A novel live attenuated Shigella vaccine

The invention relates to a live attenuated Shigella vaccine strain generated with specific targeted mutations in order to induce serotype independent cross-protection and express heterologous (non-Shigella) antigens.

BACKGROUND

Shigellae are highly human-adopted Gram-negative enterobacteria causing bacillary dysentery. The disease spreads exclusively by direct personal contact or human fecal contamination of food and water. As a result, bacillary dysentery is endemic in regions with suboptimal hygienic conditions. There are an estimated 165M cases worldwide, with as many as 1M fatalities mostly among children under the age of five Shigella was found to be the one of the most prevalent bacterial pathogen isolated in case of an acute diarrheal episode among 1-5 year-old children in Southeast Asia and sub-Saharan Africa (Kotloff et al., Bull. W.H.O. 77: 651-666, 1999). Bacillary dysentery is also common among travelers and military personnel entering endemic countries. It has long been accepted that vaccines would be crucial to control dysentery but vaccine development against Shigellae is hampered by the serotype-specific immune response, i.e upon exposure to Shigella (natural or vaccine-mediated) the immune protection is usually limited to the given serotype. The four species of the Shigella genus comprise a sum of 50 serotypes and subserotypes, which are differentiated by their LPS O-antigens.

Hong et al. (Molecular Microbiology 24:779-91, 1997) described the effect of mutations in chromosomal and plasmid-encoded lipopolysaccharide genes on invasion and serum resistance of *Shigella flexneri*. Mutations in the *rfb* and *rfaL* genes either eliminated the entire O-antigen side chains or produced chains of greatly reduced length.

Nagy et al. (J. Infect. Diseases 198: 1699-706, 2008) described the vaccine potential of a *Salmonella enterica* regulatory lipopolysaccharide mutant. Loss of the transcriptional antiterminator RfaH resulted in a heterogeneous length of LPS chains, the “gently rough” phenotype.

Regulatory protein RfaH is shown to be involved in the growth-phase dependent upregulation of long-chained (i.e. high number of O-antigen repeat) LPS molecules of *S. flexneri* (Carter et al. Microbiology. 2007 Oct; 153 (Pt 10):3499-507).

Major virulence factors of Shigellae other than LPS O-antigens are surprisingly conserved. This implies a lack of immune-mediated evolutionary pressure on these antigens substantiating the accepted view about O-antigen being the sole protective antigen. Nevertheless, there is a marked antibody response against the so-called "invasion plasmid antigens" (Ipa-s), especially following repeated exposure. These antigens encoded on the large virulence plasmid form components of a type three secretion system (T3SS) that is indispensable for invasion and hence virulence.

The structure-function analysis of the Shigella virulence factor invasion plasmid antigen B (ipaB) was disclosed by Guichon et al. (J. Bacteriol. 183:1269-76, 2001). ipaB mutants were generated to correlate function with protein subdomains.

Menard et al. (J. Bacteriol. 17518: 5899-5906, 1993) described that mutagenesis of the ipa genes ipaB, ipaC and ipaD of *Shigella flexneri*, resulted in the loss of invasive potential of Shigella.

Antibodies against Ipa proteins (such as to minor conserved antigens) are considered non-protective, as otherwise cross-protection among serotypes could be triggered. Current vaccine approaches rely almost exclusively on O-antigen mediated immunity exploiting the fact that five or six serotypes would provide high protection against the majority of endemic and epidemic dysentery cases. Nevertheless, considering the fact that most of the suggested multivalent vaccines are based on either purified subunits (O-antigens) or several live attenuated bacteria with different LPS O-antigen types, they would, most probably, be too complex and hence expensive. Moreover, a partial serotype coverage is expected to induce serotype replacement due to herd immunity based immune pressure on vaccine serotypes and escape and increase in prevalence of non-vaccine serotypes, as demonstrated for other multi-serotype pathogens, such as *Streptococcus pneumoniae*. Therefore, an ideal Shigella vaccine is expected to provide substantial cross-protection against all circulating serotypes.

Besides Shigella, Enterotoxigenic *Escherichia coli* (ETEC) is a major bacterial pathogen responsible for travelers' diarrhea and represent one of the leading cause of death in children in endemic countries. Therefore efforts are undertaken to develop vaccines addressing these two pathogens simultaneously.

Travelers' diarrhea is currently treated by antibiotics; however, there is an increasing rate of resistance among Shigella strains that makes the management of the disease more and more difficult. Moreover, ETEC infections can have long-term consequences related to irritable colon syndrome. It is widely accepted that vaccination would be the most effective way to address this high unmet medical need; yet, no vaccines are currently available for the prevention of these conditions.

Two types of enterotoxins have been identified in ETEC strains, the heat labile toxin (LT) and the heat stable toxin (ST), either as ST associated with porcine disease (STp) or ST associated with human disease (STa). LT is highly homologous in structure to the cholera toxin. The A subunit is the active component of the toxin, which functions to increase the activity of adenylate cyclase. This is delivered into host cells by the B subunits, which bind to gangliosides on the cell surface. STa is a small (19 amino acid) non-immunogenic polypeptide that has guanylate cyclase stimulating activity. STm is a mutated form of ST that is non-toxic, but still immunogenic. Such STm is considered to be safely employed as vaccine antigen (Taxt et al. Infect. Immun. 78:1824-31, 2010).

It has been demonstrated that ETEC strains also produce EAST1, a heat-stable toxin similar in size and mode of action to ST but different in sequence, originally identified in enteroaggregative E. coli strains (Nataro and Kaper, Clin Microbiol Rev. 11: 142-201, 1998; Zhang et al., Vet Microbiol. 123: 145-152, 2007).

Zheng et al. (World J. Gastroeneterol. 11: 3411-18, 2005) constructed an *asd* mutant Shigella strain co-expressing CS3 and LTB/STm of enterotoxigenic *E.coli*. After immunization of mice by the oral route, antibodies were raised against CS3, LTB, ST, and Shigella lipopolysaccharide.

Xu et al. (Vaccine 21: 664-648, 2003) described a live attenuated invasive *Shigella flexneri* serotype 2a *rfbF* mutant as a carrier for a DNA-based HIV *gag* vaccine.

Noriega et al. (Infection and Immunity 67(2): 782-788, 1999) described a strategy for cross-protection against 14 *Shigella flexneri* serotypes, involving the use of the two serotypes 2a and 3a. The attenuated strains described are *S. flexneri 2a* strain CVD1207 (ΔguaB-A Δset1 Δsen) and *S. flexneri* 3a strain CVD 1211 (ΔguaB-A ΔvirG Δsen).

Bernardini et al. (Infection and Immunity 69(2): 1072-1083, 2001) describe mutants of *Shigella flexneri* 5, which are an *aroC* mutant and a double *purE aroC* mutant.

Levine et al. (Behring Institute Mitteilungen 98: 120-123, 1997) described an attenuated *S. flexneri* 2a strain CVD 1203 which harbors mutations in chromosomal gene *aroA* and plasmid gene *virG*, as well as an *S. flexneri 2a* vaccine candidate CVD 1205 that harbors a deletion mutation in *guaB-A* rendering it defective in nucleic acid synthesis, and a deletion mutation in *virG*.

It is the objective of the present invention to provide improved Shigella vaccines, in particular for the prevention of diarrheal diseases that are highly relevant for travelers to endemic countries and young children living in developing countries. Such vaccines can be based on a live attenuated *Shigella flexneri* vaccine strain able to heterogeneously express antigens derived from different pathogens and induce broad protection against bacterial pathogens, and particularly shigellosis.

SUMMARY

The object is solved by the subject matter as claimed.

According to the disclosure there is provided a live attenuated Shigella vaccine, which is based on a rough Shigella strain lacking LPS O antigen.

In one aspect, there is provided a live attenuated Shigella vaccine that is cross-protective against different serotypes and species of Shigella comprising a Shigella strain which is rough and non-invasive by a deletion of the *rfbF* gene, and a deletion of the *ipaB* and *ipaC* genes on the invasion plasmid.

Specifically, the Shigella strain is non-invasive by mutagenesis, in particular a mutation of the invasion plasmid.

Specifically the vaccine according to the disclosure is attenuated by mutagenesis of one or more genes involved in the LPS synthesis, transport and expression, preferably selected from the group consisting of genes in the cluster of the *rfb* operon, e.g. located on the chromosome between Gnd (6-phosphogluconate dehydrogenase, 2089155-2090561) and GalF (UTP-glucose-1-phosphate uridyltransferase, 2101928-2102821) genes of the *Shigella flexneri* 2a 2457T strain (Wei et al. Complete genome sequence and comparative genomics of *Shigella flexneri* serotype 2a strain 2457T. Infect Immun. 2003 May;71(5):2775-86.) or located on the virulence plasmid (*Shigella sonnei)*. Specifically preferred is the mutagenesis of one or more genes within the *rfb/wbb* gene cluster encoding O-antigen synthesis, *waaL* encoding the O-antigen ligase, *wzx* encoding O-antigen flippase involved in O-antigen transport, *wzy/rfc* involved in O-antigen polymerization, genes within the *rfa/waa* gene cluster encoding

LPS-core synthesis, regulatory genes affecting O-antigen expression, such as *rfaH*, or loss of function(s) of which results in at least 90% reduction in the expression of O-antigens.

According to a specific embodiment, said mutagenesis is by a deletion of one or more of the *rfb* F, D, C, E, J and/or I genes, or a deletion of a part thereof, or corresponding genes in various Shigella serotypes. Alternatively, mutagenesis by inactivation, e.g. transient, conditional or constitutive inactivation, may be employed.

Said Shigella strain is preferably selected from the genus Shigella, e.g. from any Shigella serotypes or species, in particular *S. flexneri, S. sonnei, S. dysentheriae and S. boydii.*

Specifically, said Shigella strain expresses outer membrane proteins, which can induce cross-reactive antibodies, in particular conserved proteins, including OmpC, OmpA and OmpX, or those encoded on the invasion plasmid.

The vaccine according to the disclosure is particularly cross-protective against different serotypes and species of Shigella, in particular against any of *S. flexneri 2a*, *S. flexneri 6* and *S. sonnei*, or enteroinvasive *Escherichia coli*.

According to a specific embodiment, said Shigella is non-invasive by further mutagenesis of the invasion plasmid, in particular a mutation of the invasion plasmid, which comprises a deletion of the *ipaB* and/or *ipaC* and/or other *ipa* genes.

Specifically, said Shigella comprises a recombinant endogenous invasion plasmid incorporating at least one gene encoding a heterologous antigen to secrete said antigen or to express said antigen on the bacterial cell surface.

