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**VIRULENCE OF
SALMONELLA ENTERICA
SEROVAR TYPHIMURIUM
AND INNATE
ANTIBACTERIAL HOST
RESPONSES**

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Institutet**

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Unconquerable stubbornness will wear down the thickest of walls and it is only a matter of time before you break on through to the other side

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ABSTRACT

The bacterial species *Salmonella enterica* consists of a collection of closely related enteric bacteria giving rise to diverse diseases in a wide range of hosts. In the murine infection model *Salmonella enterica* serovar Typhimurium (*S. Typhimurium*) causes an invasive disease which in many aspects resembles human typhoid fever. The ability of this pathogen to survive and replicate within macrophages of the liver and spleen is a crucial virulence determinant which largely depends on the type III secretion system coded for by the *Salmonella* pathogenicity islands 2 (SPI-2). Innate immune recognition of bacterial pattern molecules such as the lipopolysaccharide (LPS) induces immediate defence responses such as production of reactive oxygen intermediates (ROI) and reactive nitrogen intermediates (RNI), synthesized by macrophages via the action of the NADPH phagocyte oxidase (phox) and inducible nitric oxide synthase (iNOS) respectively. The newly characterized phagocyte receptor TRAPC has been shown to trigger nitric oxide (NO) production in macrophages and dendritic cells upon receptor cross-linking, suggesting a possible role for TRAPC during bacterial infection. Surprisingly we could show that in combination with bacterial infection or LPS stimulation, cross-linking of TRAPC reduces macrophage NO production. The suppression of NO associated with a slight reduction of iNOS expression possibly mediated by a dampening the TLR-4 response. For *S. Typhimurium* and many other enteric pathogens, the ability to express complete LPS molecules has conventionally been regarded as a requirement for bacterial virulence, e.g. lack of the O-antigen (the outermost part of the LPS molecule) has been shown to reduce the virulence of *S. Typhimurium* in murine infection models. However, *S. Typhimurium* has also been shown to down-regulate genes for LPS-synthesis and to reduce the chain length of the O-antigen once it resides inside macrophage-like cells. This raises the question whether *S. Typhimurium* may benefit from expression of O-antigen-deficient LPS during intracellular stages of infection. To settle this issue the fitness of defined mutants devoid of O-antigen in macrophage-like cells was studied. O-antigen-deficient mutants inhibited iNOS activity in macrophage-like cells in an apparently SPI-2 dependent manner. Consequently the mutants displayed increased growth yields within these cells compared to wild type bacteria. Production of ROI as well as RNI is critical for control of disease proliferation in the murine salmonellosis model. In *E. coli* the thioredoxin and glutathione/glutaredoxin systems have been shown to mediate protection against oxidative stress. When studying the role of these systems in *Salmonella* we could show that whereas thioredoxin 1 (TrxA) is dispensable for resistance to oxidative or NO stress *in vitro*, it is essential for bacterial growth in both epithelial and macrophage-like cells as well as for virulence *in vivo* in the murine infection model. Whereas the level of replication within macrophage-like cells correlates directly to the redox potential of TrxA, *in vivo* virulence depends on both redox dependent and independent activities of TrxA. Moreover, TrxA was shown to be required for proper function of SPI-2 and for the ability of O-antigen deficient *S. Typhimurium* to inhibit iNOS activity.

LIST OF PUBLICATIONS

- I. **Eva Bjur**, Sofia Eriksson-Ygberg and Mikael Rhen
The O-antigen affects replication of Salmonella enterica serovar Typhimurium in murine macrophage-like J774-A.1 cells through modulation of host cell nitric oxide production
Microbes and Infection (2006) 8:1826-1838
- II. Rutger van der Holst*, **Eva Bjur***, Mikael Rhen and Jonas Sundbäck
Fine-tuning of macrophage anti-bacterial responses by TRAPC
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- III. **Eva Bjur**, Sofia Eriksson-Ygberg, Fredrik Åslund and Mikael Rhen
Thioredoxin 1 promotes intracellular replication and virulence of Salmonella enterica serovar Typhimurium
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- IV. **Eva Bjur**, Aurel Negrea, Sofia Eriksson-Ygberg, Fredrik Åslund and Mikael Rhen
Thioredoxin 1 contributes to bacterial virulence through redox-dependent and redox-independent mechanisms
Manuscript

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LIST OF ABBREVIATIONS

CAMPs	Cationic antimicrobial peptides
DC	Dendritic cells
EEA1	Early endosomal antigen 1
GFP	Green fluorescent protein
HP	Hydrogen peroxidase
NO	Nitric oxide
IFN	Interferon
IL	Interleukin
iNOS	Inducible nitric oxide synthase
IRAK	IL-1 receptor associated kinase
ITAM	Immunoreceptor tyrosine-based activation motif
ITIM	Immunoreceptor tyrosine-based inhibitory motif
L-Ara4N	4-amino-4-deoxy-L-arabinose
LBP	Lipopolysaccharide binding protein
LPS	Lipopolysaccharide
Mal	MyD88 adaptor-like
MyD88	Myeloid differentiation factor 88
NK	Natural killer
PAMP	Pathogen associated molecular pattern
pEtN	Phosphoethanolamine
phox	NADPH phagocyte oxidase
PP	Peyer's patches
RNI	Reactive nitrogen intermediate
ROI	Reactive oxygen intermediate
SARM	Sterile alpha HEAT-Armadillo motifs
SIF	<i>Salmonella</i> induced filament
SPI	<i>Salmonella</i> pathogenicity island
SCV	<i>Salmonella</i> containing vacuole
TGN	Trans Golgi network
TIR	Toll-interleukin-1 receptor
TLR	Toll-like receptor
TNF	Tumour necrosis factor
TRAF	TNF receptor associated factor
TRAM	TRIF-related adaptor molecule
TRAPC	Triggering receptor expressed on antigen presenting cells
TREMs	Triggering receptor expressed on myeloid cells
TRIF	TIR-related adaptor protein inducing interferon
T3SS	Type III secretion system
VAP	Vacuole associated actin polymerization

1 INTRODUCTION

1.1 SALMONELLOSIS

Salmonellae are Gram-negative bacteria with an ability to persist and cause disease in a wide range of different hosts (202). The genus consist of two different species, *Salmonella bongori* and *Salmonella enterica*, which are further divided into eight different subspecies designated subspecies I, II, IIIa, IIIb, IV, V, VI and VII (27). *S. bongori* constitutes subspecies V whereas all others belong to *S. enterica*. The different subspecies are further subdivided into approximately 2500 serovariants most of which belong to *S. enterica* subspecies I (100). *S. bongori* is associated with infection of cold blooded animals (100) and lies beyond the scope of this thesis. Serovariants capable of infecting mammals mainly belong to subspecies I and cause a variety of diseases ranging from mild gastroenteritis to severe systemic infections, including typhoid fever (100, 180). In humans typhoid fever is caused by the human specific serovar Typhi. The disease is characterised by fever, diarrhoea (30-50% of reported cases) headache, muscle pain, loss of appetite, abdominal pain and enlarged liver and spleen due to bacterial replication in these organs (180, 203). Typhoid fever poses a serious public health problem in developing countries. World wide *S. enterica* serovar Typhi is reported to cause around 22 million cases of typhoid fever leading to approximately 220 000 deaths annually. The number of cases/deaths are most likely highly underestimated due to insufficient reporting of cases in these countries (19, 180). Infection of mice with *S. enterica* serovar Typhimurium (*S. Typhimurium*), which causes gastroenteritis in humans, gives rise to a systemic disease in mice which in many aspects resembles human typhoid fever (150, 180). Thus *S. Typhimurium* infection of mice and mouse-derived cells constitute a model system for human typhoid fever. Furthermore, due to its relatively short generation time, the ease by which *Salmonella* can be genetically manipulated, and the availability of complete genome sequences make *S. Typhimurium* suitable as a model organism for intracellular bacterial infections in general. The scenarios described below concerns the mouse infection model for *S. Typhimurium*.

1.2 PATHOGENESIS AND IMMUNE RESPONSES TO INFECTION

1.2.1 Infection and systemic dissemination

In both mice and men *Salmonella* spreads via the faecal-oral route. A proportion of the bacteria survives the acidic pH of the stomach and, in mice, reaches the distal ileum and caecum where they invade M-cells and endothelial cells of the intestinal epithelium. After breaching the epithelial barrier bacteria colonize the underlying Peyer's patches (PP) where they encounter resident phagocytic cells such as macrophages and dendritic cells (DCs) (232). Additionally, the intestinal epithelium responds to infection by producing various pro-inflammatory cytokines, notably IL-8, which leads to recruitment of neutrophils and macrophages (53). Having survived this first encounter with host immune responses, bacteria enter the mesenteric lymph nodes from where they disseminate to the liver and spleen (232). To what extent bacteria exist free in blood and/or lymph, or reside shielded within phagocytic cells while

disseminating is not well established. If free in the blood *Salmonella* would be exposed to the antibacterial actions of the complement system. Thus, as *Salmonella* is able to survive and replicate within macrophages, it would be beneficial if these cells could be exploited for transport to systemic sites. *Salmonella* has been shown to, to a small extent, be taken up directly from the intestinal lumen by CD18⁺ phagocytes and it has been suggested that *Salmonella* may be transported to systemic sites shielded in these cells (191, 233). During infection of mice with an invasion-deficient mutant tagged with green fluorescent protein (GFP), GFP-expressing bacteria exclusively resided within CD18⁺ cells when present in the blood (233). As this study only used invasion-deficient bacteria it is not possible to conclude whether the majority of wild type *Salmonella*, if the bloodstream is the main route of systemic dissemination, exists free in the blood or reside in phagocytic cells. In addition to shielded transport in the CD18⁺ phagocytes taking up bacteria directly from the intestinal lumen, it is possible that invading bacteria are taken up by phagocytes in the underlying tissue and are transported to systemic sites within these cells. Thus it would be interesting to study the location of tagged wild type *S. Typhimurium* in the blood stream.

1.2.2 Innate immune responses controlling the infection

Both neutrophils and macrophages are recruited to infected organs and several studies have shown that both cell types are important for control of the infection and survival of the host (45, 46, 143, 176, 205, 230). However, macrophages in the liver and spleen seem to be the main host cells exploited for bacterial residence and replication (194, 199). Thus, although macrophages play a crucial role in controlling the infection they also represent an important site for bacterial replication and mutants of *S. Typhimurium* that are unable to replicate inside macrophages are avirulent (62).

The infection triggers production of pro-inflammatory cytokines. TNF- α (mainly produced by neutrophils and macrophages) and IFN- γ , both of which activate and thus enhance the antibacterial activities of macrophages, are crucial for control of the early stages of infection (172). Macrophage activation by TNF- α and IFN- γ trigger expression of the inducible nitric oxide synthase (iNOS) responsible for production of nitric oxide (NO) (66, 204). IFN- γ additionally triggers expression of the NADPH phagocyte oxidase (phox) and MHC-II thereby promoting induction of the oxidative burst and antigen presentation to T-cells respectively (204). Thereby IFN- γ together with TNF- α trigger of the two most important defence mechanisms to *Salmonella* infection (151, 209, 234). IL-12 and IL-18 secreted by activated macrophages and DCs have also been shown to be important presumably by triggering and enhancing the production of IFN- γ (53, 217). NK cells, NKT cells and T-cells have all been reported to produce IFN- γ during *Salmonella* infection but the relative importance of each cell type during the earlier stages of infection is not clear (120). At later stages of infection however, IL-12 mediated maintenance of IFN- γ production from CD4 T-cells is crucial for clearance of the infection (113). In addition to NK cells, NKT cells and T-cells, macrophages and neutrophils have been shown to produce IFN- γ in response to *Salmonella* infection *in vivo*. However the importance of these phagocyte sources for control of infection is not clear (120).

