick disease type A were apparent. This excluded that the effects observed in the Asm-deficient cells were due to altered cellular processes (as described above) but instead, were completely dependent on the lack of Asm.

5.2. Discussion of the Results

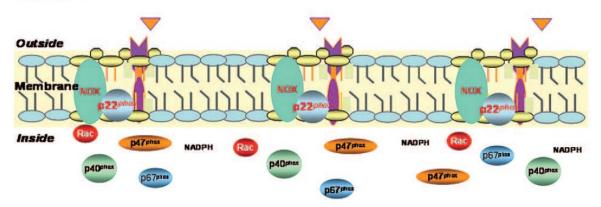
5.2.1. Role of the Asm/ceramide system in redox signaling

Our findings indicate that infecting endothelial cells with *S. aureus* activates Asm and thereby triggers the release of ceramide. Asm leads to the production of ROS by endothelial cells. Asm plays a critical role in *S. aureus*-triggered ROS release. *S. aureus* induces ROS accumulation in endothelial cells. These events were all absent in amitriptyline-treated mice that have a reduced Asm activity or in mice lacking the Asm genetically. Consistently, Reinehr and co-workers demonstrated that inhibiting Asm blocks the release of ROS, a finding suggesting that ROS functions downstream of Asm in hepatocytes (Reinehr et al 2006). Similarly, inhibiting Asm attenuates the ceramide and ROS production induced by histone deacetylase/perifosin (Rahmani et al 2005), fenretinide (Lovat et al 2004), sodium nitroprusside (Sanvicens et al 2006), or *P. aeruginosa* (Manago et al 2015, Zhang et al 2007, Zhang et al 2008). Taken together, these data confirmed the notion that Asm activation and ceramide production are upstream signals of ROS production.

NADPH oxidases (Nox), which are localized to various cellular membranes, are classically known as important ROS producers (Geiszt et al 2000, Lambeth 2004, Suh et al 1999). Ceramide induces the activation of ROS-generating enzymes, including NADPH oxidase, xanthine oxidase, NO synthase, and the mitochondrial respiratory chain (Corda et al 2001, Lecour et al 2006). In particular, ceramide has been shown to activate NADPH oxidase and to increase the production of ROS in a variety of mammalian cells, including human aortic smooth muscle cells (Bhunia et al 1997), endothelial cells (Zhang et al 2007), macrophages

(Zhang et al 2008) and erythrocytes (LaRocca et al 2014). The precise mechanism that how ceramide activates NADPH oxidase is not well understood. Because many stimuli activate NADPH oxidase by translocation and aggregation, it has been proposed that ceramide mediates the fusion of small raft domains to ceramide-enriched membrane platforms, which facilitate the aggregation of subunits of NADPH oxidase and enhances interactions between subunits of NADPH oxidase, thereby stimulating the production of ROS (**Figure 5.2.1.**) (Boini et al 2010, Jin et al 2008, Li et al 2007, Zhang et al 2006). Yi and colleagues demonstrated that ceramide in platforms may also directly enhance NADPH oxidase activity by activating small G protein Rac1/2 by activation of guanine nucleotide exchange factors (GEFs) such as Vav2 (**Figure 5.2.1.**) (Li et al 2007, Yi et al 2007).

RESTING



STIMULATED

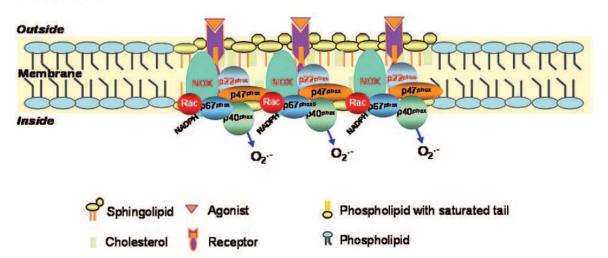


Figure 5.2.1. A hypothetic model showing lipid rafts (LRs) and LRs clustering to form a redox signaling platform

Under resting condition, individual LRs with attached receptors are present in the membrane of ECs (panel for resting cells). These individual LRs are dynamic microdomains and carry several membrane-bound or attached proteins or enzymes such as G-proteins, protein kinases, or the subunits of NADPH oxidase gp91^{phox} and p47^{phox}. When ligands or agonists bind to their receptors on individual LRs, the clustering is activated to form a number of LR macrodomains or platforms with aggregation or recruitment of receptors, NADPH oxidase subunits, and other proteins such as Rac GTPase. Clustering of these proteins and enzymes leads to activation of NADPH oxidase and production of O₂·-, which results in a prominent amplification of the transmembrane signal (panel for stimulated cells) (Li et al 2007).