Preferred embodiments refer to such vaccine, wherein said antigen is a protective antigen derived from a pathogen, e.g. selected from the group consisting of

- a bacterial antigen preferably a toxin or colonization factor,

-a viral antigen, preferably from a pathogen causing enteral or mucosal infections,

-a fungal antigen, preferably from a pathogen causing enteral or mucosal infections, and

- a parasitic antigen, preferably from a pathogen causing enteral infections.

Specifically, the bacterial antigen is originating from enteropathogenic bacteria, preferably selected from the group consisting of

a. *E. coli* antigens, in particular an enterotoxin selected from the group consisting of LTB, mutated LTA and ST of ETEC, subunits, or fusions thereof, antigens from enteroaggregative *E. coli* (EAEC), or Shiga-like toxin 1 or 2
b. *Campylobacter jejuni* antigens,
c. *Clostridium difficile* antigens, specifically toxins A and B
d. *Vibrio cholera* antigens, specifically the CT-B antigen, and
e. mutants or fusion proteins of a), b) c) or d).

Specifically, the bacterial antigen is an enterotoxin (ETEC) comprising the B subunit of heat labile toxin (LTB), the heat stable toxin (ST) or subunits or fusions thereof, preferably LTB/STm comprising an STm with an amino acid sequence as shown in SEQ ID 1, which optionally excludes the wild-type sequence of human ST.

In particular, said ETEC antigen is a fusion protein of the B subunit of LT and mutant ST, preferably a fusion protein LTB/STm with an amino acid sequence as derived from Figure 7 SEQ ID 11-18 (LTA-promoter-LTB-ST-LTB terminator nucleotide and LTB-ST amino acid sequences for 4 constructs), for example with ST mutations at position 13 and/or 12, such as P13F or P13G, and/or N12R or N12K).

Specifically, the viral antigen is originating from diarrheal viruses, preferably selected from the group consisting of rotaviruses and Norwalk virus (caliciviruses).

Specifically, the parasite antigen is originating from diarrhea-causing protozoa, preferably selected from the group consisting of *Giardia lamblia*, Cryptosporidium species and *Entameba histolytica*.

Specifically, the fungal antigen is originating from diarrhea-causing fungi, preferably selected from the group consisting of *Blastomyces dermatiditis* and Histoplasma spp.

According to a specific embodiment of the disclosure, the Shigella vaccine strain further comprises a deletion of an essential chromosomal gene and an insertion of said gene into the invasion plasmid, in particular the *ppa* gene, or any of *accD*, *acpS*, *dapE*, *era*, *frr*, *ftsI*, *ftsL*, *ftsN*, *ftsZ*, *infA*, *lgt*, *lpxC*, *msbA*, *murA*, *murI*, *nadE*, *parC*, *proS*, *pyrB*, *rpsB*, *trmA*, *rho* and *rhoL*.

Yet, according to a specific embodiment of the disclosure, the vaccine is provided for use in the prophylaxis or immunoprophylaxis of a subject to prevent infectious diseases, in particular enteral disease, such as diarrheal disease. In one aspect, there is provided a vaccine as described herein for use in the prophylaxis of a subject to prevent infectious diseases. Specifically, the disease is selected from the group consisting of Shigellosis, dysentery and diarrhea.

According to the disclosure, there is further provided a method of preventing infectious disease in a subject, in particular enteral disease, specifically by vaccination and immunizing said subject, respectively.

Specifically, said enteral disease is caused by any Shigella serotype or species.

Preferably, said (immune) prophylaxis comprises administration of the vaccine in a mucosal or oral formulation.

Specifically, the vaccine is administered orally or intranasally.

A specific embodiment refers to a vaccine for use according to the disclosure, wherein

- a polyvalent vaccine is used expressing protective antigens of Shigella and at least one other one of a species other than Shigella by the incorporation of a protective antigen of said pathogen into the endogenous modified recombinant invasion plasmid, and wherein

- said infectious disease is caused by any Shigella serotype or species and/ or said pathogen.

According to a further embodiment of the disclosure, there is provided a Shigella strain, which is a *S. flexneri* 2a strain, such as *S. flexneri* 2a 2457T, with a deletion of the *rfbF* and at least one of the *ipaB* and/or *ipaC* genes, or a deletion of essential parts thereof.

In one aspect, there is provided a Shigella strain, which is a *S. flexneri* 2a strain comprising a deletion of the *rfbF* gene, and the *ipaB* and *ipaC* genes on the invasion plasmid.

Specifically, said Shigella strain may further comprise a deletion of an essential chromosomal gene and an insertion of said gene into the invasion plasmid.

Preferably, said Shigella strain comprises a recombinant invasion plasmid incorporating at least one gene encoding a heterologous antigen to express and/or secrete said antigen.

Yet, according to a further embodiment of the disclosure, there is provided a recombinant plasmid vector based on a mutated Shigella invasion plasmid comprising a nucleotide sequence encoding at least one heterologous antigen, wherein the plasmid is mutated in at least one of the *ipaB* and/or *ipaC* genes. This specifically refers to a mutation for the deletion and/ or inactivation of a non-coding or coding region, such as regulatory sequences operably linked to a gene and a gene, respectively, preferably a deletion of the genes that renders the bacterial host cell non-invasive, in particular a deletion of the *ipaB* and/ or *ipaC* genes, or a deletion of a (substantial) part thereof.

A further specific embodiment of the disclosure relates to a bacterial host cell comprising the vector according to the disclosure, wherein said host cell is specifically selected from the genera Shigella, Escherichia, Salmonella, Campylobacter or Yersinia.

Said host cell specifically comprises a mutation in the endogenous invasion plasmid. Specifically, the vector according to the disclosure is an endogenous invasion plasmid, i.e. a plasmid endogenous or homologous to the host cell.

FIGURES

Figure 1. **Cross-protective capacity of live attenuated non-invasive strains of *S. flexneri* and *S. sonnei* lacking LPS O-antigen synthesis.**

Groups of 8 week-old BALB/c mice were immunized intranasally with CRP (10^6 CFU) and CRN (10^8 CFU) variants of *S. flexneri* 2a (a and b) mutants or alternatively phase I ($10^{5.5}$ CFU) and phase II ($10^{7.5}$ CFU) variants of *S. sonnei* (c) twice with two week-intervals. Control groups were mock vaccinated with saline. Subsequently, mice were challenged with either 10^6 CFU of wild-type *S. flexneri* 6 (a and c) or $10^{6.5}$ CFU of wild-type *S. sonnei* (b) via the same route. Survival was monitored subsequently for 14 days. Figures show combined data of three (b) or two (a and c) independent experiments with 5 mice in each group and repeat. Statistical analysis of the survival curves was performed by the Log-rank (Mantel-Cox) test. In case survival was significantly different from that of mock-vaccinated mice, the *p* value is shown on the graph.

Figure 2. **Schematic representation of antigenic phenotypes of the various mutants used as well as the proposed difference in antibody levels they might induce.**

O-antigens, its genetic determinants, and the antibodies triggered by them are shown. Ipa and minor conserved surface antigens are shown. Mutants expressing both Ipa and O-antigens (*S. flexneri ΔaroC* CRP and *S. sonnei* Phase I) trigger an antibody response mainly against these major antigens. In contrast, loss of these antigens in the vaccine strains allows a higher response to minor conserved antigens. ip: invasion plasmid, chr.: chromosome, T3SS: type tree secretion system, LPS: lipopolysaccharide.

Figure 3. **Broad-reactive mucosal IgA obtained from mice vaccinated with live attenuated *S. flexneri* 2a strains.** Immune reactivity of sIgA in BAL samples collected after 2 immunizations with the smooth ipa-positive strain (*ΔaroC* CRP) and the double mutant (*ΔrfbF* CRN) were determined in ELISA on different target bacterial cells. Reactivity is expressed as ratio (reactivity of the *ΔaroC* CRP sample divided by reactivity of the *ΔrfbF* CRN sample) at the same dilution in order to make repetitions comparable. Graph shows means + standard error of the means of four experiments performed with BAL samples obtained from independent vaccinations. Data were statistically compared by the Mann-Whitney non parametric test to the value obtained on the double (ipa and O antigen) positive target (*ΔaroC* CRP; black column).

Figure 4. **Supplementary Table 1: Oligonucleotides used for the generation and confirmation of deletion mutants.** (SEQ ID 3 - 10)

Figure 5. **Schematic presentation of an attenuated *Shigella flexneri* 2a 2457T strain.**

A. The *Shigella flexneri* 2a 2457T fully sequenced strain. O-antigen is the serotype determinant of Shigellae. The *rfbF* gene on the Shigella chromosome encodes a factor essential for the synthesis of the O-antigen component of LPS. The invasion plasmid present in all pathogenic Shigella strains encodes the invasion plasmid antigens (IpaA-D) which are important molecular components of the type III secretion system (T3SS). T3SS mediates key processes of target cell-Shigella interactions and eventually leads to the transmission of Shigella factors into the target cell that enables the pathogen to invade and spread. Ipa B and IpaC are key and essential components of this system.

B. In the *Shigella flexneri* 2a T2457 rfbF⁻ipaB/C⁻ mutant two deletions are introduced. Deletion of the rfbF gene from the chromosome eliminates the synthesis of the O-antigen and results in a "rough" strain that is attenuated and induces serotype independent immunity upon vaccination. Deletion of the ipaB and C genes on the invasion plasmid disrupts T3SS, thus rendering the Shigella mutant non-invasive (and Congo Red negative).

C. In order to stabilize the invasion plasmid of the mutant Shigella strain, an essential chromosomal gene (inorganic pyrophosphatase, *ppa* (Fig. 7 SEQ ID 24)) is deleted from the chromosome and re-introduced as a part of the synthetic construct into the invasion plasmid.

Figure 6: **Schematic illustration of the invasion plasmid pCP301 of the *Shigella flexneri* 2a** 301 strain with the *ipa* cluster, the primer positions for *ipa*B/C deletion (pKD1,2) and the control primers for monitoring deletion of *ipa*B/C (ko1,2). Position of the insertion site of the synthetic gene between ipaJ and an IS100 element is also indicated.