The complement system consists of a collection of proteins present in the blood, which may be activated through a cascade of enzymatic events during infection. Activation, which can be antibody dependent (classical pathway) or antibody independent (alternative and lectin pathways), leads to activation of factor C3. Activated C3 opsonizes bacteria and may thereby facilitate phagocytosis. Additionally, other components of the complement system have, in their active form, a chemoattractive effect on neutrophils, and complement activation via the classical pathway or via the lectin pathway may cause bacterial lysis by assembly of complement factors into the membrane attack complex.

The level of C3 activation by *Salmonella* has been implicated to associate with bacterial virulence. However, this suggestion was initially based on indirect evidence where C3 activation *in vitro* was compared to virulence *in vivo* (137, 138). C3 activation has also been shown to affect bacterial clearance from the bloodstream and to participate in the control of the infection (139, 174). However, existing *in vivo* data regarding the role of C3 during infection with *S. Typhimurium* have been obtained from studies on mice challenged by the intravenous route of infection (139, 174), a process that does not represent the normal infection route. Thereby the relevance of C3 activation during a normal per oral infection is unclear. Complement activation by *Salmonella* is known to occur via the alternative pathway (137, 138). In a study by Warren *et al.* however, mice deficient in C1q, a component required for activation of the classical pathway, showed increased susceptibility to infection with *S. Typhimurium*. Interestingly the increased susceptibility seemed to be unrelated to C1q dependent activation of the complement cascade and it was hypothesized that C1q may affect macrophage bacterial killing mechanisms (229). Taken together existing data do not provide a clear picture regarding the role of the complement system during *Salmonella* infection and more studies are needed to settle this issue.

1.2.3 Adaptive immunity and clearance of the infection

A small percentage of splenic DCs contain bacteria during *Salmonella* infection. As material from *Salmonella*-induced apoptotic macrophages are phagocytosed by both bystander DCs and bystander macrophages but presented to T-cells only by bystander DCs, it has been suggested that DCs rather than macrophages are the antigen presenting cells responsible for triggering of the adaptive response necessary for clearance of the infection (239). The requirement of an efficient T-cell response for clearance of *S. Typhimurium* and survival of the host is well established (149, 163, 190). Depletion experiments and transfer of specific subsets of T-cells from vaccinated animals have shown that CD8 T-cells play a role but CD4 T-cells are more important (152, 171, 185). Regarding B-cells and the antibody response the picture is less clear. *Salmonella* infection induces a strong antibody response (28) yet the importance of this response seems to vary depending on the susceptibility of the mouse strain used, the virulence of the bacterium and the route of infection (163). However, from experiments using B-cell deficient mice, it seems clear that during infection with virulent wild type *Salmonella* of a susceptible host, B-cells play an important role in controlling the infection (164).

1.3 VIRULENCE FACTORS

Salmonella uses a number of different virulence factors to establish infection and cause disease. Many of these are encoded within *salmonella* pathogenicity islands (SPIs). Pathogenicity islands are genomic elements, present in pathogenic bacteria and absent in non-pathogenic bacteria, coding for genes required for virulence. They are believed to have been acquired by horizontal transfer indicated by their altered GC content compared to the rest of the bacterial chromosome and that they often are flanked by tRNA genes, which are known hot-spot sites for insertions (147). To date more than 15 different SPIs have been identified in *S. enterica* differing in their distribution between different serovars (97, 206, 237). SPI-1 and 2, which are required for invasion of the intestinal epithelium and survival/replication within host cells respectively, are best characterized and encode two different type III secretion systems (T3SSs) and their corresponding effector proteins (68, 98, 162, 179, 208). These systems mediate transfer of proteins from the bacterial cytoplasm into the host cell cytosol, enabling *Salmonella* to manipulate the host cell thus favouring infection and bacterial survival/replication (90). SPI-3 and SPI-4 have been suggested to participate in survival within macrophages (13, 22, 244). SPI-5 encodes effector proteins for both SPI-1 and SPI-2 and thus contributes to both invasion of the host and intracellular survival/replication of *Salmonella* (121). Some virulence factors are encoded by genes on prophage elements integrated into the bacterial chromosome. The *gipA* gene encoded by the prophage Gifsy-1 was shown to be required for bacterial replication in PP. GipA is however dispensable for epithelial invasion and systemic disease during intraperitoneal infection of mice (214). The prophage Gifsy-2 on the other hand is of major importance for virulence (64), apparently mediated by *sodCI*, encoding a superoxide dismutase which is involved in protection against oxidative stress (50, 61), and *gtgE* whose function is unknown (101). Additional virulence factors worth mentioning are the lipopolysaccharide (LPS), which will be discussed in more detail below, and the *spv* genes. The *spvRABCD* genes are expressed on the virulence plasmid of *S. Typhimurium*, and have been shown to be important for bacterial virulence, most likely by affecting the ability to replicate within phagocytic cells in the liver and spleen (95). To date a function has been ascribed only for SpvR, which regulates *spv* transcription (34, 218), and SpvB which is a mono-ADP-ribosyl transferase causing actin depolymerization (135, 182, 223). Both SpvR and SpvB are important for virulence in mice whereas SpvA is dispensable (195). The mechanism by which the SpvB-mediated actin depolymerization contributes to virulence is not known. The role of SpvC and SpvD is unclear but they may partially contribute to virulence (195).

Virulence factors of specific relevance for this thesis; SPI-1, SPI-2, the LPS and defence mechanisms against oxidative and nitrosative stress, as well as virulence gene regulation is discussed in more detail below.

1.3.1 SPI-1

The SPI-1 T3SS is required for efficient invasion of the intestine and colonization of PP (68, 144, 165). Secretion of the SPI-1 effector proteins SopE and SopE2 into the host cell cytosol leads to activation of the Rho-family GTPases Cdc42 and Rac1 (91, 215). In their active form Cdc42 and Rac1 mediate actin rearrangements and membrane ruffling, which facilitate bacterial uptake (40). The inositol phosphate phosphatase

SopB acts in concert with SopE and SopE2 to induce membrane ruffling and bacterial uptake. In addition to its phosphatase activity SopB has been suggested to activate Rac1 (251). Additionally SipA and SipC have been reported to, in a cooperative manner, be important for formation of the membrane ruffles, mediated by their ability to nucleate and bundle F-actin filaments (39, 156). The GTPase activating effector SptP inactivates Cdc42 and Rac1 thus ensuring reestablishment of an intact host cell membrane (69). When *Salmonella* reaches the PP SipB-mediated induction of caspase-1-dependent apoptosis of macrophages has been shown to be essential for colonization of PP and for the ability to disseminate to deeper tissues and cause systemic disease (165). These results were however recently challenged by Lara-Tejero *et al.* who were unable to detect any differences in PP colonization or systemic dissemination by *S. Typhimurium* in wild type or caspase-1 deficient mice (131). Additionally, in contrast to Monack *et al.* who reported increased resistance to *S. Typhimurium* infection in caspase-1 deficient mice (165), lack of caspase-1 was shown to increase the susceptibility to infection (131). The reason for these contradicting results is unclear but could possibly relate to use of different mouse strains. Evidently more studies are needed to establish the role of caspase-1 during infection with *S. Typhimurium*.

1.3.2 SPI-2

The SPI-2 T3SS secretes effector proteins across the vacuolar membrane of the *Salmonella* containing vacuole (SCV), the specialised vacuolar compartment in which *Salmonella* resides during intracellular stages of infection, into the host cell cytosol (90). SPI-2 is essential for intracellular survival and replication of *Salmonella* (42, 179, 231) evidently through interference with phagosomal maturation and macrophage oxidative and NO responses, mediated by secreted effector proteins (1, 231). The role of SPI-2 during infection will be discussed in more detail in section 1.4.

1.3.3 The lipopolysaccharide (LPS)

LPSs, complex highly conserved glycolipids, constitute the major component of the outer membrane of Gram-negative bacteria and are important for membrane stability. The LPS molecule can be divided into three different parts; the glycolipid lipid A which anchors the LPS to the outer membrane, the oligosaccharide core and the polysaccharide O-antigen (Fig. 1). Mutants that express LPS devoid of the O-antigen are designated as “rough” due to a rough colony morphology when grown on LB agar plates, whereas the wild type LPS is designated as “smooth” (241). The LPS also constitutes a conserved pattern molecule which is recognized by the host, mainly by Toll-like receptor (TLR) 4, leading to induction of innate immune responses (65). The consequences of this are discussed in section 1.4.3.1. Although LPSs are highly conserved molecules they are far from being static; the sugar composition of the core region and the O-antigen as well as the number of acyl chains on lipid A differ between different bacteria. As a consequence of this LPS from different bacteria differ in their bioactivity (225). Additionally, *Salmonella* modifies its LPS in response to environmental conditions to increase its fitness.

Salmonella Lipid A is known to be decorated with 4-amino-4-deoxy-L-arabinose (L-Ara4N), phosphoethanolamine (pEtN), palmitate and 2-hydroxymyristate, and may

also be deacylated (57, 189). L-Ara4N, pEtN and palmitate are added to lipid A during growth in acidic low $[Mg^{2+}]$ medium and during growth in macrophage-like cells but not when bacteria are grown in tissue culture medium or in a high $[Mg^{2+}]$ mildly alkaline medium. The 2-hydroxymyristate decoration on the other hand is present under all these growth conditions (74) and the role of this modification in bacterial virulence is not known (225). L-Ara4N and pEtN decoration of phosphate groups on lipid A (L-Ara4N and pEtN) and the core region (pEtN) result in increased resistance to cationic antimicrobial peptides (CAMPs) (84, 133). Genes mediating the L-Ara4N modification have been shown to be required for full bacterial virulence in BALB/c mice. (85). As addition of L-Ara4N and pEtN renders the bacterial surface less anionic it has been assumed that the increased resistance to CAMPs is mediated by a decreased heterophilic attraction. In a study by Tamayo *et al.* lack of L-Ara4N dramatically decreased the resistance to CAMPs and virulence *in vivo*, whereas lack of pEtN only had a slight effect on CAMP resistance and bacterial virulence was essentially unaffected (221). As both modifications render the bacterial surface less anionic, they argued that the resistance to CAMPs is likely to be mediated by a mechanism that is not based on charge. However, Zhou *et al.* have reported that, at least under certain conditions, pEtN modifications occur to a less extent than the L-Ara4N modification (252), and Tamayo *et al.* did not provide data to show whether the L-Ara4N and pEtN modifications occurred to the same extent. In other bacteria, unable to modify lipid A with L-Ara4N however, the pEtN modification is important for resistance to CAMPs. Thus a likely explanation for the minor effect on CAMP resistance and lack of effect on virulence *in vivo*, observed for *Salmonella* in the absence of pEtN, is a compensatory increase in L-Ara4N modification (225).