5.2.2. Role of ROS in Asm activation

Our findings demonstrated that pretreating endothelial cells with the antioxidants N-acetylcysteine (NAC) and Tiron substantially inhibited Asm activation and the signaling events downstream of Asm activation, such as junctional proteins degradation induced by systemic *S. aureus* infection, thus indicating that ROS release is required for Asm activation. Moreover, several recent studies have indicated that the generation of ROS may be involved in the activation of Asm in response to various stimuli (Charruyer et al 2005, Dumitru et al 2006, Scheel-Toellner et al 2004), which seems to conflict with the above conclusion that Asm activation results in ROS production. This conundrum is discussed below and an amplifying concept is presented.

Scheel-Toellner and colleagues demonstrated that Asm activation, ceramide generation, and CD95 clustering play a crucial role in the spontaneous apoptosis of neutrophils; apoptosis was substantially delayed in Asm-deficient mice (Scheel-Toellner et al 2004). These events were pretreated by antioxidants indicating the dependence of the Asm on ROS. In accordance, pretreatment with the antioxidant pyrrolidine dithiocarbamate (PDTC) abolished Asm activation by ultraviolet (UV)-C light in U937 cells, a finding suggesting that ROS functions downstream of Asm (Charruyer et al 2005).

In addition, Dumitru and colleagues also demonstrated the involvement of ROS in TNF-related apoptosis-inducing ligand (TRAIL)-induced activation of Asm and apoptosis (Dumitru et al 2006). Stimulation with TRAIL/DR5 led to activation of Asm and the

subsequent formation of ceramide-enriched membrane platforms, DR5 clustering, and consequent apoptosis. Pretreatment with antioxidants NAC and Tiron substantially inhibited TRAIL-induced Asm activation, ceramide/DR5 clustering, and apoptosis, demonstrating that ROS play a crucial role in TRAIL-induced Asm/ceramic activation (Dumitru et al 2006). Finally, studies investigating the cellular effects of Cu²⁺ showed that Cu²⁺ also promotes the ROS-dependent activation of Asm and leads to the death of hepatocytes (Lang et al 2007). It was shown that the accumulation of Cu²⁺, as occurred in Wilson disease, activates Asm in hepatocytes and triggers the release of ceramide in these cells. This process leads to Cu²⁺-induced hepatocyte death, which can be prevented by a deficiency in Asm (Lang et al 2007).

In summary, these studies demonstrate that Asm activity is regulated by ROS upon systemic *S. aureus* infection, but the enzyme also stimulates ROS release. Therefore, we proposed a positive feed-back loop and a vicious cycle of–induced Asm activation and ROS release. In this amplification model, initial activation of Asm results in ROS production, which further enhance activation of Asm thus forms a feed-forward loop for ROS production. This finding is similar to the results of previous studies showing a positive feedback loop between the Asm and ROS after infection of macrophages with *P. aeruginasa* (Zhang et al 2008).

5.2.3. Role of the Asm/ceramide system and ROS for lung edema induced by systemic *S. aureus* infection

The results of the present study demonstrate that genetic deficiency or pharmacologic inhibition of the Asm/ceramide system in mice protects against lung edema induced by systemic *S. aureus* infection. The Asm/ceramide system triggered the formation of ROS, resulting in degradation of tight junction proteins and neutrophil trafficking, followed by lung edema. Pretreatment of mice or treatment of already infected mice with amitriptyline, a potent functional inhibitor of Asm, both protected mice from lung edem caused by systemic *S. aureus* infection. All the data presented above indicate that Asm/ceramide is a novel key molecule for the induction of lung edema by systemic *S. aureus* infection. Furthermore, pretreatment of mice with the antioxidants N-acetylcysteine (NAC) and Tiron substantially

inhibited the events downstream of Asm activation, such as junctional proteins degradation, neutrophil trafficking and lung edema, thus indicating that ROS release is also required for lung edema induced by systemic *S. aureus* infection.