Figure 7: **Sequences**

gene for LT-B/mST fusion protein encoding ST with a mutation at amino acid position 13 (from Pro to Phe) together with the *eltAB* promoter and termination sequences

GP-P13F (nucleotide sequence, SEQ ID 11),

LT-B/mST fusion protein with a mutation in ST at amino acid position 13 (from Pro to Phe)

GP-P13F (amino acid sequence, SEQ ID 12),

gene for LT-B/mST fusion protein encoding ST with a mutation at amino acid position 13 (from Pro to Gly) together with the *eltAB* promoter and termination sequences

GS-P13G (nucleotide sequence, SEQ ID 13),

LT-B/mST fusion protein with a mutation in ST at amino acid position 13 (from Pro to Gly)

GS-P13G (amino acid sequence, SEQ ID 14),

gene for LT-B/mST fusion protein encoding ST with a mutation at amino acid position 12 (from Asn to Arg) together with the *eltAB* promoter and termination sequences

GS-N12R (nucleotide sequence, SEQ ID 15),

LT-B/mST fusion protein with a mutation in ST at amino acid position 12 (from Asn to Arg)

GS-N12R (amino acid sequence, SEQ ID 16),

gene for LT-B/mST fusion protein encoding ST with a mutation at amino acid position 12 (from Asn to Lys) together with the *eltAB* promoter and termination sequences

GS-N12K (nucleotide sequence, SEQ ID 17),

LT-B/mST fusion protein with a mutation in ST at amino acid position 12 (from Asn to Lys)

GS-N12K (amino acid sequence, SEQ ID 18),

Forward control PCR primer for confirming ipa deletion mutant strains

ipa co1 (SEQ ID 19),

Reverse control PCR primer for confirming ipa deletion mutant strains ipa co2 (SEQ ID 20),

Forward PCR primer to generate ipa deletion mutant strains

ipa pKD1 (SEQ ID 21),

Forward PCR primer to generate ipa deletion mutant strains

ipa pKD2 (SEQ ID 22),

Nucleotide sequence of the ipaB and ipC genes removed from the invasion plasmid

ipaBC (SEQ ID 23).

Nucleotide sequence of the ppa gene inplanted from the chromosome to the invasion plasmid

Shigella ppa gene (SEQ ID 24).

Forward PCR primer to generate ppa deletion mutant strains

ppa pKD-F (SEQ ID 25)

Reverse PCR primer to generate ppa deletion mutant strains

ppa pKD-R (SEQ ID 26)

Forward control PCR primer for confirming ppa deletion mutant strains

ppa ko1 (SEQ ID 27)

Reverse control PCR primer for confirming ppa deletion mutant strains

ppa ko2 (SEQ ID 28)

Linker peptide inserted between LT-B and mST for flexible folding

GGGGS (SEQ ID 29)

Figure 8:

PCR amplification of the chromosomal region where the rfbF gene is deleted. M: DNA size marker; WT: wild type *Shigella flexneri* 2a 2457T, rfbF gene with flanking region, 1100 bp fragment; mt: ΔrfbF mutant, gene replacement with chloramphenicol gene, 1300 bp.

Figure 9:

PCR amplification of the invasion plasmid region where the ipaC and ipaB genes were deleted. M: DNA size marker; WT: wild type *Shigella flexneri* 2a 2457T, ipaB and ipaC genes with flanking region, 1600 bp fragment; mt: ΔipaBC mutant invasion plasmid, gene replacement with kanamycin gene, 2570 bp.

Figure 10:

A. **Structure of the multi-gene constructs encoding the essential gene Ppa, the LTB-mST fusion protein and the kanamycin resistance protein.** Expression of the LTB-mST fusion protein is driven by the LTA-promoter and transcription is terminated with the LTB terminator.The LTB-ST amino acid sequences of 4 constructs with detoxifying ST mutations (P13F, P13G, N12R, N12K) are indicated (mutated codons underlined). Abbreviations: CS: cloning site; H1 and H2: homologous regions 1 and 2 on the invasion plasmid to aid homologous recombination; ppa: inorganic pyrophosphatase gene; pro: promoter; term: terminator; GGGGS: Gly-Gly-Gly-Gly-Ser (SEQ ID 29 penta-amino acid linker between LTB and mST; kan: kanamycin resistance gene.

B. **Insertion of ETEC genes into the Shigella invasion plasmid.** M: DNA size marker; WT: wild type *Shigella flexneri* 2a 2457T, invasion plasmid intergenic region, 450 bp fragment; mt: LT-B + STm gene mutant invasion plasmid, gene replacement with the kanamycin gene, 2800 bp,

C. **Immunoblot analysis to detect LTB.** The recombinant LT-B, as well *E. coli* and Shigellla culture supernatant fractions (secreted proteins) were separated by SDS-PAGE, proteins transferred to nitrocellulose membrane and detected with the anti-LTB monoclonal antibody. Lane 1: wild type *Shigella flexneri* (negative control); lane 2: *Shigella flexneri* carrying the fusion gene in the invasion plasmid; lane 3: DH5α *E. coli* transformed with pGET vector containing the synthetic construct as shown in Fig. 10A lane 4: ETEC strain expressing LT (positive control).

Figure 11:

Heterologous protection induced by *Shigella flexneri* 2a vaccine strain with engineered rfbF and ipaC/ipaB combined mutation. Groups of 5 mice were immunized intranasally with sublethal doses of either wild-type strain *Shigella flexneri* 2a 2457T (5×10^5 cfu/ mouse) or its isogenic deletion mutants 2457TΔrfb, 2457TΔipaBC, 2457TΔrfbΔipaBC (all at 10^8 cfu/mouse), or mock immunized with PBS buffer. Three identical immunizations were performed with 2-week intervals. One week following the last booster immunization, mice were challenged with a lethal dose of a *S. sonnei* strain (2×10^6 cfu/mouse). Survival of animals was monitored daily.

DETAILED DESCRIPTION OF THE INVENTION

Specific terms as used throughout the specification have the following meaning.

The term "attenuated" is used herein to describe a virulent strain of Shigella that has been modified so that it is no longer capable of causing disease, i.e., the modified strain is avirulent. The term "live" regarding the attenuated Shigella is used herein to describe Shigella that is able to grow and reproduce. Accordingly, the live Shigella strain of the present invention is used in the attenuated live vaccine and is specifically able to colonise the colon of a subject, but not cause the clinical symptoms associated with enteral diseases caused by the enteral or diarrheal pathogens. Further, the live strain of the present invention is specifically capable of limited replication in the vaccinated subject and of inducing a protective immune response which is protective against virulent strains of Shigella. An attenuated bacterium of the invention may be genetically engineered to express a heterologous antigen that is not expressed by the native bacterium, so that the attenuated bacterium acts as a carrier of the heterologous antigen.

The term "antigen" as used according to the present invention shall in particular refer to any antigenic determinant, which can be possibly recognised by a binding site of an antibody. Specifically preferred antigens are those molecules or structures, which have already been proven to be or are capable of being immunologically or therapeutically relevant, especially those, for which a clinical efficacy has been tested. The term as used herein shall in particular comprise molecules or structures selected from antigens comprising immunoaccessible and immunorelevant epitopes, in particular

conserved antigens found in one or more species or serotype. Immunoaccessible epitopes are typically presented by or comprised in antigens expressed on a cell surface. The term "protective antigen" as used herein shall refer to those antigens that trigger an immune response *in vivo*, so to induce neutralizing antibodies against the antigen. This provides for the effective protection upon active immunization with the antigen. Protein antigens are preferred antigens due to their inherent ability to elicit both cellular and humoral immune responses.

The term "heterologous" is herein used specifically with regard to an antigen, and understood as an antigen foreign to the cell expressing said heterologous antigen. With regard to a Shigella cell or strain, the term specifically refers to antigens foreign to the Shigella cell or strain, respectively. Thus, such heterologous or foreign antigen would not be expressed in a wild-type cell or strain, but by the recombinant one comprising a heterologous gene encoding said antigen. Thereby said recombinant cell or strain would express said heterologous antigen, e.g. on the cell surface. The cells of the invention may be genetically engineered to express a heterologous antigen, e.g. a non-toxic component or form of LT and/or ST or STm. Such cells induce an immune response against the heterologous antigen as well as the native antigens and hence improve the protection provided by a vaccine.

The term "cross-reactive" with respect to antigens as used herein shall mean antigens with epitopes shared between different pathogens, including e.g. different serotypes of the same species or different bacterial species. Cross-reactive antigens typically are conserved structures. Cross-reactive epitopes may originate from the same antigens expressed by different pathogens, or else from different antigens with similar structure.

Specific cross-reactive antigens are recognized by cross-reactive antibodies, e.g. antibodies of antisera, isolated antibodies or recombinant ones. Such cross-reactive antibodies may recognize the cross-reactive antigens of different pathogens. Specific cross-reactive antibodies are neutralizing antibodies.

A "cross-protective" vaccine or immune response is understood as one which protects against infection by at least one different pathogen, e.g. a different species or serotype, which is not identical to the one used to elicit the response. Cross-protective efficacy typically may be tested with different antisera from subjects that had been exposed to the different pathogens.

When a cross-reactive antigen is designed to induce cross-protective immunity, this may be tested in animal models, e.g. by immunising the animals with the cross-reactive antigen derived from one pathogen triggering an immune response, and challenging the animals with at least one pathogen different form the one used to elicit the response. As an example, such cross-protective immunity against more than one Shigella serotype or other enteroinvasive bacteria with cross-reactive antigens, such as *E.coli*, specifically refers to protection against distinct variations within the species of bacteria of different individuals, e.g. variations at the sub-species level. The group of serovars with common antigens is called a serogroup or serotype.

The basis for the development of a broad spectrum, e.g. multi-strain and/or multi-serotype and/or multi-species Shigella vaccine is the identification of cross-reactive antigens which are prevalent in Shigella serovars. This particularly includes isolates associated with human infections.

When a polyvalent vaccine is designed to induce cross-protective immunity against different pathogens, the immune response typically is elicited by several antigens, e.g. individual antigens from the different pathogens. As an example, such polyvalent vaccine may be based on at least two different protective antigens from different species, such as derived from Shigella and Escherichia, but also other bacterial, viral, fungal or parasitic antigens. The cross-protective, polyvalent vaccine may e.g. be tested in an animal model by immunising the animals with the vaccine comprising different protective antigens derived from at least two different pathogens triggering an immune response, and challenging the animals with one, two or more of the pathogens.

The basis for the development of a multi-species vaccine candidate based on specific attenuated Shigella bacteria, as used according to the invention, is the identification of protective antigens, either cross-reactive to address a series of different serotypes or not, which are prevalent in the different pathogenic species, against which protection is sought.