The number of acyl chains on lipid A may differ and lipid A can be both acylated, by addition of palmitate, or deacylated to generate hepta- and penta-acylated lipid A respectively. Like the L-Ara4N and pEtN modifications, the addition of palmitate leads to increased CAMP resistance thought to be mediated by increased membrane density (86). Both penta- and hepta-acylated lipid A exhibit reduced ability to trigger signalling through TLR-4 and it has been suggested that these modifications occur to reduce host innate antibacterial responses (117). It has also been shown that not only the number but also the length of the acyl chains, as well as their position on lipid A, affect TLR-4 signalling (116). Disruption of the bacterial membrane was shown to induce deacylation and formation of penta-acylated lipid A and it was hypothesized that in the case of bacterial membrane damage within the host release of penta-acylated LPS may reduce TLR-4 signalling and thus benefit the bacteria (118). However, deacylation does not take place in the presence of L-Ara4N (118), which is added to lipid A in macrophage-like cells (74). Palmitoylation giving rise to hepta-acylated lipid A, which can co-exist with the L-Ara4N modification, also gives reduced TLR-4 signalling (117) and should serve the same function if released during the course of membrane damage. Possibly, penta-acylated LPS is required only under conditions other than those encountered within the host, a hypothesis that is strengthened by the finding that a mutant unable to deacylate lipid A is not attenuated in the mouse infection model (16).

Salmonella is evidently able to modify its lipid A in a multitude of ways in response to environmental stimuli. However the specific composition of lipid A under a given

condition is not fully understood. Possibly heterogeneity may be desirable from a bacterial point of view to maximise protection against antibacterial host responses.

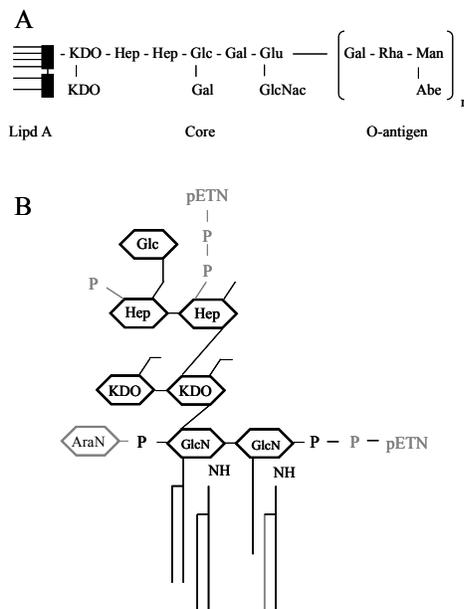


Figure 1. The full length LPS structure is shown in **A**. **B** shows lipid A and the inner core with the different modifications shaded in grey.

In addition to flagellin, Lipid A is considered as the major inducer of host responses during *Salmonella* infection (104, 225), and its modification is evidently important for increased bacterial resistance to host responses. However the core region and the O-antigen are also important for bacterial virulence and protection from host responses. Despite providing the bacterial surface with negative charge, phosphorylation of the core heptose region is required for resistance to polymyxin, a peptide antibiotic thought to act by the same mechanism as CAMPs, possibly mediated by affecting membrane stability. Phosphorylation of the core is furthermore required for virulence *in vivo* (247). The host complement system is activated at the tip of the LPS. By providing a distance between the site of complement activation and the bacterial surface the O-antigen mediates protection against the membrane attack complex (76). The composition of the polysaccharide backbone as well as the type of side chains is highly variable both between and within Gram-negative bacterial species e.g in *Salmonella* more than 50 different variants are known (134). When the abequose (Abe) side chain of *S. Typhimurium* (Fig.1) was exchanged for the tyvelose side chain found in *S. enterica* serovar Enteritidis, *S. Typhimurium* showed increased activation of complement, increased phagocytosis by macrophage-like cells and reduced virulence during intravenous infection of mice (112, 137-139). Additionally, expression of complete smooth LPS is a prerequisite for bacterial virulence, not only for *Salmonella*

but also for other enterobacteria such as *Yersinia enterocolitica*. Strains of both *Y. enterocolitica* and *S. Typhimurium* which lack the O-antigen display a reduced ability to colonize the murine host and a reduction in virulence in mouse infection models (5, 173, 211, 224). However recent studies from our laboratory (Paper I) and others (21, 130, 238) indicate that under certain conditions bacteria may benefit from expressing reduced amounts of O-antigen. This will be discussed in more detail in the Results and Discussion section for Paper I.

1.3.4 Defence mechanisms against oxidative and nitrosative stress

To be able to replicate within the host and cause disease *Salmonella* must withstand the host immune responses such as the oxidative burst and NO production of macrophages (151, 209, 234). Bacterial defence mechanisms against these host responses will be discussed in section 1.4.2.

1.3.5 Virulence regulation

During the course of infection and spread to new hosts *Salmonella* has to be able to survive/replicate outside the host e.g. in food, water and soil, in the host gastrointestinal tract, while passing through epithelial cells and finally inside macrophages. Survival/replication under such diverse conditions requires tight gene regulation ensuring that the appropriate genes are expressed in the correct environment. Use of alternative σ -factors may alter promoter preferences of the RNA polymerase and thereby also the gene expression profiles (192). The alternative σ -factor RpoS is required for survival under stress conditions such as starvation and exposure to low pH as well as virulence *in vivo* (59, 177, 242). As deprivation of nutrients and acidic pH are conditions met by the bacteria inside macrophages it was hinted between the lines that RpoS would be required for survival and replication inside these cells (59). However, it was later shown that *S. Typhimurium* LT2 strains, which carry a defect *rpoS* gene, as well as an *rpoS* null mutant survive inside J774-A.1 macrophage-like cells and bone marrow-derived murine macrophages to the same extent as an isogenic strain carrying the wild type allele (242). Survival/replication inside macrophages was later shown to largely depend on another alternative σ -factor, RpoE (106). In addition to intra-macrophage survival, RpoE has also been shown to mediate resistance to antibacterial peptides (106) and to play an important role during nutrient deprivation (119, 222), virulence *in vivo* and resistance to oxidative stress both *in vitro* and *in vivo* (222). However as the situation *in vivo* is much more complex than the situation in cell cultures, it is fully possible that RpoS is important for intracellular replication *in vivo*.

Regulation of virulence genes is governed by sensing of environmental changes. This is often mediated by two-component signal transduction systems. These systems consist of a response regulator whose activity is regulated by an integral membrane protein that senses changes in the environment. Activation of the sensor leads to autophosphorylation followed by transfer of phosphate to and thus activation of the response regulator, which in turn activates or repress expression of different subsets of target genes (15).

The PhoP/PhoQ two-component system responds to changes in $[Mg^{2+}]$ and $[Ca^{2+}]$. It is activated by low concentrations, conditions which are encountered within the SCV, and inhibited by high (“extracellular”) concentrations (72). PhoP/PhoQ has also been reported to respond to acidic pH within macrophages (6), and an *rpoS/phoP* double mutant was shown to be more sensitive to acidic pH than an *rpoS* single mutant (14). Garcia Véscovi *et al.* on the other hand reported that induction of PhoP/PhoQ regulated genes in response to low pH occurs independently of PhoP/PhoQ (72). Thus the results regarding induction of PhoP/PhoQ in response to low pH are inconsistent and the use of differential experimental setups in the different reports makes it difficult to definitely conclude whether or not acidic pH has a role in the activation of the PhoP/PhoQ system. Nevertheless, the PhoP/PhoQ system is important for intracellular survival and virulence, and regulates the expression of several virulence functions, e.g. it activates transcription of *sodCI*, which is involved in protection against oxidative stress (77). Via the action of PmrD, the PhoP/PhoQ system activates the PmrA/PmrB two-component system which regulates genes mediating the modifications of lipid A that render *Salmonella* more resistant to CAMPs (81, 84, 124, 133). As mentioned above PmrA and PmrA-controlled genes mediating these modifications have been shown to be required for full bacterial virulence in BALB/c mice during per oral but not intraperitoneal infection (85). It was therefore suggested that this modification would be required for defence against antibacterial host responses present within the intestine. Recently it was reported that genes required for the L-4AraN modification are expressed not only inside murine macrophage-like cells and mouse liver and spleen, but also in the intestine of BALB/c mice in a PhoP and PmrA dependent manner (158). This was a surprising finding and contradictory to the dogma that PhoP and PhoP dependent induction of PmrA are induced exclusively during intracellular stages of infection. Possibly these systems may be induced differentially under different conditions. Furthermore, considering the complex network of regulatory systems in *Salmonella*, one can envision that induction of genes controlled by these systems is more complex than what is known to date and that a combination with other regulatory systems may control which PhoP regulated genes that are induced under a given condition. Intestinal expression of the L-4AraN modification appears logical in the sense that it would mediate protection against CAMPs present in the intestine. Interestingly, the PhoP/PhoQ system was recently reported to respond to the presence of antibacterial peptides, implying that the changes in surface composition that mediate resistance to antibacterial peptides are induced directly by sensing their presence. (9). Possibly sensing of CAMPs is the inducer of PhoP regulated genes in the intestine. The PmrA/PmrB system also responds to mildly acidic pH or high iron concentrations independently of PhoP/PhoQ (213, 246). Within the host, high iron concentrations are encountered only transiently in the gastro intestinal tract but the relevance of this for PmrA/PmrB induction during infection is unclear. Furthermore the induction of PmrA in the intestine reported by Merighi *et al* was indicated to occur independently of the concentration of iron (158). However, outside the host high iron concentrations are encountered e.g. in soil and the PmrA/PmrB mediated modifications of lipid A have been shown to promote bacterial survival in this environment (175). Thus, the PmrA/PmrB system is important for adaptation to environmental conditions both inside and outside the host.

Expression of the SPI-1 T3SS and its effector proteins have been shown to be induced by high osmolarity, low oxygen and slightly alkaline pH, conditions which are all found in the small intestine. Additionally growth in rich medium to the late logarithmic phase of growth induces SPI-1 thus facilitating the study of SPI-1 functions (144). The PhoP/PhoQ system is known to mediate inhibition of SPI-1 by repressing expression of the main activator of SPI-1, the transcription factor HilA (11). How *Salmonella* senses the environmental conditions which induce SPI-1 is not completely understood. SirA, a member of the two-component response regulator family known to act together with the membrane sensor BarA, has been shown to participate in SPI-1 induction (7). The OmpR/EnvZ two-component system responds to changes in osmolarity as well as low pH and has been shown to be involved in the regulation of SPI-1 (145). Induction of SPI-1 expression is mainly regulated by the transcription factor HilA. SPI-1-inducing conditions activate the HilD transcription factor, which activates expression of *hilA*. HilA in turn, either directly or by inducing the transcription factor InvF, activates transcription of genes within SPI-1 (7). HilD and HilC are also reported to activate InvF independently of HilA (3). However a *hilA* mutant is essentially non-invasive (10, 21) and the role of HilA independent mechanisms is unclear.