It has been speculated that membrane rafts (MRs) and ROS may constitute an amplification system of redox signals and ceramide signaling cell membranes, which insures the efficiency of signal transduction (Li et al 2013a). The formation of such feed forward amplifying loop for MR redox and ceramide signaling may also be responsible for the temporospatial regulation of a complex signalosome that precisely and efficiently control cell function. If the activity of this regulatory loop is excessively enhanced, excessive production of both ROS and ceramide may result in the progress and development of different diseases or pathological processes (Li et al 2013a).

With respect to the role of these domains for the regulation of vascular endothelial functions, it has been described by numerous studies. Zhang and colleagues demonstrated that transfection of Asm siRNA markedly attenuated CD95 ligand in isolated small bovine coronary arteries, and induced inhibition of endothelium-dependent vasorelaxation (a response to bradykinin) by 60 % (Zhang et al 2007). The results suggest that Asm, the release of ceramide, and MR-derived ceramide-enriched membrane platforms are involved in the activation of NADPH oxidase in response to cytokines in coronary ECs, consequently leading to endothelial dysfunction (Jin et al 2007, Zhang et al 2006, Zhang et al 2007).

Moreover, the MR redox signaling platform associated with NADPH oxidase has been demonstrated to be responsible for endothelial dysfunction induced by various stimuli such as death receptor activation, homocysteine, cytokines, or adipokines (Jin et al 2008, Xia et al 2011, Zhang et al 2006). As a commonly used functional study, endothelium-dependent vasodilation (EDVD) response in isolated perfused arteries was tested. It was found that various stimulations which led to the formation of MR redox signaling platforms such as CD95 ligand, endostatin, homocysteine, and visfatin all led to impairment of EDVD. This

impairment was homeostatically recovered by NADPH oxidase inhibition using apocynin, or Asm siRNA, suggesting that MR redox signaling platforms with NADPH oxidase participate in the impairment of endothelial function (Jin et al 2008, Zhang et al 2007).

In addition, platelet-activating factor (PAF), lipopolysaccharide (LPS) or acid instillation treatment induces Asm-dependent production of ceramide and results in pulmonary edema and has a key role in ALI. Agents that interfere with PAF-induced ceramide release, such as steroids or the xanthogenate D609, attenuate pulmonary edema formation induced by PAF, endotoxin or acid instillation. These results identify Asm and ceramide as possible therapeutic targets in acute lung injury (Goggel et al 2004).

During sepsis, ALI results from activation of innate immune cells and endothelial cells by endotoxins, leading to systemic inflammation through pro-inflammatory cytokine overproduction, oxidative stress, and intracellular Ca²⁺ overload. Recent data by Gandhirajan and co-workers indicate that ROS-driven Ca²⁺ signaling promotes vascular barrier dysfunction and induce pulmonary edema (Gandhirajan et al 2013).

All the experiments confirmed the notion that feed forward amplifying loop of Asm/ceramic and ROS is involved in systemic *S. aureus*—induced pulmonary edema.

5.2.4. Role of junctional proteins degradation for lung edema induced by systemic S. aureus infection

As we known endothelial barrier dysfunction occurs during stimulation by inflammatory agents, pathogens, activated blood cells, or disease states. The pathophysiology is characterized by excessive flux of plasma across the exchange micro-vessel wall into the surrounding tissues. Traditionally, compromised endothelial cell–cell junctional integrity is considered to account for the leak response.

A principal hallmark of lung edema is degradation of junctional proteins, which induces the disruption of endothelial cell barrier, followed by excessive flux, neutrophil trafficking and

consequently lung edema. Clinicians have long recognized the problem of vascular leak but had no tools to reverse it.

Out data presented here indicate that systemic *S. aureus* infection induces lung edema via degradation of junctional proteins. Genetic deficiency of the Asm/ceramide system in mice protects against junctional proteins degradation and reduces lung edema induced by systemic *S. aureus* infection. Furthermore, pre-treatment of the mice or treatment of already infected mice with amitriptyline both protected mice from junctional proteins degradation and reduces lung edema. Likewise, pretreatment of mice with the antioxidants N-acetylcysteine (NAC) and Tiron substantially inhibited junctional proteins degradation and reduces lung edema.