The term “enteral” also known as “enteric”, as used herein specifically in connection with a disease or pathogen shall refer to a disease condition or pathogen relating to, or affecting the intestines, e.g. dysentery or diarrheal disease. Specifically such enteral disease refers to infectious disease of the colon. Specific symptoms include bloody, mucus-filled diarrhea; abdominal pain; fever and loss of fluids from the body. Diarrheal disease refers to conditions resulting in three or more loose or liquid

stools per day, or as having more stools than is normal for that person. An enteral pathogen is understood to cause enteral disease in a subject, either upon infection with said pathogen, or intoxication of the subject with a toxin, in particular an enterotoxin.

There are many causes of infectious enteral disease, such as dysentery or diarrhea, which include viruses, bacteria, funghi and parasites. Examples are provided as follows: Norovirus is the most common cause of viral diarrhea in adults, but rotavirus is the most common cause in children under five years old. Adenovirus types 40 and 41, and astroviruses cause a significant number of infections. The bacterium Campylobacter is a common cause of bacterial dysentery or diarrhea, but infections by Salmonellae, Shigellae and some strains of *Escherichia coli* (*E.coli*) are frequent in some territories. In the elderly, particularly those who have been treated with antibiotics for unrelated infections, a toxin produced by *Clostridium difficile* often causes severe diarrhea. Examples of parasites include *Giardia lamblia*, which can cause chronic infections, and *Entamoeba histolytica*. Examplary enteral disease as possibly addressed by the vaccine of the invention is Shigellosis and ETEC-related diarrhea.

The term “endogenous” as used herein with respect to a plasmid shall mean the plasmid that originates in a particular host cell. An endogenous plasmid may be genetically engineered to obtain a recombinant endogenous plasmid, e.g. by recombinant techniques to engineer the plasmid *in situ*, i.e. within the host cell harbouring the native endogenous plasmid, or else upon removal from the host cell, subjecting it to laboratory manipulation, and then reintroduced into a host cell of the same type. The invasive phenotype of Shigella is specifically conferred by the endogenous 220-kb virulence plasmid, also called invasion plasmid, or native or endogenous invasion plasmid. The endogenous invasion plasmid of Shigella is specifically provided according to the invention for recombination purposes, either as isolated invasion plasmid or for *in situ* recombination.

The term “essential” as used herein with respect to a gene is understood to refer to a gene necessary for a living organism to survive, e.g. for a bacterial cell to replicate. Mutation of an essential gene, such as a deletion and/ or inactivation, would cause a lethal phenotype or a non-replicable cell. Essential genes of Shigella may be mutated to delete the gene(s) of the Shigella chromosome, and further to incorporate the gene(s) into the invasion plasmid to stabilize the invasion plasmid. This provides

for cultivation of a Shigella with a stable recombinant endogenous invasion plasmid. Among the essential genes of Shigella there are the *ppa*, *accD*, *acpS*, *dapE*, *era*, *frr*, *ftsI*, *ftsL*, *ftsN*, *ftsZ*, *infA*, *lgt*, *lpxC*, *msbA*, *murA*, *murI*, *nadE*, *parC*, *proS*, *pyrB*, *rpsB*, *trmA*, *rho* and *rhoL* genes.

Herein "inactivation" of a gene is always understood to refer to transient, inducible or constitutive down-modulation of a gene, so to reduce or inhibit expression of a gene product. This may specifically be done by mutation of a gene or regulatory sequence operably linked to the gene, such as promoters, enhancers, etc. that regulate the expression of a gene. Among the inactivating mutations there are particularly those that result in the reduction or suppression of expression of polynucleotides or genes, e.g. genes encoding virulence factors, or lead to the expression of respective non-functional proteins, e.g. non-functional virulence factors.

The term "invasive" or "non-invasive" as used herein with respect to a gene is understood in the following way. Invasive pathogenic bacteria are capable of invading eukaryotic cells. For example, after invasion, Shigella may multiply intracellularly and spread to neighbouring epithelial cells, resulting in tissue destruction and characteristic pathology of Shigellosis. Among the genes mediating invasiveness of Shigella there are e.g. the *ipa* genes encoding invasion plasmid antigens. Deletion and/ or inactivation of at least one of such genes may lead to a non-invasive Shigella.

The Sereny test is a standard test for determining the invasiveness of organisms such as Shigella or *Escherichia coli*. (Wood et al. J. Clin. Microbiol. 24: 498–500, 1986). It is done by inoculating suspension of bacteria into guinea pig's eye. Severe mucopurulent conjunctivitis and severe keratitis indicates a positive test.

The term "isolated" or "isolation" as used herein with respect to a nucleic acid, and in particular with respect to a vector, plasmid and specifically the invasion plasmid of Shigella, shall refer to such compound that has been sufficiently separated from the environment with which it would naturally be associated, so as to exist in "substantially pure" form. The term "substantially pure" or "purified" as used herein shall refer to a preparation comprising at least 50% (w/w), preferably at least 60%, 70%, 80%, 90% or 95% of a compound, such as a nucleic acid molecule or a plasmid. Purity is measured by methods appropriate for the compound (e.g. chromatographic methods, polyacrylamide gel electrophoresis, HPLC analysis, and the like).

"Isolated" does not necessarily mean the exclusion of artificial or synthetic mixtures with other compounds or materials, or the presence of impurities that do not interfere with the fundamental activity, and that may be present, for example, due to incomplete purification. In particular, isolated nucleic acid molecules of the present invention are also meant to include those chemically synthesized.

With reference to the isolated invasion plasmid of the invention, this term refers to a plasmid that is separated from the cytoplasm in which it originated. An "isolated plasmid" may further represent a plasmid produced directly by biological or synthetic means and separated from other components present during its production.

The term “mutagenesis” with respect to a gene as used herein shall mean the mutation of a genetic sequence, in particular any of deletion, substitution, insertion of at least one nucleotide, or any combinations thereof, to obtain a mutated gene. This shall particularly refer to entire gene(s) or a significant part thereof, e.g. a deletion of at least 50% of the gene. The terms “mutagenesis” and “mutation” are herein used interchangeably.

The term “rough” with respect to a gram-negative bacteria, such as Shigella, means other than smooth, and shall specifically include “gently-rough” (i.e. O-ag synthesis downregulated) or “deep-rough” bacteria. The term "rough" as used herein may include characteristics such as an irregular colony morphology, and may include for instance undulate and/or lobate morphology. The term specifically means that a strain is unable and/or substantially unable to produce O- polysaccharide. A repetitive glycan polymer contained within an LPS is referred to as the O-antigen, O-poly-saccharide, or O-(side-) chain of the bacteria. The O antigen is attached to the core oligosaccharide, and comprises the outermost domain of the LPS molecule. The presence or absence of the O-chains determine, whether the LPS is considered rough or smooth. Bacterial strains that have altered O-antigen structures change their appearance from smooth to dull when grown on agar plates. Full-length O-chains make the LPS smooth, while the absence or reduction of O-chains renders the LPS rough. "Smooth" bacteria include the complete core and O-antigen. "Rough" bacteria include a lack of LPS O-antigen, meaning no O-antigen or a reduced chain length of O-antigen or a reduced number of smooth LPS chains. The term “Gently-rough” refers to a subgroup of rough bacteria, which have a reduced chain length of O-antigen or a reduced number of smooth LPS chains. "Deep rough" bacteria have lost parts of the LPS core, consequently lack O-antigens as well.

The term "lack of LPS O-antigens" as used herein with respect to rough Shigella shall specifically refer to less than 50%, or less than 40%, or less than 30%, or less than 20%, or less than 10%, or essentially no or no LPS O-antigen as determined in a standard assay.

A standard test may be used to determine the rough characteristics of a strain. For example, the phenotype of LPS mutants may e.g. be determined by SDS-PAGE separation of LPS and silver staining or agglutination tests using serotype-specific immune sera.

The rough Shigella may be produced by attenuation, e.g. by mutation of at least one gene or a significant part thereof, such as by deletion and/ or inactivation, which gene is involved in the LPS synthesis, transport and/or expression, preferably selected from the group consisting of genes in the cluster of the *rfb* operon, or one or more of genes within the *rfb/wbb* gene cluster encoding O-antigen synthesis, *waaL* encoding the O-antigen ligase, *wzx* encoding O-antigen flippase involved in O-antigen transport, *wzy/rfc* involved in O-antigen polymerization, genes within the *rfa/waa* gene cluster encoding LPS-core synthesis, regulatory genes affecting O-antigen expression, such as *rfaH*, or loss of function(s) of which results in at least 90% reduction in the expression of O-antigens.

Specific examples of genes involved in the LPS sugar synthesis are *rfbA*, B, D and C.

Specific examples of genes involved in the LPS sugar transferase are *rfbF* and G.

A specific example of a gene involved in the LPS O-antigen polymerase is *rfc/wzy*.

The cluster of the *rfb* operon is located either on the chromosome or on the invasion plasmid (*Shigella sonnei*). Specific genes in this cluster are *rfb* F, D, C, E, J and/or I genes.

As used herein, the term "recombinant" refers to a molecule or construct that does not naturally occur in a host cell. In some embodiments, recombinant nucleic acid molecules contain two or more naturally-occurring sequences that are linked together in a way that does not occur naturally. A recombinant protein refers to a protein that is encoded and/or expressed by a recombinant nucleic acid. In some embodiments, "recombinant cells" express genes that are not found in identical form within the native (i.e., non-recombinant) form of the cell and/or express native genes that are otherwise

abnormally over-expressed, under-expressed, and/or not expressed at all due to deliberate human intervention. Recombinant cells contain at least one recombinant polynucleotide or polypeptide. “Recombination”, “recombining”, and generating a “recombined” nucleic acid generally encompass the assembly of at least two nucleic acid fragments. In certain embodiments, recombinant proteins and recombinant nucleic acids remain functional, i.e., retain their activity or exhibit an enhanced activity in the host cell. In any case an attenuated bacterium, such as the attenuated Shigella of the invention is considered a recombinant cell. A nucleic acid construct, such as a plasmid or vector, nucleic acid (e.g., a polynucleotide), polypeptide, or host cell is referred to herein as “recombinant” when it is non-naturally occurring, artificial or engineered. A recombinant invasion plasmid of Shigella is particularly engineered to incorporate a specific deletion and/ or inactivation of one, two or more poly-nucleotide(s) or genes, such as at least one deletion of genes encoding invasion plasmid antigens, and/or further comprises one or more heterologous genes, such as genes encoding protective antigens.