The SsrA/SsrB two-component system responds to low $[Ca^{2+}]$, low osmolarity and acidic pH, environmental conditions encountered within the SCV, and is essential for induction of SPI-2 (73). It is not known whether SsrA senses these signals directly or if another sensor is involved. Additionally, expression of SPI-2 partly depends on the OmpR/EnvZ two-component system and the transcriptional regulator SlyA, both of which respond to low osmolarity and low $[Ca^{2+}]$ (73, 141). Additionally, the PhoP/PhoQ system has been reported to induce expression of SPI-2 *in vitro* (51) and in macrophage-like cells (245), indicating PhoP/PhoQ regulation of SPI-2. Another study reported that *ssrA/ssrB* is induced independently of PhoP/PhoQ in macrophage-like cells (132, 160). Beuzon *et al.* later reported that PhoP/PhoQ and SPI-2 contribute independently to virulence *in vivo* (18). However the data were not conclusive and a partial role for PhoP/PhoQ cannot be excluded based on these data. Moreover, PhoP was recently shown to regulate transcription of *ssrB* and to bind to the *ssrB* promoter region both *in vitro* and in macrophages (20). Thus existing data do not provide a clear cut picture regarding the role of PhoP/PhoQ in SPI-2 regulation. Taken together it seems like PhoP/PhoQ may have a partial effect on SPI-2 induction. If so, that would explain the apparently conflicting data obtained from studies on macrophage-like cells as different SPI-2 genes were studied in the different reports (132, 160, 245).

Evidently virulence gene regulation in *S. enterica* serovar Typhimurium is highly complex with a multifaceted network of regulators responding to different stimuli. The details on how and which of the different regulators that interact to ensure expression of the appropriate set of genes in a given environment is far from clear.

1.4 SALMONELLA AND THE MACROPHAGE

1.4.1 Macrophage responses to infection

Upon infection or tissue damage monocytes circulating in the bloodstream migrate into the infected/damaged tissue where they differentiate into macrophages. Macrophages

are professional phagocytic cells serving both a cleaning function, ingesting and degrading e.g. apoptotic and necrotic host cells, as well as pro-inflammatory antimicrobial functions (79). Upon phagocytosis the ingested material are taken up into a phagosome which matures, through ordered sequential vesicle fusion/fission events with early endosomes, late endosomes and finally with lysosomes, into a highly microbicidal phagolysosome. The maturation is accompanied by a progressive decrease in phagosomal pH and acquisition of hydrolytic enzymes, such as cathepsin D. Additionally within the phagosome/phagolysosome microbes are deprived of nutrients and exposed to reactive oxygen and nitrogen intermediates (ROI and RNI) (240). The regulation of the fusion/fission events leading to formation of the phagolysosome is largely unknown. It is thought to be partly controlled by members of the Rab family of small GTPases. Rab5 is present on early phagosomes and is believed to mediate fusion events with later endosomal compartments through its downstream effector early endosomal antigen 1 (EEA1) (184). Phagosomal maturation occurs along microtubules, which together with actin filaments constitute the cytoskeleton of eukaryotic cells (240). Microtubules are polarized tracks which guide organellar traffic within the cell. Movement along microtubules in the + (towards the cell surface) or - (towards the centre of the cell) direction is driven by the motor proteins kinesin and dynein respectively (240). Rab7 present on late endosomes has been shown to be recruited to intermediate phagosomes and to mediate interaction between the phagosome and microtubule, through its effector Rab interacting lysosomal protein (RILP), thereby promoting phagosomal movement and formation of phagolysosomes (92).

ROI, produced during the oxidative burst, and production of NO and other RNI are the most important macrophage defence mechanisms during infection with *S. Typhimurium* of macrophage-like cells, primary macrophages as well as of mice *in vivo* (55, 151, 209, 234). ROI and RNI have been shown to mainly act sequentially during the infection with the bactericidal ROI being important initially and the bacteriostatic RNI at later time points (151, 234). For production of ROI the macrophage relies on phox, which is composed of seven different subunits which assemble in the phagosomal membrane upon macrophage activation to produce superoxide (108). Superoxide passes through the outer membrane of Gram-negative bacteria and may damage periplasmic proteins but is unable to penetrate the cytoplasmic membrane. However, in the periplasm superoxide undergo both spontaneous and enzyme-mediated dismutation to generate the more reactive hydrogen peroxide which is able to enter the bacterial cytoplasm. Hydrogen peroxide may react further to generate the even more toxic hydroxyl radical and, in combination with NO, peroxynitrite (108). In phagocytic cells, NO is produced by iNOS from L-arginine and oxygen in a NADPH dependent process, and may undergo further reactions to generate an array of RNI (58, 250).

NO is highly diffusible and toxic not only to microbes but also to the host, and its production therefore needs to be tightly regulated (250). NF- κ B is the main transcription factor involved in induction of iNOS transcription. Whereas direct interaction between NF- κ B and the IFN- γ inducible transcription factor IRF-1 has a synergistic effect on iNOS expression, the transcription factor STAT3 interacts with NF- κ B to inhibit transcription of iNOS (201, 249). Protein dimerization is necessary for iNOS activity and depends on binding of L-arginine, heme and tetrahydrobiopterin

(BH₄) as well as the formation of a disulphide bridge that covalently links the two monomers. In addition to its requirement for iNOS dimerization, L-arginine has been shown to control iNOS translation. Reduced levels of L-arginine inhibits translation without affecting the level of iNOS mRNA (54). The activity of iNOS is also controlled by protein-protein interactions. Kalirin and NAP110, expressed in neuronal cells and macrophages respectively, interact directly with iNOS to inhibit its activity (250). On the other hand Rac2, a member of the Rho family of small GTPases which is also the driving force for phox, has been shown to interact with iNOS to increase its enzymatic activity and was indicated to affect iNOS distribution within macrophage-like cells (129).

The distribution/localisation of iNOS has been suggested to constitute yet another possible level of control of iNOS activity as it was shown that iNOS partly localises to a vesicular compartment in macrophages (236, 243). That is, vesicular localisation would enable recruitment of iNOS-containing vesicles to phagosomes upon infection, thereby focusing the response onto the bacterial localisation. While Webb *et al.* observed iNOS to associate with the cortical submembranous actin as well as being localised to cytoplasmic vesicles and free in the cytoplasm, they could not detect any relocalisation or recruitment to phagosomes of iNOS upon particle ingestion or infection with *S. Typhimurium* (236). Later iNOS has been shown to associate with latex bead-containing phagosomes whereas both *S. Typhimurium* and *Mycobacterium tuberculosis* have been reported to dislocate iNOS from the SCV/phagosomal membrane (38, 161). A possible explanation for the contradicting results regarding iNOS localization and its recruitment to phagosomes may be that iNOS distribution and tendency to associate with phagosomes depends on the activation state of the cells, a possibility that has been suggested previously by Webb *et al.* (236). Additionally iNOS was recently shown to form aggresomes in both human and murine macrophage cell lines (123). Aggresomes are discrete cytoplasmic inclusion bodies whose formation is triggered by the synthesis of misfolded proteins. However, this did not appear to be the rationale for formation of iNOS-aggresomes. Aggregation of iNOS was shown to limit iNOS mobility within the cell and it was suggested that iNOS-aggresome formation occurs to control iNOS activity (123). However no data showing the enzymatic activity of aggregated iNOS was presented and the biological relevance of iNOS aggresome formation remains to be determined. Taken together, existing data on iNOS localisation and its possible redistribution upon phagocytosis do not provide a clear picture and more studies are evidently needed to settle this issue.

1.4.2 Bacterial defence mechanisms and manipulation of host responses

Protection against host antibacterial mechanisms occurs at two levels, *i*) induction of stress responses which detoxify ROI and RNI or repair the damage imposed by these substances and *ii*) manipulation of host responses in order to create a less hostile environment which promotes bacterial survival and replication.

Salmonella possesses several different systems which mediate detoxification of harmful substances, and DNA damage-repair mechanisms. The superoxide dismutase SodCI, shown to be an important virulence factor, converts superoxide into hydrogen peroxide

(50, 125). Although this ROI is more toxic than superoxide, its formation is a necessary step in the superoxide-detoxification process (108). Exposure to hydrogen peroxide activates the transcription factor OxyR, which induce expression of genes involved in protection to oxidative stress, e.g. *katG* encoding hydrogen peroxidase (HP) I, a catalase which reduces hydrogen peroxide to generate water and oxygen (80). However a mutant lacking HPI and HPII, the only other catalase known to be expressed by *Salmonella*, is unaffected for survival in macrophages and virulence in mice (31). It is thus unclear what mechanisms *Salmonella* uses to resist hydrogen peroxide in macrophages *in vitro* or *in vivo*. Glucose-6-phosphate dehydrogenase has been shown to be important for protection against hydrogen peroxide and an NO donor compound *in vitro* as well as virulence in mice, presumably through its participation in the production of NADPH which serves as a source of reducing equivalents (146). In the closely related bacteria *Escherichia coli* the glucose-6-phosphate dehydrogenase is regulated by the SoxR/SoxS system. However, this system has been shown to be dispensable for survival of *Salmonella* in phagocytic cells and virulence in mice (60). Hence expression of glucose-6-phosphate dehydrogenase is most likely induced by another regulator in *Salmonella*. DNA damage activates the RecA protein which induces expression of genes mediating DNA repair. This is known as the SOS response and ensures bacterial survival under DNA-damaging conditions (168, 200, 212, 227). RecA as well as the DNA-repairing enzyme RecBCD have been shown to be important for resistance to the macrophage oxidative burst and virulence *in vivo* (32, 35).

1.4.2.1 Manipulation of macrophage responses

As mentioned above, phagocytosis of a microbe is followed by phagosomal maturation into a highly bactericidal phagolysosome. *Salmonella* manipulates this development in order to generate a specialised vacuolar compartment, the SCV, which allows bacterial survival and replication. The biogenesis and details regarding the composition of the SCV is largely unclear. This is partly due to use of different cell types and bacterial strain backgrounds in existing studies. Knowledge regarding SCV maturation has largely been acquired from epithelial cells which are fundamentally different from macrophages. Certain aspects of SCV maturation may however be easier to study in epithelial cells whereby these cells may serve as a tool when deciphering the SCV maturation process. However, findings derived from epithelial cells need to be verified in macrophages, and, to avoid the risk of essential features of SCV maturation being missed, it is important to study this process also directly in macrophages. It seems clear that the SCV fuses with early endosomes, as evidenced by the transient acquisition of the early endosomal markers EEA1 and the transferrin receptor, in a Rab5 dependent manner in both epithelial cells and macrophages (1). These early markers are rapidly replaced by late endosomal markers such as Rab7, lysosomal glycoproteins e.g. LAMP-1, and the vacuolar ATPase which is responsible for phagosome acidification. SCV acidification is a requirement for secretion of SPI-2 effectors and thereby for bacterial replication (1, 103).