The experiments further suggest, on one hand, the feed forward amplifying loop for Asm/ceramide and ROS is required for degradation of junctional proteins induced by systemic *S. aureus* infection; on the other hand, junctional proteins degradation is responsible for lung edema induced by systemic *S. aureus* infection. This concept is consistent with findings that superoxide can directly down-regulate TJ proteins and indirectly activate matrix metalloproteinases (MMPs) that contribute to disrupt the integrity of endothelial cell layers (Gu et al 2011). Moreover, superoxide directly activates several inflammatory cytokines, which in turn activate MMPs (Abdul-Muneer et al 2015, Gu et al 2011, Rochfort et al 2014). Furthermore, in some pathological conditions, ROS induce the degradation of tight junctional proteins, following by vascular leakage and neutrophil trafficking with consequent pulmonary edema (Catanzaro et al 2015, Naik et al 2014).

All the data presented above indicate that antidepressant amitriptyline and antioxidants N-acetylcysteine (NAC) and Tiron might be very useful for future therapies for lung edema induced by degradation of junctional proteins. At the same time, the development of agents or mediators that reinforce intercellular junctional proteins should be a goal of drug research.

5.2.5. Role of neutrophil recruitment for lung edema induced by systemic S. aureus infection

Lung edema, endothelial and epithelial injury are accompanied by an influx of neutrophils into the interstitium and broncheoalveolar space. Neutrophils are considered to play a key role in the progression of ALI/ARDS since activation and transmigration of neutrophils is a hallmark event in the progression of ALI/ARDS (Abraham 2003).

The importance of neutrophils in ALI/ARDS is affirmed by clinical data and animal models. In patients with ARDS, the concentration of neutrophils in the bronchoalveolar lavage (BAL) fluid correlates with severity of ARDS and outcome (Matthay et al 1984, Parsons et al 1985, Steinberg et al 1994). Furthermore, depletion of neutrophil in mice reduces the severity of lung injury (Abraham et al 2000). Interestingly, blocking interleukin-8 (IL-8), a major chemoattractant for neutrophils, protects rabbits from acid aspiration-induced lung injury (Folkesson et al 1995). Further to emigration, neutrophils are irreplaceable in bacterial clearance, much of which is mediated by phagocytosis and intracellular bacterial killing (Soehnlein 2009). Even so, ALI/ARDS can occur in children and adults with neutropenia (Laufe et al 1986, Ognibene et al 1986, Sivan et al 1990), which indicates that neutrophil-independent mechanisms alone allow for development of ALI/ARDS under specific conditions. Despite that, a multitude of experimental and clinical data point at the causative role of neutrophils in lung injury.

The present study indicates that neutrophil trafficking plays a key role in lung edema induced by systemic *S. aureus* infection. Genetic deficiency of the Asm/ceramide system in mice reduces neutrophils trafficking, consequently protects the mice against lung edema induced by systemic *S. aureus* infection. Furthermore, pre-treatment of the mice or treatment of already infected mice with amitriptyline both protected mice from neutrophil trafficking and reduces lung edema. Furthermore, pretreatment of mice with the antioxidants N-acetylcysteine (NAC) and Tiron substantially inhibited neutrophils trafficking and reduces lung edema.

The experiments further suggest, on one hand, the feed forward amplifying loop for Asm/ceramide and ROS is required for neutrophil trafficking induced by systemic *S. aureus* infection; on the other hand, neutrophil trafficking is involved in lung edema induced by systemic *S. aureus* infection. Consistently, it has recently been shown that recruitment of neutrophils is a key event in development of ALI, linking to plasma leakage and deterioration of oxygenation (Grommes et al 2011, Ware et al 2000). LPS inhalation mimics human Gram-negative ALI, inducing neutrophil recruitment, pulmonary edema and finally impairment of gas exchange (Matute-Bello et al 2008). Moreover, the importance of neutrophils in ALI is supported by studies where lung injury is abolished or reversed by depletion of neutrophils (Looney et al 2006, Soehnlein et al 2008).

Hence, antidepressant amitriptyline and antioxidants N-acetylcysteine (NAC) and Tiron might be very useful for future therapies for lung edema induced by neutrophils trafficking. At the same time, the development of agents or mediators that decrease neutrophils recruitment should be a goal of drug research.