A “stable” recombinant invasion plasmid of Shigella is a Shigella plasmid that displays at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or greater than 90% retention in a Shigella cell culture under conditions selected to maintain the plasmid in the cell culture. A specific example of a stable recombinant invasion plasmid of Shigella refers to a recombinant Shigella host cell that has been mutated to delete and/ or inactivate an essential gene located at a chromosomal locus, and integrated at a locus of the invasion plasmid. While a Shigella without the invasion plasmid would not grow or not be replicated, the Shigella bearing the endogenous invasion plasmid would be able to grow and replicate *in vivo*.

As used herein, the term “vector” refers to a vehicle by which a DNA or RNA sequence, e.g. a foreign (heterologous) gene, can be introduced into a host cell, so as to transform the host and promote expression (e.g. transcription and translation) of the introduced sequence. Plasmids are preferred vectors of the invention, in particular the invasion plasmid of Shigella, including specifically an endogeneous invasion plasmid.

Vectors typically comprise the DNA of a transmissible agent, into which foreign DNA is inserted. A common way to insert one segment of DNA into another segment of DNA involves the use of enzymes called restriction enzymes that cleave DNA at specific sites (specific groups of nucleotides) called restriction sites. A “cassette” refers to a DNA coding sequence or segment of DNA that codes for an expression product

that can be inserted into a vector at defined restriction sites. The cassette restriction sites are designed to ensure insertion of the cassette in the proper reading frame. Generally, foreign DNA is inserted at one or more restriction sites of the vector DNA, and then is carried by the vector into a host cell along with the transmissible vector DNA. A segment or sequence of DNA having inserted or added DNA, such as an expression vector, can also be called a "DNA construct." A common type of vector is a "plasmid", which generally is a self-contained molecule of double-stranded DNA, usually of bacterial origin; that can readily accept additional (foreign) DNA and which can readily introduced into a suitable host cell.

The Shigella of the present invention preferably comprises the recombinant endogenous invasion plasmid used as a vector to express one or more heterologous genes. Thus, according to a preferred embodiment, the Shigella is a "no artificial vector" strain, meaning that the strain does not comprise an artificial plasmid, besides any (recombinant) endogenous plasmid.

A plasmid vector often contains coding DNA and promoter DNA and has one or more restriction sites suitable for inserting foreign DNA. Coding DNA is a DNA sequence that encodes a particular amino acid sequence for a particular protein or enzyme. Promoter DNA is a DNA sequence which initiates, regulates, or otherwise mediates or controls the expression of the coding DNA. Promoter DNA and coding DNA may be from the same gene or from different genes, and may be from the same or different organisms. Recombinant cloning vectors will often include one or more replication systems for cloning or expression, one or more markers for selection in the host, e.g. antibiotic resistance, and one or more expression cassettes. The term "expression system" means a host cell and compatible vector under suitable conditions, e.g. for the expression of a protein coded for by foreign DNA carried by the vector and introduced to the host cell.

Therefore, the attenuated Shigella according to the invention is specifically used in the development of a live vaccine.

The attenuated Shigella specifically is derived from a virulent strain of any of the Shigella species and serogroups (serotypes). For example, any of the following groups:

- Serogroup *A*: *S. dysenteriae* (12 serotypes)
- Serogroup *B*: *S. flexneri* (15 serotypes and subserotypes)
- Serogroup *C*: *S. boydii* (18 serotypes)
- Serogroup *D*: *S. sonnei* (1 serotype)

The virulent Shigella strain as used herein for the purpose of attenuation may be a clinically known virulent strain or a strain that is identified as containing virulence factors. Specifically the strain is selected from any of *S. flexneri, S. sonnei, S. dysenteriae and S. boydii, in particular S. flexneri 2a, such as S. flexneri 2a 2457T* (ATCC 700930, DNA=700930D-5), or CIP 107659 (Institute Pasteur, France).

The virulent Shigella strain may be modified by methods known in the art including multiple serial passage, temperature sensitive attenuation, mutation, or the like such that the resultant strain is attenuated, specifically avirulent, not capable of causing disease in a subject.

In some embodiments, the modification to the virulent strain results in the deletion and/ or inactivation of a gene, including reduction or suppression of expression of polynucleotides or genes encoding virulence factors or leads to the expression of non-functional virulence factors.

There are a number of techniques well known in the art to obtain attenuating mutations, e.g. for reducing or abolishing polynucleotide expression. For example, a mutation may be introduced at a predetermined site, such as the promoter region or within the coding sequence to produce a nonsense mutation, using recombinant DNA-technology. Recombinant DNA techniques comprise cloning the gene of interest, modification of the gene sequence by site-directed mutagenesis, restriction enzyme digestion followed by re-ligation and subsequent replacement of the wild type gene with the mutant gene.

Suitable standard recombinant DNA techniques are known in the art and described inter alia in Sambrook et al., “Molecular Cloning: A Laboratory Manual” (1989), 2nd Edition (Cold Spring Harbor Laboratory press).

The attenuating mutations may be performed employing methods well-known in the art, including cloning the DNA sequence of the wild-type gene into a vector, e.g. a plasmid, optionally inserting a selectable marker into the cloned DNA sequence or deleting a part of the DNA sequence, resulting in its inactivation. A deletion may be introduced by, for example, cutting the DNA sequence using restriction enzymes that cut at two points in or just outside the coding sequence and ligating together the two ends in the remaining sequence. Alternatively, a mutant allele in which the flanking regions of a target gene are amplified separately and linked directly together in a separate overlap PCR reaction, with omission of the intervening target sequence, can be constructed. A plasmid carrying the mutated DNA sequence can be transformed into the bacterium by known techniques such as electroporation chemical transformation or conjugation. It is then possible by suitable selection to identify a mutant wherein the inactivated DNA sequence has recombined into the chromosome of the bacterium and the wild-type DNA sequence has been rendered non-functional by homologous recombination.

Furthermore, if an antibiotic resistance gene was used, it is generally removed from the bacteria before they are used in a vaccine. According to the method of Datsenko et al. (Proc. Natl. Acad. Sci. U. S. A 97, 6640-6645 (2000)) mutagenesis is based on the lambda bacteriophage Red recombinase system that allows specific disruption of both plasmid encoded and chromosomal genes. The strategy is to replace such genes, e.g. with a selectable antibiotic resistance gene, which is generated by PCR using primers with 40-60 nt homology extensions to the targeted gene. The Red-based recombination is mediated in these homologous sequences. Following selection, the antibiotic resistance gene can also be eliminated using a helper vector that expresses the FLP recombinase, which uses FRT direct repeats (FLP recognition target) flanking the antibiotic resistance gene.

In some embodiments, a mutation may be introduced at a predetermined site in chromosomal or extrachromosomal DNA, e.g. a plasmid, via an insertion, a deletion, or a substitution of one nucleotide by another, such as a point mutation, which leads to a mutated gene that has reduced or no expression. The mutation should produce a Shigella strain that has a reduced capacity to cause dysentery. Preferably, the mutation is a deletion mutation, where disruption of the gene is caused by the excision of nucleic acids. Such a mutation can, for example, be made by the deletion of a contiguous span of base pairs. Even very small deletions such as stretches of 10 base

pairs can cause the gene to encode no protein or a non-functional protein. Even the deletion of one single base pair may lead to no protein or a non-functional protein, since as a result of such a mutation, the other base pairs are no longer in the correct reading frame or transcription has been inhibited or diminished. More preferably, a longer stretch is removed e.g. 100 base pairs or at least the significant part of a gene, e.g. at least 50% of the gene. Even more preferably, the whole gene is deleted.

Well-defined and deliberately made mutations involving the deletion of fragments or the whole gene, or combinations thereof, have the advantage, in comparison to classically induced mutations, that they will not revert to wild-type. Thus, in some embodiments of the invention the vaccine strain comprises a live attenuated Shigella strain in which a mutation in a gene encoding a virulence factor comprises a deletion or an insertion to disrupt the polynucleotide sequence encoding the virulence factor so that no corresponding protein is produced or the protein is non-functional.

Exemplary virulence factors selected to engineer an attenuated Shigella strain are *rfb*, *ipaB*, *ipaC* or *aroC*.

The attenuation may, for example, be brought about by deleting and/or inactivating one or more of the following genes, or (a significant) part thereof, or any of the modulators of said gene effecting attenuation of said genes: *rfb*, *aroA*, *aroC*, *aroD*, *aroE*, *virG* and *ipaA-D*. Preferred attenuated Shigella strains of the invention are double mutants or multiple mutant strains with at least three or more attenuating mutations. Preferred combinations of target genes for attenuating mutations include at least one *rfb* gene (e.g. *rfb* F, D, C, E, J and/or I genes) and at least one *ipa* gene (e.g. *ipaB*, *ipaC*).

As an alternative to attenuating mutations resulting from genetic engineering, it would also be possible to identify naturally occurring strains of Shigella that are avirulent or comprise one or more preexisting mutations in a polynucleotide or gene encoding a virulence factor which can be used as live vaccine strains. These naturally occurring Shigella strains, once isolated by standard techniques, may be subjected to further mutagenesis or recombinant DNA techniques to construct double or multiple mutant strains.

Techniques for identifying bacteria that have one or more mutations in genes encoding virulence factors are known by one skilled in the art. Accordingly, routine techniques for the detection of Shigella strains that have been mutated by the techniques described above include Northern and Western blotting, PCR, ELISAs and

cytotoxicity assays as described elsewhere herein. Mutant strains with no functional genes encoding specific virulence factors can easily be selected employing standard techniques.

Genes encoding the virulence factors to be attenuated may be plasmid-borne. Therefore, in some embodiments the modification to a virulent Shigella strain comprises mutating one or more endogenous Shigella plasmids. The term "plasmid", specifically refers to cytoplasmic DNA that replicates independently of the bacterial chromosome. The mutation of parts of the Shigella virulence or invasion plasmid or even the elimination of a plasmid may be envisaged. However, it is preferred that the attenuated Shigella still comprises the endogenous invasion plasmid, more preferable a stable invasion plasmid. This ensures the stability of the attenuated strain, in particular with respect to the potential loss of the invasion plasmid by the attenuated cell, or the potential uptake of a (native) invasion plasmid derived from a wild-type Shigella, which may occur with an instable strain or instable invasion plasmid.

The Shigella invasion plasmid is endogenous in most strains of Shigella. Though the invasion plasmid may be lost on cultivating a Shigella strain, it may be engineered to obtain a recombinant one exhibiting a high level of stability, which renders it an attractive target for development as a useful vector to incorporate heterologous genes encoding antigens, in particular protective antigens.

The recombinant invasion plasmid of the present invention obtained in the examples described hereinafter has the features as indicated in Figure 5 and 10A.