The function of the SPI-1 T3SS in *Salmonella* as well as T3SSs in other bacterial species, have been shown to depend on host cell cholesterol (94). At this point it is not clear whether the SPI-2 T3SS also requires cholesterol for proper function. However, bacterial replication, in epithelial cells as well as in macrophages, has been shown to

depend on the accumulation of host cell cholesterol around the SCV (36, 37). Another characteristic of the SCV, in both epithelial cells and macrophages, is the SifA dependent formation of membrane extensions from the vacuole known as *Salmonella* induced filaments (SIFs) (71, 122). SIFs are formed and extend towards the periphery of the cell along microtubules, and are required for maintenance of SCV membrane integrity (17, 29, 71). In addition to SifA, the SPI-2 effector SseJ has been shown to contribute to SCV membrane dynamics (196) and was recently shown to affect virulence *in vivo* (181).

The vesicles of the endosomal pathway as well as maturing phagosomes, are normally transported along microtubules in the cell to reach their intended target. *S. Typhimurium* has been shown to target the SCV to the Trans Golgi network (TGN) in epithelial cells (198). Retention of SCVs in this juxtannuclear position is required for bacterial replication in epithelial cells, and depend on the SPI-2-effector proteins SseF and SseG and their ability to interact with the microtubule network (127, 198). Furthermore, an *sseG* mutant exhibits reduced fitness in macrophage-like cells, primary peritoneal macrophages as well as in mice *in vivo*, thereby providing indirect evidence for the importance of *S. Typhimurium*-Golgi interactions in macrophages (99, 198). Microtubules were shown to accumulate around SCVs during infection of both epithelial cells and macrophages, a bacteria-driven process as indicated by the large dependency on bacterial protein synthesis. In epithelial cells, the accumulation of microtubules was accompanied by accumulation of both kinesin and dynein, a process shown to promote bacterial replication as well as being important for SCV membrane dynamics, including SIF-formation (82). However *Salmonella* has also been reported to inhibit the recruitment of kinesin to the SCV membrane (26). This may seem contradictory however excessive recruitment of kinesin to the SCV leads to SCV-displacement towards the periphery of the host cell and disruption of the SCV membrane presumably due to increased kinesin-mediated pulling force on the SCV (26). Hence, a balanced interaction of the SCV with both dynein and kinesin seems to be required for retention of the SCV in a juxtannuclear position, SCV membrane integrity and bacterial replication. Guignot *et al.* reported that the recruitment of dynein to the SCV depends on Rab7, possibly mediated by its downstream effector RILP (82). Rab7 is also required for SIF formation, SCV membrane integrity and bacterial replication (30, 82). Recruitment of Rab7 to the SCV membrane would thereby benefit the bacteria. The Rab7/RILP dependent recruitment of dynein to the SCV was confirmed by Marsman *et al.*, however these authors showed that this leads to fusion of SCVs with lysosomes and inhibition of bacterial replication (148). The latter study is based on experiments where RILP is overexpressed. Considering the balanced interaction of the SCV with both dynein and kinesin that seems to be required for proper maintenance of the SCV, and that RILP mediates interaction with dynein it is possible that the results by Marsman *et al.* are caused by a tilting of this balance due to overexpression of RILP. Additionally, *S. Typhimurium* was recently shown to interfere with the transport of vesicles from Golgi to the cell surface as evidenced by the accumulation of exocytic vesicles in the vicinity of SCVs. This process was shown to depend on the SPI-2 effector proteins SifA, SseF and SseG. It was suggested that the recruitment of exocytic vesicles may serve as a source for nutrients and membrane material (126).

SPI-2 has been shown to mediate formation of an F-actin meshwork around the SCV known as vacuole associated actin polymerization (VAP). VAP formation occurs in both epithelial and macrophage-like cells and was indicated to be important for intracellular replication of *S. Typhimurium* as well as for maintenance of the SCV membrane (157). However, after their initial appearance VAP formation in epithelial cells was shown to be reduced with time post infection (159). As mentioned in section 1.3, SpvB is a bacterial mono-ADP-ribosyl transferase which inhibits host cell actin polymerization by ADP-ribosylation of G-actin (135, 223). SpvB is important for virulence *in vivo* and replication within the mesenteric lymph nodes and the spleen (95). Although no defect for intracellular replication has been demonstrated for *spvB* mutant bacteria, *spvB* expression is induced during bacterial growth in macrophage-like cells *in vitro* (63, 96, 193) and the study by Heffernan *et al.* provides indirect evidence that SpvB enables growth within macrophages *in vivo* (95). This raises the question whether the virulence function of SpvB is related to VAP. However conflicting data exist regarding this (159, 207). Furthermore as the importance of VAP has been established only by the use of actin depolymerising substances which may have other adverse effects, it has been argued that these data should be interpreted with caution until the role of VAP can be confirmed by genetic evidence (83). Thus more studies are required to verify the importance of VAP and to determine how the actin depolymerising activity of SpvB contributes to virulence.

S. Typhimurium is also capable of excluding both pHOX and iNOS from the SCV in a SPI-2 dependent manner, thereby minimising the encounter with the highly antibacterial ROI and RNI produced by these enzymes (38, 235).

1.4.3 Receptors mediating recognition and/or uptake

Macrophages express a wide variety of receptors on their surface mediating recognition and/or phagocytosis. These include Fc receptors, complement receptors, scavenger receptors, C-type lectin receptors, TLRs and triggering receptors expressed on myeloid cells (TREM2) (2, 43, 78). Some of these recognise both host and pathogen derived ligands and are able to mediate either inhibitory or activating signals depending on the ligand. This can be exemplified by scavenger receptors which mediate inhibitory signals e.g. during phagocytosis of apoptotic host cells and activating signals while mediating phagocytosis of bacteria (2, 78). During an infection a pathogen is likely to be recognized simultaneously by multiple receptors. Additionally, certain infections e.g. with *Salmonella*, are associated with host cell apoptosis which may induce inhibitory signals upon phagocytosis of bacteria-containing apoptotic bodies (248). Thus a given macrophage may receive both inhibitory and activating signals in a given situation and the outcome, i.e. the activation state of the macrophage is likely to be the sum of all input signals. Of the receptors expressed on macrophages TLR-4 and TREM2 are of particular importance for this thesis and will be described in more detail below.

1.4.3.1 TLR-4

TLRs belong to a large group of receptors known as pattern recognition receptors due to their ability to recognise pathogen associated molecular patterns (PAMPs). The mammalian TLR family (so far) consist of ten human (TLR-1 to 10) and twelve murine (TLR-1 to 9 and TLR-11 to 13) TLRs (115). TLRs were initially considered as being expressed exclusively on the cell surface. Later however it has been shown that whereas e.g. TLR-1, 2 and 4 are expressed on the cell surface and are recruited to phagosomes upon activation, TLR-3, 7 and 9 are expressed intracellularly (4). TLRs are expressed by both immune and non-immune cells and recognize a wide variety of PAMPs from a broad range of pathogens. Ligand recognition is mediated by a leucine-rich repeat domain and triggers homo- or hetero-dimerisation depending on the specific TLR (4, 183). Receptor dimerisation triggers signalling via the cytoplasmic Toll-interleukin-1 receptor (TIR) domain through which they interact with TIR containing adaptor proteins to induce intracellular signalling. To date five TLR-associated adaptor proteins have been identified; myeloid differentiation factor 88 (MyD88), MyD88 adaptor-like (Mal), TIR-related adaptor protein inducing interferon (TRIF), TRIF-related adaptor molecule (TRAM) and sterile alpha HEAT-Armadillo motifs (SARM) (178). The response of the activated cell differs depending on which TLR that triggers the activation. The molecular basis for how different TLRs induce diverse responses is poorly understood but differential adapter usage is believed to be part of the mechanism by which the different TLRs discriminate between different pathogens (178).

TLR-4 is mainly known as an LPS receptor but has also been shown to recognise a variety of PAMPs in addition to LPS (4, 183). With its ability to respond to LPS, TLR-4 is the main inducer of host responses to Gram-negative bacteria (105, 186, 188). The details regarding LPS-TLR-4 interactions are poorly understood. LPS-mediated signalling through TLR-4 has been shown to depend on LPS binding protein (LBP), CD14 and MD2. According to the current model LBP binds to LPS and the LPS/LBP complex in turn binds soluble or membrane bound CD14 which presents the complex to TLR-4. Additionally TLR-4 needs to be bound to the secreted protein MD2 to be able to signal (65). TLR-4 uses (at least) four different adaptors which are thought to act in pairs, MyD88/Mal and TRIF/TRAM, with Mal and TRAM acting as bridging adaptors which recruit MyD88 and TRIF respectively upon receptor activation and dimerization (4, 178). MyD88 recruits IL-1 receptor associated kinase (IRAK) 4 and IRAK-1. Phosphorylation of IRAK-1 by IRAK-4 enables release of IRAK-1 from its inhibitor Toll-interacting protein (Tollip) and MyD88 where after IRAK-1 associates with TNF receptor associated factor 6 (TRAF-6). Signalling downstream of TRAF-6 leads to activation of the transcription factor AP-1 and early activation of NF- κ B which trigger the production of pro-inflammatory cytokines such as TNF- α and IL-1 β (65, 115, 178). Signalling mediated through TRIF/TRAM, known as the MyD88 independent pathway, appears to be more complex and is still incompletely understood. It seems clear that MyD88 independent signalling leads to activation of the interferon regulatory factor (IRF) 3 transcription factor, late activation of NF- κ B and production of IFN- β and iNOS (102, 169, 178). Although TNF- α was initially shown to be induced solely by the MyD88 dependent pathway a recent study suggests that TNF- α is produced also by the MyD88 independent pathway in an IRF-3 dependent manner. MyD88 independent production of TNF- α was shown to be required for the late

activation of NF- κ B in this pathway (47). It has also been suggested that two different pathways exist downstream of TRIF. One where TRIF, either directly or via RIP-1, interacts with TRAF-6 to activate NF- κ B, and one where IRF-3 and possibly also IRF-7 induces e.g. IFN- β expression (169). Adding to the complexity, the transcription factor IRF-5 has recently been shown to be required for triggering of the pro-inflammatory cytokines IL-6, IL-12 and TNF- α via the MyD88 dependent pathway (219).

Activation of TLR-4 triggers both the MyD88 dependent and independent pathways (65). The rationale for two separate signalling pathways downstream of TLR-4 is not known. However recent data may provide a clue. Jiang *et al.* have shown that macrophages from mice with non-functional CD14 respond differentially to smooth and rough LPS isolated from *Salmonella*. CD14 deficient macrophages were unable to trigger the MyD88 independent pathway and the MyD88 dependent pathway was triggered only in response to rough LPS (111). Another study has compared TLR-4 responses to LPS from different Gram-negative bacteria. This showed that the relative contribution of MyD88 dependent and independent signalling differed in the response to the different LPS (253). Although the biological relevance of this is not yet clear it opens up the possibility that TLR-4 may discriminate between LPS from different bacteria and it is intriguing to speculate that this may be used by the host to optimise the response to a specific Gram-negative bacterium.