5.2.6. Clinical significance of combination of amitriptyline and antibiotic

S. aureus is a leading cause of septic infections, and S. aureus—induced sepsis is one of the most serious infections acquired in hospitals or in the community. However, even with the use of appropriate antibiotics, fatal lung edema often develops (Cortes Garcia et al 2012, Moore et al 2011, Moore et al 2012). Despite many clinical trials, no FDA-approved drug is available for use in sepsis, a lack that underscores the importance of future sepsis research. Interestingly, our studies with wt and Asm-deficient mice seem to mimic the situation in hospitals showing a high lethality in septic S. aureus infections even if adequately treated with antibiotics (Cortes Garcia et al 2012, Moore et al 2011, Moore et al 2012).

Our findings demonstrate that treating mice with amitriptyline 1 or 2 h after infection reduces *S. aureus*—induced pulmonary edema and also inhibits myeloid cell trafficking and the degradation of junctional proteins. The reduced capacity of mice treated with amitriptyline or Asm-deficient mice to kill *S. aureus* is consistent with the previous notion that myeloid cells

lacking Asm are unable to cluster and activate NADPH oxidases resulting in a defect of the production of superoxide and a reduced killing of pathogens. Finally, amitriptyline-treated or Asm-deficient mice died by the inability to eliminate the bacteria. In contrast, antibiotics kill the bacteria, but did not reduce lung edema. Thus, the combination of amitriptyline and antibiotics combines the advantages of inhibiting lung edema and eliminating systemic bacteria, protecting mice from lethality.

It is very interesting that Goggel and co-workers demonstrate that steroids or the xanthogenate D609, which can interfere with PAF-induced ceramide synthesis, inhibit pulmonary edema formation induced by platelet-activating factor (PAF), lipopolysaccharide (LPS) or acid instillation (Goggel et al 2004). These results indicate that Asm/ceramide signaling plays an important role in pulmonary edema induced by PAF instillation.

However, the molecular mechanisms how the Asm/ceramide system induces lung edema is largely unknown. According to previous studies, eNOS/eNO might be involved in this role. It has been reported that pharmacological inhibition of the Asm pathway with imipramine, D609 or dexamethasone blocks the PAF-induced increase of caveolin-1 and eNOS in caveolae, and the decreases in eNO production and edema formation in rat lung (Yang et al 2010). These results suggest that inhibition of eNOS/eNO signaling decreases PAF-induced lung edema.

More recently, Samapati and colleagues indicate PAF increases lung edema and endothelial Ca²⁺. This response is abrogated by inhibitors of Asm or in Asm-deficient mice, and replicates by lung perfusion with exogenous Asm or C₂-ceramide. Further experiments demonstrate that PAF increases the caveolar abundance of TRPC6 channels via Asm activation, subsequently induces increases in lung endothelial Ca²⁺, vascular filtration coefficient, and edema formation , which were attenuated by the TRPC inhibitor SKF96365 and in TRPC6-deficient mice, whereas direct activation of TRPC6 replicated the Ca²⁺ and edema response to PAF. The exogenous NO donor PapaNONOate or the cyclic guanosine

3',5'-monophosphate analog 8Br-cGMP blocked the endothelial Ca²⁺ and permeability response to PAF (Samapati et al 2012).

According to our data, the Asm/ceramide system induces lung edema by junctional proteins degradation and neutrophil trafficking, which is a novel viewpoint to explain how the Asm/ceramide system induces lung edema upon systemic *S. aureus* infection.

5.2.7. Possible additional roles of Asm as activator of ADAM 10

S. aureus expresses multiple toxins, such as alpha-toxin, Panton-Valentine leukocidin, and enterotoxin B and A, which cause membrane damage, infiltration of myeloid cells and macrophages, cytokine production, and increased vascular permeability resulting in severe pulmonary edema and lung injury (Bhakdi et al 1984, Diep et al 2010, Mattix et al 1995, Menoret et al 2012).

Pore-forming cytotoxins (PFTs) are a family of bacterial virulence factors that cause eukaryotic cell injury and death (Gonzalez et al 2008). *S. aureus* encodes multiple PFTs, the best-studied being α-hemolysin (Hla), which is expressed by almost all strains (Tomita et al 1997). Hla is involved in the pathogenesis of skin infections, pneumonia, corneal infection and toxic shock syndrome (Brosnahan et al 2009, Bubeck Wardenburg et al 2007a, Bubeck Wardenburg et al 2007b, Kennedy et al 2010, O'Callaghan et al 1997), including those caused by MRSA.