The plasmid of the present invention includes derivatives thereof autonomously replicable in Shigella. Such a derivative may be one corresponding to the invasion plasmid of which portion other than the region responsible for the invasion is removed therefrom, or one corresponding to the invasion plasmid of which part is inserted with another (heterologous) DNA sequence. Thereby a suitable shuttle vector autonomously replicable in Shigella may be obtained. Such vector may be used in any of the attenuated Shigella live vaccine strains according to the invention, or in any other bacteria capable of incorporating an invasion plasmid, including enteroinvasive Escherichia.

The endogenous Shigella invasion plasmid is well characterized in the art, and this knowledge informs selection of sites for recombination in such plasmids, as well as appropriate propagation conditions, e.g. at position between ntds 103187-103328 between an IS100 and *ipaJ* genes (these positions are determined for the pCP301 invasion plasmid of the *Shigella flexneri* 2a 301 strain)

The plasmid preferably is employed as a single copy plasmid.

The plasmid of the present invention may be provided in the isolated form, e.g. by preparing a DNA fraction of cytoplasm from the Shigella cells by a common method for preparing a plasmid DNA from cells. Further, the DNA fraction may be purified by density-gradient centrifugation method, agarose gel electrophoresis and the like.

For the construction of a shuttle vector, the whole sequence or a part thereof may be used. When a part thereof is used, such a part typically contains the region responsible for the replication of the plasmid, but a region unnecessary for the replication may be excluded. For example, the region required for the replication can be determined by ligating a part obtained by digesting the plasmid with a restriction enzyme to a plasmid autonomously replicable in Shigella, transforming another bacterium, such as another Shigella strain or an Escherichia strain, with the obtained recombinant plasmid, and determining if the recombinant plasmid is harbored by the transformant.

The vaccine according to the invention may be formulated using known techniques for formulating attenuated bacterial vaccines. The vaccine is advantageously presented for oral administration, for example as an aqueous solution or dried powder for reconstitution in a suitable buffer prior to administration. Reconstitution is advantageously effected in a buffer at a suitable pH to ensure the viability of the bacteria. In order to protect the attenuated bacteria and the vaccine from gastric acidity, a protective agent, such as sodium bicarbonate is advantageously administered with each administration of the vaccine. Alternatively the vaccine is presented in a lyophilized encapsulated form.

Vaccine strains may be administered in a pharmaceutically acceptable vehicle, e.g. as a spray or mixed in food and/or water or delivered in admixture with a suitable carrier, diluent, adjuvant or excipient such as sterile water, physiological saline, glucose, or the like. The vaccine strains may contain auxiliary substances such as wetting or emulsifying agents, pH buffering agents, adjuvants, gelling or viscosity enhancing additives, preservatives, flavoring agents, colours, and the like, depending

upon the route of administration and the preparation desired. Pharmaceutical carriers for preparation of pharmaceutical compositions and medicaments are well known in the art, as set out in textbooks such as "Remington's Pharmaceutical Sciences" (1990), 18th Edition (Mack Publishing Co.).

The vaccine strains of the present invention can be administered in dosages and by techniques well known to those skilled in the medical or veterinary arts, taking into consideration such factors as the age, sex, weight, species and condition of the recipient subject, and the route of administration. The route of administration can be percutaneous, via mucosal administration (e.g., oral, nasal, anal, vaginal) or via a parenteral route (intradermal, intramuscular, subcutaneous, intravenous, or intra-peritoneal). Vaccine strains can be administered alone, or can be co-administered or sequentially administered with other treatments or therapies. Forms of administration may include suspensions, syrups or elixirs, and preparations for parenteral, subcutaneous, intradermal, intramuscular or intravenous administration (e.g., injectable administration) such as sterile suspensions or emulsions.

The vaccine may be used in the vaccination of a subject, particularly a human being, or else a warm-blooded mammalian, specifically including pigs.

Once produced the vaccine strain of the present invention may be administered to a subject in the course of an active immunotherapy, specifically by vaccination, to prevent enteral disease, specifically dysentery caused by Shigella and optionally heterologous enteral or diarrheal pathogens. This may be achieved by any of the vaccines according to the invention, which are cross-protective and/or polyvalent.

An infection caused by Shigella and optionally other a microorganism, such as diarrheal microorganisms targeted by a cross-protective and/or polyvalent vaccine of the invention, may therefore be prevented or treated by administering an effective dose of the vaccine according to the invention. The dosage employed may ultimately be at the discretion of the physician, but will be dependent on various factors including the size and weight of the subject and the type of vaccine formulated. However, a dosage comprising the oral administration of from 10^7 to 10^{11}, e.g. from 10^8 to 10^{10}, bacteria per dose may be convenient for a 70 kg adult human host.

An infection caused by Shigella and optionally other a microorganism, especially a pathogen, may therefore be prevented or treated by administering an effective dose of a vaccine according to the invention. The dosage employed may ultimately be at the discretion of the physician, but will be dependent on various factors including the size

and weight of the subject and the type of vaccine formulated. However, a dosage comprising the oral administration of from 10^7 to 10^{11}, e.g. from 10^8 to 10^{10}, bacteria per dose may be convenient for a 70 kg adult human host.

According to specific examples, isogenic attenuated mutants of a prototype *S. flexneri* 2a strain were constructed. The mutants were either unable to synthesize O-antigens (Δ*rfbF*) or - representing a well-proven vaccine approach - were auxotrophic (Δ*aroC*). Virulence of these mutants in the mouse lung model showed a comparable level of attenuation. Subsequently, we isolated derivatives of both mutants that lacked the invasion plasmid encoding the Ipa-s (Congo red negative /CRN/ mutants). Loss of the invasive phenotype in these latter mutants increased attenuation further to an undetectable level. This series of *S. flexneri* 2a mutants lacking either O-antigens (*ΔrfbF* CRP), or ipa proteins (*ΔaroC* CRN), or both (*ΔrfbF* CRN) or none of these antigens (*ΔaroC* CRP) were used to immunize mice at sublethal doses intranasally. Subsequently, mice were challenged by lethal doses of heterologous *S. flexneri* 6 (Fig. 1a) or *S. sonnei* (Fig. 1b) wild type strains. The attenuated mutant expressing both ipa and O-antigens (*ΔaroC* CRP) could not provide protection over the level observed at mock vaccinated mice. In contrast, the double mutant lacking both major immunogenic groups of antigens elicited high protection against both heterologous challenge strains. Even loss of the virulence plasmid alone (*ΔaroC* CRN) appeared to improve cross-protection. In order to corroborate these results, groups of mice were also immunized with Phase I (Ipa and O-antigen positive) and Phase II (Ipa and O-antigen negative) variants of a *S. sonnei* isolate. The Phase II vaccine strain provided high protection against a challenge by *S. flexneri* 6, whereas immunization with the fully virulent Phase I strain afforded no significantly different survival from that provided by saline (Fig. 1c).

To support the concept that improved cross-protection originates from increased immunogenicity of minor antigens at this mutant backgrounds (i.e. upon the loss of dominant antigens – see Fig. 2), immune reactivity of serum and bronchoalveolar lavage (BAL) samples obtained from the immunized mice were compared in ELISA on whole bacterial cells that expressed both or none of the major antigenic groups (Fig. 3).

BAL obtained from mice vaccinated with the *ΔaroC* CRP (both ipa and O-antigen positive) mutant were more reactogenic to the invasive smooth homologous target verifying that these antigens, indeed, dominated the immune response. On the contrary, loss of the immunodominant antigens on the vaccine strain (*ΔrfbF* CRN)

resulted in an improved reactogenicity to the homologous target strain devoid of both O- and Ipa antigens.

Furthermore, the heterologous *S. sonnei* strain was more readily recognized by BAL obtained from mice vaccinated by the double mutant. These results corroborate that there is a higher titer of mucosal antibodies against those shared minor antigens that are accessible on these targets. Interestingly, this phenomenon was not apparent in case of serum IgG (data not shown), supporting earlier findings showing that sIgA rather than serum IgG mediates protection in this model.

Current vaccine approaches (in general as well as to *Shigella* in particular) rely on the utilization of major immunogenic antigens. In order to evade the immune response, however, evolutionary pressure has selected multiple immunologically distinct variants of these antigens, which form the basis of classifying pathogens in serotypes. Utilization of serotype-determining major antigens might therefore confer only partial protection against a pathogen, unless all serotypes can be included in the vaccine (e.g. in case of poliovirus vaccines). Combination of the most prevalent serotypes can give a relatively broad protection, however, this could be transient due to serotype replacement (i.e. less common serotypes emerge filling the gap opened by the eradication of the vaccine serotypes). This necessitates vaccine optimization from time to time, for example by including additional serotypes in the multivalent vaccines. Due to phenomena like antigenic competition and interference as well as financial considerations, however, the maximum number of serotypes to be covered is limited.

On the other hand, various serotypes of a given bacterial pathogen share a huge number of conserved antigens on their surface. The fact that they could have remained conserved implies that they are either not accessible on the surface (not protective antigens) and/or their function is so indispensible for pathogenesis that allows no modification in their antigenic structure. This is exemplified by the *Shigella* ipa proteins, which are highly conserved (due to their sophisticated function in invasion) and very immunogenic, still can not elicit cross-protection, probably because they are only expressed upon contact to the target cell, hence probably not accessible for an antibody-mediated protective mechanism.

Specifically we show (Fig. 2.), that immunodominant antigens such as Iipa and O antigens hijack the immune response in a way that allows less antibodies to be raised against minor antigens. Given that Ipa-s are not protective and O-antigens are highly variable, *Shigella* can efficiently evade the immune response. We show,

however, that deletion of these classes of antigens highly improved cross-protective potential of live vaccine strains.

As regards the invasion plasmid mutation, instead of selection for spontaneous deletion mutant of the invasion plasmid based on the loss of Congo Red positivity, the *ipaB* and *C* genes may be removed, while the rest of the plasmid is intact.

Moreover, the plasmid may be stabilized by implantation of an essential gene, such as *ppa*, from the chromosome to the invasion plasmid.

Furthermore, the expression of foreign (heterologous) antigens, such as ETEC LTB and mutated STa (STm) toxins are feasible. STm preferably contains one or more point mutations. Specifically preferred STm are

NSSNYCCELCCXXACTGCY (SEQ ID 1),

wherein

X at position 12 is N, K or R, and/or

X at position 13 is P, G, L or F,

wherein the STm excludes the wild-type sequence:

NSSNYCCELCCNPACTGCY (SEQ ID 2).

Preferred combinations of point mutations are N12K or N12R in combination with P13F.