Excessive triggering of pro-inflammatory cytokines and iNOS may cause extensive tissue damage by induction of apoptosis and/or necrosis, or induce septicaemia, and would thereby be detrimental for the host (142, 228). It is therefore not surprising that a number of negative regulators for TLR-signalling have been identified, many of which have been shown to be up-regulated in response to LPS and /or other TLR-ligands (140). Identification of a soluble variant of TLR-4 in mice lead to the hypothesis that decoy TLRs may exist to balance the response. The soluble variant of TLR-4 was shown to inhibit LPS-induced production of NF- κ B and TNF- α by an unknown mechanism (107). A short variant of MyD88, MyD88s, is recruited to the receptor but does not allow NF- κ B signalling and may thus dampen the response by competing with MyD88 (33, 109). The inhibition appears to be specific for NF- κ B as AP-1 dependent gene expression is intact in the presence of MyD88s (110). IRAK-M and alternative splice variants of IRAK-1 and IRAK-2 are believed to inhibit IRAK activity (140). The function of the non-inhibitory IRAK-2 splice variant is not known. Other intracellular proteins shown to mediate negative regulation include the PI3K, SOCS1, A20 and Tollip (140). TLR responses may also be controlled by transmembrane proteins e.g. ST2 and TNF-related apoptosis-inducing ligand receptor (TRAILR). ST2 belongs to the TIR superfamily and exists in a membrane bound (ST2L) and a soluble form (sST2). ST2L is believed to mediate inhibition by sequestration of MyD88 and Mal through its TIR domain. sST2 has been shown to inhibit LPS-induced production of pro-inflammatory cytokines in macrophages by an unknown mechanism (140). TRAILR is believed to suppress TLR responses by inhibiting the NF- κ B pathway (52).

1.4.3.2 TREMs

The recently identified TREMs belong to the Ig-superfamily of receptors. They lack a cytoplasmic signalling domain and rely on association with membrane-anchored adaptor proteins for surface expression and signalling. To date two human and three murine TREMs have been characterised, all of which associate with the adaptor DAP12 (43). The cytoplasmic domain of DAP12 contains an immunoreceptor tyrosine-based activation motif (ITAM) which is phosphorylated upon ligand binding to the receptor. Phosphorylation of the ITAM motif, mediated by a Src family kinase, allows recruitment of the tyrosine kinases Syk and/or ZAP70. This triggers several signalling pathways through a cascade of phosphorylation events. Eventually this leads to nuclear translocation of transcription factors which activate gene expression (12, 88). Human TREM-1 is up-regulated on neutrophils and monocytes in response to Gram-negative and Gram-positive bacterial as well as fungal stimuli but not during non-microbial inflammatory conditions. Activation of TREM-1 by cross-linking of the receptor triggers an inflammatory response in monocytes and neutrophils, a response that is augmented by LPS stimulation of the cells, indicating that TREM-1 synergizes with TLR-4 signalling (24, 25). Murine TREM-2 has been shown to be expressed on macrophage cell lines, immature DCs, microglial cells and osteoclasts (43, 48). Cross-linking of murine TREM-2 triggered production of NO in transfected macrophages indicating that TREM-2 mediates activating signals (48). Of the up till now characterised TREMs, murine TREM-2 is the only one for which possible ligands have been identified. TREM-2 has been shown to bind both Gram-negative and Gram-positive bacteria. The binding was inhibited by anionic bacterial products such as LPS and lipotechoic acid but also by other anionic carbohydrates, indicating that the binding is based on charge (49). Murine TREM-3 is expressed on macrophage cell lines and has, like TREM-1, been shown to be up-regulated in response to LPS stimulation and was indicated to mediate activating signals (41).

TREM-1 also exists as an alternative soluble splice variant found in the blood of patients with sepsis (75). The function of this soluble variant is not known but it has been suggested that it may act as a decoy receptor to dampen the response, a hypothesis that is strengthened by studies on murine soluble TREM-1. Experimental LPS-induced septic shock in mice caused an up-regulation of murine TREM-1. Interestingly mice could be rescued by treatment with a soluble TREM-1 fusion protein (25). As mentioned above the only signalling adaptor known to associate with TREMs is DAP12 which typically mediates activating signals. However recent data suggest that DAP12 also may mediate inhibitory signals by an unknown mechanism. Absence of DAP12 was shown to cause enhanced macrophage-production of pro-inflammatory cytokines in response to various known TLR ligands. DAP12 deficient mice accordingly showed an increased susceptibility to septic shock as well as increased resistance to bacterial infection with *Listeria monocytogenes* (89). Furthermore, although TREM-2 was initially believed to trigger macrophage activation, it has recently been shown that TREM-2 inhibits macrophage activation by certain but not all TLRs. Stimulation of macrophages from TREM-2^{-/-} mice with LPS, zymosan or CpG provoked increased levels of TNF- α compared to wild type macrophages, indicating that TREM-2 signalling dampens the response triggered by TLR-4, TLR-2/6 and TLR-9. The absence of TREM-2 did not have any effect when cells were stimulated with

TLR-3 or TLR-7/8 ligands (226). Thereby TREM-2^{-/-} macrophages responded in a similar way as DAP12 deficient macrophages to stimulation with TLR-4, TLR-2/6 and TLR-9 ligands. Additionally, TREM-2 has recently been shown to be able to mediate the TLR-inhibitory signals through DAP12 (87). DAP12-mediated inhibition has been observed for other receptors than TREMs. Cross-linking of the receptor NKp44 or Siglec-H on plasmacytoid DCs (pDC) inhibited production of IFN- α/β in response to CpG (23, 67). It has also been shown that pDCs unable to signal through DAP12 produce increased cytokine amounts in response to infection with murine cytomegalovirus compared to cells from wild type mice (210). Thus DAP12 seems to be able to mediate inhibitory as well as activating signals, however, the molecular basis for this dual function of DAP12 is not known. As mentioned above, in a given situation an immune cell may receive signals through multiple receptors and the level of the response is likely to be the balanced outcome of all input signals. Signalling by ITAM associated receptors are often counterbalanced by receptors mediating their signals through an immunoreceptor tyrosine-based inhibitory motif (ITIM). Following phosphorylation of tyrosine residues ITIMs recruits the protein tyrosine phosphatases SHP-1 or SHP-2 or the inositol lipid phosphatase SHIP which dephosphorylate signalling proteins and thereby dampens the response. However in the case of DAP12 the inhibitory signal seems to be mediated through an ITAM motif which normally induces activating signals (87).

Although little is known about the molecular mechanism underlying DAP12 mediated inhibition, it has been reported to require phosphorylation of the same tyrosine residues that are involved in mediating activation, and possibly also the activity of Syk (87). Several possible mechanisms have been suggested on how DAP12 mediates the inhibition on TLR signalling, including recruitment of a phosphatase followed by dephosphorylation and thereby inactivation of signalling molecules, sequestration of signalling molecules or activation of a specific negative TLR regulator (87). However, none of these models provide an explanation for how an ITAM bearing receptor may mediate an inhibitory signal which depends on the same tyrosine motifs as the activation, and future studies are thus needed to shed light on this enigma.

2 AIMS

This thesis focuses on *S. Typhimurium* host-pathogen interactions, in particular the interplay between *S. Typhimurium* and its macrophage host cell.

The specific aims were to:

- Establish what role the O-antigen has for intracellular fitness in macrophages
- Study the role of the thioredoxin and glutathione/glutaredoxin systems in resistance to oxidative and NO stress, intracellular fitness and virulence *in vivo*
- Study the function of the newly characterised receptor TRAPC during bacterial infection

3 RESULTS AND DISCUSSION

3.1 PAPER I

According to the dogma, many enterobacterial pathogens, including *Salmonella*, rely on expression of smooth LPS for full virulence. This is exemplified by the reduced ability of O-antigen deficient mutants of *Yersinia enterocolitica* to colonize Peyer's patches and their inability to colonize the liver or spleen. Concomitantly these mutants also display a severe reduction in virulence in the murine infection model. Likewise mutants of *S. Typhimurium* devoid of the O-antigen display a decreased capability to colonize the gut, and a reduced virulence in the murine infection model.

In addition to its important role for bacterial virulence the LPS is also a major inducer of innate host responses mainly through recognition by TLR-4, thereby triggering production of pro-inflammatory cytokines, ROI and RNI (65, Hoebe, 2003 #424, 178, 204). Recognition by TLR-4 has been attributed to lipid A and *Salmonella* is known to modify its lipid A in a multifaceted way to increase resistance to CAMPs or reduce recognition by TLR-4 (84, 86, 117, 133). However recent data indicating that CD14 is essential for the recognition of smooth but not rough LPS (111), brings to mind the possibility that the O-antigen in addition to lipid A may influence TLR-4 recognition of Gram-negative bacteria. Additionally *Shigella* was recently shown to reduce the length of its LPS by glycosylation-mediated conformational changes of the O-antigen thereby achieving more efficient type III secretion of virulence proteins into host cells (238). Furthermore, *S. Typhimurium* has been shown to down-regulate genes for LPS synthesis (56) and to reduce the chain length of the O-antigen once the bacteria reside and replicate inside macrophage-like cells (130). Combined, these findings imply that it may be beneficial to modify also the O-antigen under certain stages of infection. This possibility intrigued us to study whether *S. Typhimurium* benefits from expressing LPS devoid of O-antigen once bacteria reside and replicate inside macrophages.

To analyse this, isogenic *waaL* and *waaK* deletion mutants, lacking the O-antigen ligase and the N-acetylglucosamine transferase respectively, as well as a $\Delta waaKL$ double mutant were generated. When assayed for fitness and ability to induce host cell NO production in macrophage-like J774-A.1 cells, the $\Delta waaL$, $\Delta waaK$ and $\Delta waaKL$ mutants triggered lower production of NO and consequently displayed higher intracellular growth yields compared to wild type bacteria. If the reduction in macrophage NO production was caused by differential recognition by TLR-4, the reduced NO levels should be accompanied by reduced iNOS expression. Interestingly, immunoblotting experiments showed equal induction of iNOS expression in cells infected with wild type, $\Delta waaL$ or $\Delta waaK$ mutant bacteria. As this experiment indicated that these mutants interfere with the enzymatic activity of iNOS we continued by analysing the requirement for bacterial protein synthesis for inhibition of iNOS. When bacterial protein synthesis was inhibited during infection of J774-A.1 cells the $\Delta waaL$ mutant was unable to interfere with the activity of iNOS. Furthermore we could show that the iNOS inhibition was unrelated to SPI-1 but seemed to require the SPI-2 T3SS. Interestingly, while the $\Delta waaK$ mutant which still expressed slight amounts of O-antigen inhibited the activity of iNOS, the partial restoration of O-antigen expression

in the $\Delta waaKL$ mutant, obtained with complementation with *waaK* and *waaL* *in trans*, restored macrophage NO levels and bacterial growth yield to wild type levels. Thus a delicate balance in O-antigen expression seems to regulate the ability to inhibit iNOS activity.

Our results clearly show that *S. Typhimurium* benefits from expressing LPS devoid of the O-antigen during growth in macrophage-like cells, and provide a possible explanation for the observation by Lähteenmäki *et al.* that *S. Typhimurium* down-regulates the chain length of the O-antigen during growth in macrophage-like cells (130). That is, *S. Typhimurium* may modify the O-antigen to enable interference with iNOS activity and possibly also other antibacterial macrophage-responses. In this scenario our mutants already express the required LPS structure whereas the wild type needs time to modify the LPS rendering the mutants able to inhibit iNOS activity more efficiently. In this context it is interesting to note that *S. Typhimurium* has been shown to shed its LPS during infection of epithelial cells. Furthermore, LPS shedding was only observed with wild type bacteria expressing smooth LPS (70). Possibly the rationale for this shedding is to rapidly change the LPS structure into one containing less O-antigen to enable efficient iNOS inhibition.