Both of the *S. aureus* strains used in our study produce several hemolysins. It is possible that *S. aureus* toxins mediate the activation of the Asm observed in the present study after infection of endothelial cells with *S. aureus*. However, at present, it is unknown whether purified alpha-toxin activates the Asm in human and mouse monocytic cells. Recently, it was reported that the binding of Hla to its eukaryotic receptor A-disintegrin and metalloprotease 10 (ADAM10) leads to the up-regulation of ADAM10 activity, which is required for Hla-induced cytotoxicity (Inoshima et al 2011, Powers et al 2012, Wilke et al 2010).

Increased ADAM10 activity in epithelial and endothelial cells and following signaling cascades disrupts the cell barrier function, and this disruption contributes to the pathogenesis of lethal lung edema. However, it is unknown whether the Asm and ADAM10 function in the same signaling cascade or are independent pathways that are both required for the cellular effects of alpha-toxin.

5.2.8. Possible additional roles of Asm as activator of the Nalp3 inflammasome

Microorganisms that invade the cytosol can be recognized by cytoplasmatic pattern-recognition receptors (PRRs), most notably the nucleotide-binding oligomerization domain, leucine-rich repeat (also known as NOD-like receptors, both abbreviated to NLR) (Kawai et al 2010, Schroder et al 2010). NLRs, which detect microbial components in the cytosol and trigger the assembly of large caspase-1-activating complexes termed inflammasomes, are further subcategorized based on differences in the N-terminal domains (Schroder et al 2010, Stutz et al 2009). Amongst the various inflammasomes, the NALP3 inflammasome is particularly qualified to response to various activators, leading to caspase activation. NLRP3 inflammasome activation induces caspase-1 activation, which causes the processing of the pro-inflammatory cytokines IL-18 and IL-18 and triggers the inflammatory stress (Schroder et al 2010, Stutz et al 2009). IL-1 β is an early cytokine in ALI patients and induces alveolar permeability and causes production of other cytokines such as IL-6 and TNF-a (Ganter et al 2008).

S. aureus is a potent activator of the inflammasome in macrophages resulting in upregulation of caspase-1 upon its interaction with Asc and NALP3 (Mariathasan et al 2006). Moreover, α -hemolysin activates the NALP3-inflammasome during *S. aureus* pneumonia, inducing necrotic pulmonary injury. Moreover, Nalp3^{-/-} mice have less-severe pneumonia (Kebaier et al 2012). In addition, purified α -hemolysin activates the NALP3-inflammasome, ultimately leading to the secretion of the pro-inflammatory cytokines IL-1 β and IL-18 and the resultant tissue necrosis and inflammation (Craven et al 2009).

Recently, it was reported that the inflammasome protein complex activates caspase-1 to promote the processing and secretion of IL-1β, which is responsible for alveolar epithelial permeability. In addition, it is shown that inflammasome inhibition blocks hyperoxia-induced alveolar permeability and cytokine production (Kolliputi et al 2010). Later, Kolliputi and colleagues further reveal that ceramide causes NALP3-inflammasome activation, induction of caspase-1, IL-1β cleavage, release of pro-inflammatory cytokines, and ultimately alveolar epithelial permeability. Short-hairpin RNA silencing of NALP3-inflammasome components abrogated ceramide-induced secretion of pro-inflammatory cytokines and abolished ceramide-induced alveolar epithelial permeability in *in vitro* (Kolliputi et al 2012). However, the role of inflammasome in relation to *S. aureus*-induced Asm/ceramide activation and inflammatory cytokine production leading to endothelial permeability remains unknown.

5.2.9. Significances and perspectives

In the present study, we demonstrated that the combination of amitriptyline and antibiotics effectively protects mice from lung edema and bacteremia during sepsis. Amitriptyline is a well-known antidepressant that has been widely used in clinical practice for more than 50 years and is associated with only mild adverse effects at therapeutic doses. Thus, the major significance of the research work in this dissertation is to indicate that inhibition of the Asm/ceramide system in combination with antibiotics could be a novel approach to treat severe systemic and often lethal infections and to inhibit lung injury in patients with incipient sepsis. The results presented in this dissertation increases our understanding of the signaling mechanisms responsible for the acute ROS response in endothelial cells during host-pathogen interaction and link the function of Asm with ceramide redox signaling. The notion that Asm deficiency or antioxidants prevent *S. aureus*-induced Asm/ceramide activation, ROS release, junctional proteins degradation, neutrophil trafficking and lung edema, which may contribute to the understanding how systemic *S. aureus* infections induce lung edema. This may direct the development of new therapeutic strategy for treatment of this disease.