Furthermore, examples show that relative immunogenicity of shared conserved antigens had increased in the absence of the major antigens in the vaccine strain. As these deletions not only improve the spectrum of protection but also render the vaccine strain highly avirulent, the double mutant is considered as very safe, even at extremely high doses. Moreover, live oral vaccines are relatively cheap to manufacture, and require no trained medical personnel for administration, which are important factors when considering the target population in endemic countries.

The subject matter of the following definitions is considered embodiments of the present invention:

1. A live attenuated Shigella vaccine, which is based on a rough Shigella strain lacking LPS O antigen, preferably a non-invasive strain.

2. Vaccine according to definition 1, which is attenuated by mutagenesis of one or more genes involved in the LPS synthesis, transport and expression, preferably selected from the group consisting of genes in the cluster of the *rfb* or one or more genes within the *rfb/wbb* gene cluster encoding O-antigen synthesis, *waaL* encoding

the O-antigen ligase, *wzx* encoding O-antigen flippase involved in O-antigen transport, *wzy/rfc* involved in O-antigen polymerization, genes within the *rfa/waa* gene cluster encoding LPS-core synthesis, regulatory genes affecting O-antigen expression, such as *rfaH*, or loss of function(s) of which results in at least 90% reduction in the expression of O-antigens.

3. Vaccine according to definition 1 or 2, wherein said mutagenesis is by a deletion of one or more of the *rfb* F, D, C, E, J and/or I genes, or a deletion of a part thereof, or corresponding genes in various Shigella serotypes.

4. Vaccine according to any of definitions 1 to 3, wherein said Shigella strain is selected from the genus Shigella, e.g. from any Shigella serotype or species, in particular *S. flexneri, S. sonnei, S. dysentheriae and S. boydii.*

5. Vaccine according to any of definitions 1 to 4, wherein said Shigella expresses cross-reactive outer membrane proteins.

6. Vaccine according to any of definitions 1 to 5, which is cross-protective against different serotypes and species of Shigella, in particular against any of *S. flexneri 2a*, *S. flexneri 6* and *S. sonnei*, or enterinvasive *Escherichia coli*.

7. Vaccine according to any of definitions 1 to 6, wherein said Shigella is non-invasive by further mutagenesis of the invasion plasmid, in particular a deletion of the *ipaB* and/or *ipaC* genes and/or other *ipa* genes.

8. Vaccine according to any of definitions 1 to 7, wherein said Shigella comprises a recombinant endogenous invasion plasmid incorporating at least one gene encoding a heterologous antigen to secrete said antigen or to express said antigen, e.g. on the bacterial cell surface.

9. Vaccine according to definition 8, wherein said antigen is selected from the group consisting of

- a bacterial antigen preferably a toxin or colonization factor,
- a viral antigen, preferably from a pathogen causing enteral or mucosal infections,
- a fungal antigen, preferably from a pathogen causing enteral or mucosal infections, and
- a parasitic antigen, preferably from a pathogen causing enteral infections.

10. Vaccine according to definition 9, wherein the bacterial antigen is originating from enteropathogenic bacteria, preferably selected from the group consisting of

a. *E.coli* antigens, in particular an enterotoxin selected from the group consisting of LTB, mutated LTA and ST of ETEC, subunits, or fusions thereof, antigens from enteroaggregative *E. coli* (EAEC), or Shiga-like toxin 1 or 2
b. *Campylobacter jejuni* antigens,
c. *Clostridium difficile* antigens, specifically toxins A and B
d. *Vibrio cholera* antigens, specifically the CT-B antigen, and
e. mutants or fusion proteins of a), b) c) or d).

11. Vaccine according to definition 10, wherein said ETEC is a fusion enterotoxin of LTB and mutant ST (STm), in particular a fusion protein comprising an STm with an amino acid sequence as shown in SEQ ID 1.

12. Vaccine according to definition 10, wherein the viral antigen is originating from diarrheal viruses, preferably selected from the group consisting of rotaviruses and caliciviruses, such as Norwalk virus.

13. Vaccine according to definition 10, wherein the parasite antigen is originating from diarrhea-causing protozoa, preferably selected from the group consisting of *Giardia lamblia*, Cryptosporidium species and *Entameba histolytica*

14. Vaccine according to definition 10, wherein the fungal antigen is originating from diarrhea-causing fungi, preferably selected from the group consisting of Blastomyces dermatiditis and Histoplasma spp.

15. Vaccine according to any of definitions 1 to 14, wherein said Shigella further comprises a deletion of an essential chromosomal gene and an insertion of said gene into the invasion plasmid, in particular the *ppa* gene or any of *accD*, *acpS*, *dapE*, *era*, *frr*, *ftsI*, *ftsL*, *ftsN*, *ftsZ*, *infA*, *lgt*, *lpxC*, *msbA*, *murA*, *murI*, *nadE*, *parC*, *proS*, *pyrB*, *rpsB*, *trmA*, *rho* and *rhoL*.

16. Vaccine according to any of definitions 1 to 15, for use in the active immunotherapy of a subject to prevent infectious diseases, in particular enteral disease, such as diarrheal or dysentery disease.

17. Vaccine for use according to definition 16, wherein said enteral disease is caused by any Shigella serotype or species.

18. Vaccine for use according to definition 16 or 17, wherein the immunotherapy comprises administration of the vaccine in a mucosal or oral formulation.

19. Vaccine for use according to any of definitions 16 to 18, wherein the vaccine is administered orally or intranasally.

20. Vaccine for use according to any of definitions 16 to 19, wherein

- a polyvalent vaccine is used expressing protective antigens of Shigella and at least one pathogen of a species other than Shigella by the incorporation of a protective antigen of said pathogen into the endogenous invasion plasmid, and wherein

- said infectious disease is caused by any Shigella serotype or species and/ or said pathogen.

21. Shigella strain, which is a *S. flexneri* 2a strain with a deletion of the *rfbF*, *ipaB* and/or *ipaC* genes, or a deletion of essential parts thereof.

22. Shigella strain according to definition 21, which comprises a recombinant invasion plasmid incorporating at least one gene encoding a heterologous antigen to express said antigen or secrete said antigen.

23. Shigella strain according to definition 21 or 22, which further comprises a deletion of an essential chromosomal gene and an insertion of said gene into the invasion plasmid.

24. A recombinant plasmid vector based on a mutated Shigella invasion plasmid comprising a nucleotide sequence encoding at least one heterologous antigen, wherein the plasmid is mutated in at least one of the *ipaB* and/or *ipaC* genes.

25. Bacterial host cell comprising the vector according to definition 24, wherein said host cell is selected from the genera Shigella, Escherichia, Salmonella, Campylobacter or Yersinia.

26. Host cell according to definition 25, wherein the vector is an endogenous invasion plasmid.

The foregoing description will be more fully understood with reference to the following examples. Such examples are, however, merely representative of methods of practicing one or more embodiments of the present invention and should not be read as limiting the scope of invention.

EXAMPLES

Example 1: Preparation of an attenuated Shigella strain

METHODS

Bacterial strains and culture conditions

Bacteria were routinely grown in Luria Bertani (LB) broth or agar plates. For the detection of an intact invasion plasmid expressing the ipa proteins tryptic soy agar (TSA) plates supplemented with 0.01% Congo Red dye (Sigma-Aldrich) were used. Fresh cultures were always started from a Congo Red-positive (CRP) colony ensuring plasmid carriage. Where appropriate media were supplemented by the following concentration of antibiotics: ampicillin 100 µg/ml, kanamicin 100ug/ml, chloramphenicol 25 µg/ml.

The sequenced prototype *Shigella flexneri* 2a strain 2 (strain 2457T, ATCC 700930) was used as a parental strain for mutagenesis. Inactivation of the *aroC* and *rfbF* genes was performed by the Red recombinase technique described earlier (Levine, M.M., et al. Nat. Rev. Microbiol. 5, 540-553 (2007)). Deletion of *aroC* results in an auxotrophic mutant unable to synthesize aromatic compounds. RfbF is involved in the synthesis of the O-antigen subunits, loss of which results in a rough LPS phenotype. The oligonucleotides used for the generation and confirmation of the mutations are provided as Supplementary Table 1 in Figure 4 (SEQ ID 3 - 10). Mutants 2457TΔ*aroC*::*kan* and 2457TΔ*rfbF*::*cat* were subsequently cultured on Congo Red (CR) agar plates to select CR-positive (CRP) and CR-negative (CRN) colonies. The loss of virulence determinants encoded on the invasion plasmid was confirmed by PCR. Similarly, phase I and phase II variants of *S. sonnei* were differentiated on CR plates. Phase I is the traditional designation of invasion plasmid-bearing wild-type *S. sonnei* strains, whereas phase II refers to plasmid-lost strains. As O-antigen synthesis is also encoded on the virulence plasmid in this species, phase II variants are both non-invasive and rough. The wild-type *Shigella flexneri* 6 and *S. sonnei* strains used for the challenge studies had been isolated from clinical cases of bacillary dysentery. Their serotypes were determined by slide agglutination using commercial typing sera (Mast AssureTM; Mast Group Ltd., Merseyside, UK).

Animal experiments

All in vivo studies were performed in the formerly described mouse lung model (van de Verg et al., Infect Immun 63: 1947-1954, 1995). 6-8 weeks old female BALB/c mice were anesthetised intraperitoneally with a mixture of 5 mg/ml ketamine (Calipsol, Richter Gedeon, Hungary) and 0.3 mg/ml xilazine (Primasine, Alfasan).

Infections were performed intranasally with 50 µl of inoculum (diluted in saline) containing the required CFU of bacteria. Bacterial counts were justified by plating of serial dilutions from the inocula. 50 percent lethality doses (LD50 values) were calculated from infections by 0.5 log-serial dilutions (10^5-10^8 CFU) according to Reed and Muench (Oaks, EV, et al. Infect. Immun. 53: 57-63, 1986). Vaccinations were done with sub-lethal doses of bacteria (10^6 CFU of CRP mutants and 10^8 cfu of CRN mutants from strain 2457T; $10^{5.5}$ CFU of phase I and $10^{7.5}$ CFU of phase II *S. sonnei*) two times with 2-week intervals. Control group received saline. In a pilot study it has been shown that all vaccine strains have been cleared within 3 days p.i. Two weeks after the booster immunization mice were challenged with a lethal dose of either the *S. flexneri* 6 or the *S. sonnei* wild-type strain.