In recent experiments J774-A.1 cells were primed by a 2h treatment with IFN- γ (1000 U/ml) prior to infection. This did not affect the background levels of NO in uninfected cells, but deprived the $\Delta waaL$ mutant of its ability to suppress macrophage NO production compared to wild type bacteria (Fig. 2 unpublished data). Hence, the level of *Salmonella*-mediated iNOS inhibition seems to correlate with the activation state of the cells. One explanation for this could be that the level of iNOS inhibition dependent on the dose of the inhibitor as well as on the kinetics of iNOS expression. Possibly, priming with IFN- γ enables the J774-A.1 cells to trigger iNOS expression, and thereby NO production, more rapidly in response to infection compared with non-primed cells. Bearing in mind that the suppression of iNOS activity is indicated to depend on SPI-2 and that macrophage NO production is reported to inhibit SPI-2 expression (154), one can envision that a more rapid induction of NO production may inhibit SPI-2 to the extent that it cancels out the benefit of lacking the O-antigen.

Whatever the identity of the bacterial protein/s (factor X) mediating the inhibition of iNOS activity, the inhibition may occur at one or several different levels. Production of NO depends on the presence of L-arginine, and iNOS activity is partly controlled by arginase-mediated degradation of L-arginine. Furthermore, the intracellular storage of L-arginine is not enough to support the NO production and iNOS activity also rely on transport of L-arginine into the cell by arginine transporters (167). Thus factor X may control iNOS activity by inducing expression of host cell arginases or inhibiting arginine transport. Treatment of cells with an arginase inhibitor did not affect the ability of the $\Delta waaL$ mutant to suppress iNOS activity (unpublished data) but the possible effect on L-arginine transport remains to be studied. Additionally, iNOS is active only as a dimer and requires a number of co-factors for dimerization, hence factor X may also inhibit iNOS dimerization by inducing degradation, inhibit expression or sequester cofactors required for activity. Factor X may also inhibit iNOS activity by inducing expression of inhibitory proteins, or by reducing the disulfide bridge necessary for dimerization.

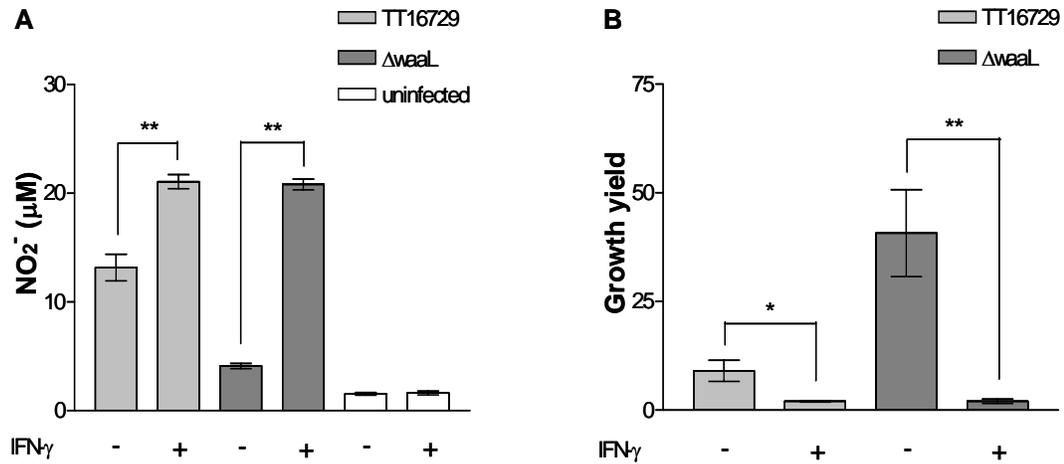


Figure 2. J774-A.1 cells were pretreated with IFN- γ for 2h prior to infection with wild type or $\Delta waaL$ mutant bacteria. NO production (A) and bacterial growth yields (cfu at 16h/cfu at 2h) (B) were measured 16h post infection.

3.2 PAPER II

The recently characterized novel member of the mouse TREM receptor family triggering receptor expressed by antigen presenting cells (TRAPC) is, like TREM-1, transcriptionally up-regulated by LPS on macrophage-like cells, and cross-linking of TRAPC induces production of NO in macrophage-like cells and DCs (manuscript under revision in Eur. J. Immunol.). The production of NO by murine phagocytic cells is important for the control of intracellular bacterial replication not only of *Salmonella* but also other important pathogens, including *Listeria monocytogenes* and *Mycobacterium tuberculosis*. Thereby the ability of TRAPC to induce NO expression strongly suggests a role for TRAPC in the defence against bacteria and intrigued us to study the effect of TRAPC-cross-linking during bacterial infection of macrophage-like cells.

When combined with infection with the Gram-negative bacteria *E. coli* TG1 or *S. Typhimurium*, or stimulation with LPS, cross-linking of TRAPC on J774-A.1 cells, in contrast to what would be expected considering the priming effect of TRAPC-cross-linking on macrophages, inhibited host cell NO production. For *S. enterica* serovar

Typhimurium the reduction in NO levels correlated with increased intracellular bacterial replication.

Like all other up till now identified members of the TREM receptor family, TRAPC contains an ITAM motif in its cytoplasmic domain through which it associates with the ITAM-containing membrane-anchored adaptor protein DAP12. ITAM mediated signalling typically generates activating signals (12, 88), however, an increasing number of reports show that DAP12 also may mediate inhibitory signals (23, 67, 87, 89, 210). TREM-2 was recently shown to have an inhibitory effect on TLR signalling and to be able to mediate this effect through DAP12 (87, 226). In one set of samples, the suppression of macrophage NO production, obtained when TRAPC cross-linking was combined with infection or LPS stimulation, was accompanied by slightly reduced iNOS levels indicating that the suppression of NO production occurs on the level of signalling rather than interference with iNOS activity. The transcription factor NF- κ B has a crucial role for induction of iNOS expression, and is activated during TLR-4 signalling through degradation of I κ B (115, 201). Immunoblotting experiments with cross-linked non-infected macrophage-like cells show that cross-linking of TRAPC triggers degradation of I κ B. Ongoing experiments will reveal whether the inhibition of macrophage NO production, obtained with TRAPC cross-linking combined with Gram-negative infection or LPS stimulation, is a consequence of inhibition of the NF- κ B pathway.

It may seem puzzling that while IFN- γ has a synergistic effect on host cell NO production triggered by cross-linking of TRAPC (manuscript under revision in Eur. J. Immunol.), bacterial infection or LPS stimulation acts inhibitory. One can however envision at least two explanations for this apparent contradiction. *i*) TREM-2 has been shown to bind specifically to Gram-negative and Gram-positive bacteria as well as to yeast, and this binding can be inhibited by bacterial products such as LPS, lipoteichoic acid, and peptidoglycan but also anionic carbohydrate molecules, including dextran sulfate, suggesting that ligand recognition is based partly on charge. It is tempting to speculate that bacteria have evolved to use certain DAP12 associated receptors to their advantage. In this scenario, by inducing DAP12 mediated inhibition of antibacterial macrophage responses, bacteria would promote their own survival. It remains to be investigated if bacteria are able to bind these DAP12 associated receptors, including TRAPC, directly, and what mechanism(s) underlies the TRAPC-mediated regulation of innate immune effector functions. *ii*) A full scale pro-inflammatory signalling will inevitably cause a certain degree of tissue damage to the host, and is therefore undesirable unless absolutely necessary. It is possible that TRAPC participates in the decision whether full scale signalling should be triggered or not and that the signal mediated by TRAPC (activating or inhibitory) is determined by the activation state of the cell. That is, triggering of TRAPC in conjunction with TLR-4 signalling in activated cells or in combination with other pro-inflammatory stimuli, e.g. IFN- γ may be a signal of high level of danger and that full scale signalling is required. Triggering of TRAPC in combination with TLR-4 signalling on naive cells in the absence of additional pro-inflammatory stimuli on the other hand may lead to TRAPC mediated dampening of the TLR-4 mediated response to avoid unnecessary damage to the host. This scenario may however be too simplistic. DAP12 $-/-$ mice are more susceptible to septic shock due to excessive induction of inflammatory responses (89) i.e. a certain

degree of inhibition seems to be required to avoid detrimental damage to the host. Most likely in a given situation a given macrophage receives signals from a multitude of receptors, and there may also be cross-talk between some of these receptors. Several inhibitory and activating signals may be required to fine tune the response to ensure induction of the appropriate one.

3.3 PAPER III AND IV

Host cell production of ROI is, together with production of RNI, the most important host defence mechanism towards infection with *S. Typhimurium* in the murine infection model. Thus it is not surprising that a number of defence mechanisms, which protect *Salmonella* from these host responses, have been identified. However, there are still genes potentially important for protection against ROI/RNI but whose importance has not been evaluated in *Salmonella*.

ROI may affect the redox status of cytosolic proteins and oxidize cysteine sulfhydryl side chains essential for protein folding, enzymatic activity or for the chelating of essential metal cofactors. In *E. coli*, the thioredoxin and glutathione/glutaredoxin systems encode enzymes which shuttle redox potential from NADPH to cytosolic substrates, thereby providing a repair system for oxidized sulfhydryl groups in cytosolic proteins (Fig. 3). Through thioredoxin 1 (TrxA) and 2 (TrxC) the thioredoxin system transfers reducing equivalents to DsbD, located in the cytoplasmic membrane, for transfer to the periplasmic space thus providing the periplasmic oxidoreductase DsbC with electrons. DsbC in turn, by reducing wrongly paired disulfides, plays an important role in assuring correct protein folding of periplasmic proteins. Both thioredoxin 1 and 2 are in turn continuously reduced, mainly by thioredoxin reductase (TrxB) which derives its reducing equivalents from NADPH.

The glutathione/glutaredoxin system, which relies on glutathione as a redox-shuttle from NADPH to oxidized targets, consists of the glutathione-synthesizing enzymes γ -glutamylcysteine synthetase (GshA) and glutathione synthetase (GshB), the glutathione oxido-reductase (Gor) and glutaredoxin 1 (GrxA), 2 (GrxB) and 3 (GrxC) (8). For *E. coli* it has been shown that null mutants for single components of the thioredoxin or glutathione/glutaredoxin system do not have any profound effects on viability during standard *in vitro* growth conditions (187, 197). However, when *trxA*, *trxC* and *grxA* are deleted simultaneously the combination is lethal (216). Hence, the thioredoxin and glutathione/glutaredoxin pathways could be envisioned to formally constitute parallel mechanisms for transfer of electrons. Deficiencies in the thioredoxin or glutathione/glutaredoxin pathways are indeed reported to sensitize bacteria such as *E. coli*, *Helicobacter pylori* and *Rhodobacter sphaeroides* to hydrogen peroxide *in vitro* (44, 136, 220), whereas inactivation of a homologue for glutathione peroxidase (*gpxA*) in *Neisseria* is reported to cause increased sensitivity to paraquat (166). Additionally, in *E. coli* glutaredoxin has been suggested to act as a “S-nitrosyl sink” in the protection against nitric oxide stress (93).