6. SUMMARY

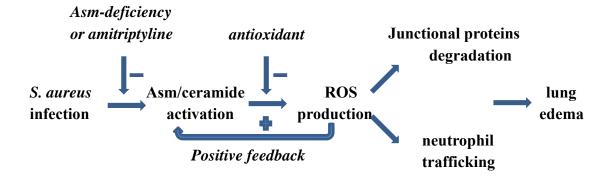
Pulmonary edema associated with increased vascular permeability is a severe complication of *S. aureus*—induced sepsis and an important cause of human pathology and death. Antibiotics alone are often insufficient to cure patients with *S. aureus*—induced sepsis. Although treatment with effective doses of bactericidal antibiotics indeed prevents the bacterial burden, antibiotics often fail to prevent fatal lung edema after septic infection with *S. aureus*.

The present study investigated the role of the Asm/ceramide system in the development of lung edema caused by *S. aureus*. Furthermore, the present study identified signaling mechanisms responsible for lung edema caused by *S. aureus*. Most importantly, the present study identifies a novel approach to patients with *S. aureus*-induced sepsis with bactericidal antibiotics applied in combination with amitriptyline. The major findings are:

- *S. aureus* rapidly activates Asm and induces ceramide release in the plasma membranes.
- The Asm/ceramide system mediates S. aureus-induced ROS production.
- The Asm/ceramide system and ROS form a positive feedback loop.
- Asm and ceramide activation are crucial for *S. aureus*-induced lung edema.
- ROS is essential for *S. aureus*-induced lung edema.
- The Asm/ceramide system and ROS activation lead to junctional proteins degradation.
- The Asm/ceramide system and ROS activation lead to neutrophil trafficking.
- Both junctional proteins degradation and neutrophil trafficking contribute to lung edema induced by *S. aureus* infections.
- Genetic deficiency or pharmacologic inhibition of the Asm/ceramide system in mice protects against lung edema induced by systemic *S. aureus* infection.

- Pretreating endothelial cells with the antioxidants N-acetylcysteine (NAC) or Tiron substantially inhibited Asm activation and the signaling events downstream of Asm activation.
- The combination of antibiotics and amitriptyline reduced both pulmonary edema and bacteremia protecting mice from lethal sepsis and lung dysfunction.

Therefore, the proposed signaling pathway is depicted as bellow:



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8. PUBLICATIONS

- 1. **Huiming Peng**, Cao Li, Stephanie Kadow, Brian D. Henry, Jörg Steinmann, Katrin Anne Becker, Andrea Riehle, Natalie Beckmann, Barbara Wilker, Pin-Lan Li, Timothy Pritts, Michael J. Edwards, Yang Zhang, Erich Gulbins, Heike Grassmé. Acid sphingomyelinase inhibition protects mice from lung edema and lethal Staphylococcus aureus sepsis. J Mol Med (2015) 93:675–689
- 2. Rolf Hilker, Antje Munder, Jens Klockgether, Patricia Moran Losada, Philippe Chouvarine, Nina Cramer, Colin F. Davenport, Sarah Dethlefsen, Sebastian Fischer, **Huiming Peng**, Torben Schönfelder, Oliver Türk, Lutz Wiehlmann, Florian Wölbeling, Erich Gulbins, Alexander Goesmann and Burkhard Tümmler. Interclonal gradient of virulence in the *Pseudomonas aeruginosa* pangenome from disease and environment. Environmental Microbiology (2015) 17(1), 29–46
- 3. Cao Li, **Huiming Peng**, Lukasz Japtok, Aaron Seitz, Andrea Riehle, Barbara Wilker, Matthias Soddemann, Burkard Kleuser, Michael Edwards, David Lammas, Pin Lan Li, Krishna M. Boini, Yang Zhang, Erich Gulbins, Heike Grassmé. Neutral sphingomyelinase reduction protects mice against systemic tuberculosis through autophagy stimulation via ROS-downregulation. Front Biosci (Elite Ed). (2016) 1(8), 311-25.

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