Subsequently, lethality was monitored for 14 days. Alternatively, immunized mice were sacrificed two weeks after the booster and bronchoalveolar lavage (BAL) fluid and blood samples were collected. For the collection of BAL the trachea of euthanised mice was prepared for cannulation with a blunted needle and 200 µl saline was injected and retracted from the bronchi of each mouse.

ELISA

Bacteria inoculated from fresh CR plates were grown overnight in LB broth. 96-well plates (C.E.B., France) were coated overnight with 0.1 ml washed bacterial suspensions ($5x10^8$ CFU/ml) in carbonate buffer (pH 9.5) at 4°C. The following day, plates were washed with PBS containing 0.05% Tween 20, and then blocked with PBS containing 2% BSA (Sigma-Aldrich) for 1h at room temperature. BAL and serum samples were diluted in PBS containing 0.5% BSA and incubated with the antigen-coated plates for 1h at 37°C. Serial dilutions were conducted across the plates. After three washes, plates were probed with anti-mouse IgG (for serum IgG) or anti-mouse IgA (for BAL samples) immunoglobulin conjugated with HRPO (Dako A/S, Denmark). The ELISA substrate was *o*-phenylenediamine (Sigma-Aldrich) dissolved in citric acid buffer containing H_2O_2. The OD was measured at 492 nm on a conventional ELISA

plate reader. Immunoreactivity was expressed in relation to the reactivity of the Δ*aro* CRP BAL sample at the same dilution (1:10). Means+SEM were calculated from 4 independent assays.

Statistical analysis

The 50% lethality dose was calculated with the statistical method of Reed and Muench 6. The statistical analysis of the survival curves was performed with the LogRank (Mantel-Cox) test using GraphPad Prism version 5.00 for Windows. The IgA titers of BAL were compared with the Mann-Whitney non parametric analysis. The *p* value was considered significant if lower than 0.05.

RESULTS

Based on the survival curves of animal immunized with the attenuated *Shigella flexneri* 2457T (serotype 2a) vaccine strains and challenged with the wild type Shigella strains, synergistic protective effect was observed by combining the rfbF gene deletion with the loss of invasion plasmid in the heterologous challenge setting. Significantly better protection was achieved by immunization with the Congo Red negative (CNR, with invasion plasmid deletion) *Shigella flexneri* 2457T (2a) ΔrfbF strain relative to that of the Congo Red positive (CNP, intact invasion plasmid) *Shigella flexneri* 2a ΔrfbF strain when the animals were challenged with the heterologous *Shigella flexneri* 6 strain (Fig. 1b). In case of homologous challenge with the wild type *Shigella flexneri* 544 strain (2a), both vaccine strains were equally protective, suggesting that for homologous challenge even the deletion of the rfbF gene is sufficient (Fig. 1a). The difference in vaccination efficacy is likely to be partially related to the higher allowable sub-lethal challenge dose with the ΔrfbF – invasion plasmid double mutant, but not fully accountable for, since the CRN Δaro (control) strain used at comparable challenge dose as the double mutant, induced partial protection in both homologous and heterologous challenge experiments (Fig. 1a,b).

Further evidence for the beneficial effect of mutations inactivating the rfbF gene and invasion plasmid achieving significant protection against heterologous challenge is provided by using *Shigella sonnei* vaccine strains. Immunization with the *Shigella sonnei* Phase II variant (deleted invasion plasmid responsible for expression of both the invasion complex and rfbF gene) afforded high level protection against lethal

challenge with the wild type *Shigella flexneri* 542 strain (serotype 6), while the wild type *S. sonnei* strain phase I variant (intact invasion plasmid carrying the invasion complex and the rfbF gene) exhibited low (statistically not significant) protective effect (Fig. 1c).

Example 2: Preparation of *Shigella flexneri* 2a 2457 mutant with synthetic gene construct on the invasion plasmid

The source material for mutant construction is the ATCC strain *Shigella flexneri* 2a 2457T as described above. Deletion of the *rfbF* and *ipaB* and *ipaC* genes as well as the *ppa* gene is performed using the Red recombinase technique (Datsenko,K.A. & Wanner,B.L. One-step inactivation of chromosomal genes in Escherichia coli K-12 using PCR products. *Proc. Natl. Acad. Sci. U. S. A* **97**, 6640-6645 (2000)).

Step 1: the rfbF gene was removed from the chromosome. The lack of RfbF is associated with a phenotypic change: the Shigella strain becomes “rough”, a typical morphological change that can be detected by naked eye on agar plates. This phenotypic change was observed, but the successful removal of the rfbF gene was also confirmed by PCR analysis. It was based on the different length of the PCR product obtained with genomic DNA from wild type or mutated Shigella (Fig. 8).

Step 2: the ipaB and ipaC genes were removed from the invasion plasmid. These genes are neighbors and were deleted together with the same Red recombinase technique applied to the rfbF gene deletion. This gene deletion also results in a phenotype: the Shigella loses the ability to take up the dye Congo Red and therefore forms a white colony on Congo Red containing agar plates in contrast to Shigella carrying the wild type plasmid which are red. Since Shigella can lose its plasmids spontaneously during *in vitro* culture, the deletion of the ipaB and ipaC genes was confirmed by PCR analysis of the mutants, and it was based on shorter PCR fragments obtained with the mutants, compared to the wild type plasmid (Fig. 9).

Step 3: Insertion of the synthetic gene that drives the expression of the ETEC toxins LT-B and ST, as well as transplants an essential gene (ppa) from the chromosome into the invasion plasmid (see Figure 10A). The successful introduction of the LTB-mST fusion gene was proved by site specific PCR amplification of the region of genetic manipulation (Fig. 10B). Expression of the toxin fusion gene from Shigella was tested by immunoblotting (Fig. 10C). Removal of the ppa gene from the chromosome (essential for the growth of Shigella) was proved by PCR based on shorter length of amplicon from the final vaccine strain.

All genetic manipulations involved the insertion of antibiotic resistance genes. After each step the genes responsible for antibiotic resistance were removed with helper plasmids as described by Datsenko and Wanner (*Proc. Natl. Acad. Sci. U. S. A* **97**, 6640-6645 (2000)).

Example 3: Animal protection studies to test the mutant strain of Example 2

Virulence attenuation of the isogenic mutant strains vs. their parental wild-type strain was shown in the mouse lung model of shigellosis. Groups of mice were infected intranasally with 10-fold serial dilutions (between 10^6 and 10^8 cfu) of the different bacterial strains in order to determine the minimal lethal dose for each strains. In case of the wild-type strain, there was a 30, 50, and 100% lethality found at 10^6, 10^7, and 10^8 cfu/mouse doses, respectively. In contrast, no mice died from any of the isogenic mutants 2457TΔrfb, 2457TΔipaBC, or double mutant 2457TΔrfbΔipaBC at any of the tested doses. These results suggest high virulence attenuation in all mutants upon deletion of the corresponding genes.

Subsequently, groups of mice were immunized in the same model with sublethal doses of either wild-type strain 2457T (5×10^5 cfu/ mouse) or its isogenic deletion mutants 2457TΔrfb, 2457TΔipaBC, 2457TΔrfbΔipaBC (all at 10^8 cfu/mouse), or mock immunized with PBS only. Three identical immunizations were performed with 2-week intervals. One week following the last booster mice were challenged with a (previously optimized) lethal dose (2×10^6 cfu/mouse) of a *S. sonnei* strain. As depicted on Fig. 11, immunization with the wild-type strain could not provide protection, whereas each of the single locus mutants (either 2457TΔrfb or 2457TΔipaBC) elicited partial protection, only. In contrast, the double mutant (2457TΔrfbΔipaBC) could provide full protection against infection by the heterologous Shigella species.

CLAIMS

1. A live attenuated Shigella vaccine that is cross-protective against different serotypes and species of Shigella comprising a Shigella strain which is rough and non-invasive by a deletion of the *rfbF* gene, and a deletion of the *ipaB* and *ipaC* genes on the invasion plasmid.

2. Vaccine according to claim 1, wherein said Shigella strain is selected from the genus Shigella, in particular *S. flexneri, S. sonnei, S. dysenteriae and S. boydii.*

3. Vaccine according to claim 1 or 2, which is cross-protective against any of *S. flexneri 2a*, *S. flexneri 6* and *S. sonnei*, or enteroinvasive *Escherichia coli*.

4. Vaccine according to any of claims 1 to 3, wherein said invasion plasmid is a recombinant endogenous invasion plasmid incorporating at least one gene encoding a heterologous antigen to secrete said antigen or to express said antigen on the bacterial cell surface.

5. Vaccine according to claim 4, wherein said antigen is selected from the group consisting of

- a bacterial antigen, preferably a toxin or colonization factor,
- a viral antigen, preferably from a pathogen causing enteral or mucosal infections,
- a fungal antigen, preferably from a pathogen causing enteral or mucosal infections, and
- a parasitic antigen, preferably from a pathogen causing enteral infections.

6. Vaccine according to claim 5, wherein the bacterial antigen is an enterotoxin (ETEC) comprising the B subunit of heat labile toxin (LTB), the heat stable toxin (ST) or subunits or fusions thereof, preferably LTB/STm comprising a STm with an amino acid sequence as shown in SEQ ID 1.

7. Vaccine according to any of claims 1 to 6, wherein said Shigella further comprises a deletion of an essential chromosomal gene and an insertion of said gene into the invasion plasmid.

8. Vaccine according to any of claims 1 to 7, for use in the prophylaxis of a subject to prevent infectious diseases.

9. Vaccine for use according to claim 8, to prevent enteral disease.

10. Vaccine for use according to claim 8 or 9, wherein the vaccine is administered orally or intranasally.

11. Vaccine for use according to any of claims 8 to 10, wherein

- a polyvalent vaccine is used expressing protective antigens of Shigella and at least one pathogen of a species other than Shigella by the incorporation of a protective antigen of said pathogen into the endogenous invasion plasmid, and wherein
- said infectious disease is caused by any Shigella serotype or species and/ or said pathogen.

12. Shigella strain, which is a *S. flexneri* 2a strain comprising a deletion of the *rfbF* gene, and the *ipaB* and *ipaC* genes on the invasion plasmid.

13. Shigella strain according to claim 12, wheren said invasion plasmid incorporates at least one gene encoding a heterologous antigen to express and/or secrete said antigen.

14. Shigella strain according to claim 13, wherein the heterologous antigen is a bacterial enterotoxin (ETEC) comprising the B subunit of heat labile toxin (LTB), the heat stable toxin (ST) or subunits or fusions thereof, preferably LTB/STm comprising a STm with an amino acid sequence as shown in SEQ ID 1.