The annotated *S. enterica* serovar Typhimurium LT2 genome sequence contains close homologues to the components of the *E. coli* thioredoxin and glutathione/glutaredoxin

systems, however, apart from the role of DsbA and its paralogue SrgA for SPI-2 secretion and virulence, the importance of these systems for *Salmonella* virulence have not previously been studied. Thus deletion mutants of the *trxA*, *trxB*, *trxC*, *gshA*, *grxA* and *dsbC* genes were generated to establish the importance of the thioredoxin and glutathione/glutaredoxin systems for protection against ROI and RNI, intracellular replication and *in vivo* virulence of *S. Typhimurium*. These mutants were subsequently probed for sensitivity to oxidative and NO donor substances *in vitro*, intracellular fitness in epithelial and macrophage-like cells as well as for virulence *in vivo*. Surprisingly, except the *gshA* mutant, which was more sensitive to oxidative substances when grown under SCV-like conditions, none of the mutants displayed increased sensitivity to the substances tested. Furthermore, the *trxA* mutant was the only mutant that showed a reduced growth yield in both epithelial and macrophage-like cells as well as a severe reduction in virulence *in vivo*. In addition to its role as a reductase *E. coli* TrxA has been shown to harbour a chaperone function and to be able to interact with a large number of different proteins some of which are involved in oxidative stress response (128). By complementing the $\Delta trxA$ mutant with a collection of *trxA* constructs differing in their redox potential we could show a straight correlation between TrxA redox-activity and fitness in macrophage-like cells. Additionally, competition experiments *in vivo* between *trxA* mutants complemented *in trans* either with wild type *trxA* or redox-inactive *trxA* clearly showed that *Salmonella* virulence depends on redox active TrxA.

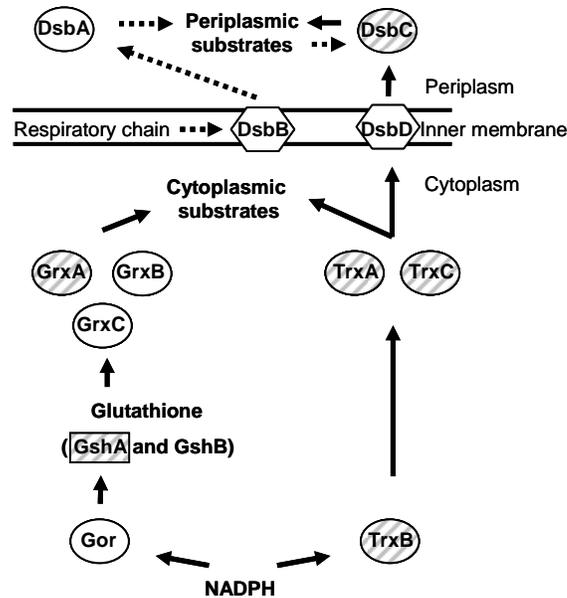


Figure 3. A schematical overview of the thioredoxin and glutathione/glutaredoxin systems in *Escherichia coli* is shown. Reduction and oxidation are indicated by solid and broken arrows respectively. Double arrows indicate disulfide bond isomerization. Members of either of these systems covered in this study are shaded in grey.

The phenotype of the *trxA* mutant, with its pronounced decrease in intracellular fitness and *in vivo* virulence, strongly resembles the phenotype of an *ssaV* mutant, which is unable to secrete SPI-2 effector proteins. In paper IV we therefore continued by studying if the phenotype of the *trxA* mutant was connected to SPI-2. Initial experiments in which macrophage-like cells were infected with wild type, $\Delta trxA$, $\Delta ssaV$ or $\Delta trxA \Delta ssaV$ mutant bacteria indicated a possible mechanistic connection between TrxA and SPI-2. SPI-2 is required for growth within the SCV, and we could furthermore show that catalytically active TrxA is required for bacterial adaptation to a sudden shift from rich medium to growth under SCV-like conditions as well as for SPI-2 functionality under these conditions. In paper I we showed that a strong reduction of the O-antigen levels or complete absence of O-antigen enables *S. Typhimurium* to inhibit the iNOS activity of macrophage-like cells. The inhibition of iNOS was furthermore indicated to depend on SPI-2. Accordingly, a compound recently shown to inhibit T3SS in *Yersinia* (114), *Chlamydia trachomatis* (170) and *S. Typhimurium* (Negrea et al. submitted manuscript) deprived the $\Delta waaL$ mutant of its ability to inhibit macrophage NO production (unpublished data). As we in paper I show that the inhibition of iNOS is independent of SPI-1, these results provide further evidence for the involvement of SPI-2 in the inhibition of iNOS activity. As SPI-2 depends on TrxA for proper function (Paper IV), and the inhibition of iNOS activity by O-antigen deficient *S. Typhimurium* seemed to depend on SPI-2, the next question was whether TrxA is required for iNOS inhibition.

When analyzing the importance of TrxA redox activity for iNOS inhibition, in contrast to the $\Delta trxA$ single mutant (Paper III), no linear correlation could be established between TrxA redox potential and intracellular fitness in the $\Delta waaL$ background. However, a correlation was observed in the sense that complementation with the more reducing variants of TrxA restored the intracellular fitness, whereas the more oxidizing variants of TrxA, in spite of inducing NO levels similar to the $\Delta waaL$ single mutant, only caused a partial restoration of the growth yield that did not differ significantly from that of $\Delta trxA \Delta waaL$ complemented with the empty cloning vector pBAD33. Surprisingly, while complementation with a catalytically inactive variant of *trxA* did not reduce the NO levels of infected J774-A.1 cells, it partially restored the intracellular growth yield of the $\Delta waaL \Delta trxA$ double mutant. In the very stringent statistical analysis used in this study the partial complementation mediated by catalytically inactive *trxA*, was not significant but in an ordinary two-sided T-test it gave a p-value < 0.05. In contrast, the catalytically inactive *trxA* did not mediate any complementation of the $\Delta trxA$ single mutant. Combined these observations imply that under certain conditions TrxA may contribute to intracellular fitness of *S. enterica* serovar Typhimurium through a redox-independent mechanism. Furthermore, competition experiments *in vivo*, where a *trxA* mutant complemented with the empty pBAD33 cloning vector was competed against *trxA* mutant bacteria complemented with either wild type *trxA* or catalytically inactive *trxA*, clearly showed that TrxA contributes to virulence, mainly through a redox- dependent but also through a redox-independent mechanism.

Considering the major importance of ROI and RNI in the defence against *Salmonella*, both during infection of macrophages *in vitro* and *in vivo* (151, 234), and the role of TrxA as a reductase, it may seem surprising that the *trxA* mutant does not show

increased sensitivity to oxidative or NO stress *in vitro*. However this does not in any way rule out an important role for TrxA in the protection against ROI and/or RNI. If TrxA is required for inhibition of production of ROI/RNI rather than repair of the damage or ROI/RNI detoxification, absence of TrxA will not affect the sensitivity to these compounds.

4 CONCLUDING REMARKS

The ability to adapt to host environment is essential for bacterial virulence. In the murine model system for typhoid fever adaptation of *S. Typhimurium* to the intramacrophage environment is crucial for virulence, and largely depends on SPI-2. This thesis defines important, SPI-2 related, roles for the O-antigen of the LPS and TrxA, a component of the thioredoxin system, for bacterial adaptation to macrophage and host conditions.

Expression of a full length O-antigen has conventionally been regarded as a requirement for enterobacterial virulence. The importance of smooth LPS for colonization of the host is well established for *Salmonella* as well as for other enteric bacteria. However, the role of the O-antigen during intracellular stages of infection has not previously been studied with clearly defined LPS mutants. O-antigen depletion in *S. Typhimurium* was accompanied by a higher bacterial fitness in non-activated murine macrophage-like cells. This macrophage-adapted phenotype associated with suppression of iNOS activity and thereby the production of NO, and strongly depended on SPI-2 and TrxA. Interestingly, *S. Typhimurium* was recently shown to down-regulate the O-antigen chain length during growth in macrophage-like cells (130), providing our data with a possible biological relevance. TrxA was in turn shown to affect SPI-2 activity under SCV-like conditions. By its requirement for proper function of SPI-2 it is possible that TrxA contributes to macrophage-adaptation and virulence through SPI-2. The following question is whether TrxA mediates suppression of iNOS activity by a direct interaction with iNOS i.e. is TrxA a SPI-2 effector protein? However, TrxA does not have the translocation motif found in many, but not all, SPI-2 effector proteins (153, 231). Furthermore, considering its effect on SPI-2 functionality it seems more likely that the requirement for TrxA is secondary and that TrxA is required for the secretion and/or function of one or more SPI-2 effector proteins.

At this stage we cannot conclude whether the SPI-2-dependency for iNOS inhibition originates from the ability of SPI-2 to promote bacterial intracellular replication through its effect on vesicular trafficking, or whether there is a specific iNOS-targeted SPI-2 effector protein. It is also unclear how O-antigen deficiency relates to the SPI-2 dependent inhibition of iNOS. In *Shigella*, a reduction in LPS length, mediated by a conformational change of the O-antigen, potentiates the T3SS, thereby enabling more efficient secretion of effector proteins into host cells (238). Possibly, the efficiency of the SPI-2 T3SS correlates with the length of the LPS also in *S. Typhimurium*, with T3SS activity being enhanced in an O-antigen deficient background. Regarding the SPI-2 dependency, a simple explanation could be that SPI-2-assisted bacterial intracellular replication associates with consumption of host L-arginine. If one further assumes that SPI-2 activity is enhanced in an O-antigen deficient background, and that this translates into increased intracellular replication, host cell resources of L-arginine would be depleted, and iNOS would be inactivated in lack of the key substrate. However this would require up-regulated transport of host L-arginine across both the vacuolar membrane of the SCV and the bacterial membranes. Thereby it seems more likely that the inhibition of iNOS is a direct consequence of SPI-2 activity. Here it is

interesting to note that TrxA recently was shown to act as a chaperone for a *Helicobacter pylori* encoded arginase. Furthermore, the *H. pylori* TrxA, in conjunction with the arginase, protected the bacterium against ROI and RNI (155). Possibly *S. Typhimurium* affects iNOS by encoding a SPI-2-secreted and iNOS-targeting effector, e.g. an arginase that requires TrxA either for its function or translocation.

Subsequent studies focusing on host cell immune response regulators opened yet another potential bacterial strategy for coping with host cell NO expression. Cross-linking of the novel TREM-family member protein TRAPC previously found to induce a moderate NO production in uninfected macrophage-like cells and DCs. However, in contrast to what would be expected, when combined with infection with wild type *S. Typhimurium*, cross-linking of TRAPC on macrophage-like cells suppressed host cell NO production. This pathway of NO inhibition appeared unrelated to the one dependent on SPI-2, in that a similar suppression was achieved upon infection with a laboratory *E. coli* strain devoid of SPI-2 as well as with LPS stimulation. It remains to be determined whether bacteria are able to exploit TRAPC to their own benefit or whether the inhibitory function of TRAPC is a mechanism used by the host to balance the response to an invading pathogen to avoid unnecessary damage to the host inflicted by an excessive pro-inflammatory response.

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