

COMPOSITIONS AND METHODS OF ENHANCING IMMUNE RESPONSES

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. Provisional Application No. 60/825,983, filed September 18, 2006, which is incorporated herein by reference in its entirety.

5 STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

This invention was made with United States government support awarded by National Institutes of Health grant R21 AI063137. The United States may have certain rights in this invention.

INTRODUCTION

10 Influenza virus infection, particularly avian influenza H5N1, presents a mounting health and economic concern. Evidence clearly indicates that H5N1 is continuing to circulate between susceptible birds and swine in widening regions of the world. Many scientists believe that if left unchecked, the current H5N1 avian influenza will mutate to allow for human to human transmission and cause a world-wide pandemic. With a mortality rate of
15 over 50%, such an outbreak would be devastating. Regardless of the ability of the virus to cause human disease, avian influenza H5N1 is already threatening to have a huge economic impact due to the eradication of poultry flocks in affected areas. Therefore, development of a vaccine to protect humans, poultry, swine and other domesticated animals from H5N1 influenza is needed. An influenza vaccine that is capable of protecting against H5N1 as well
20 as other influenza viruses would be optimal.

SUMMARY

Salmonella enteritidis 13A strains having ATCC deposit numbers PTA-7871, PTA-7872 or PTA-7873 are disclosed. Also disclosed is a composition comprising an attenuated Salmonella strain and a pharmaceutically acceptable carrier.

25 In another aspect, methods of enhancing an immune response in a subject by administering a vaccine vector to the subject are provided. A polynucleotide encoding a polypeptide of CD154 capable of binding CD40, the polypeptide having fewer than 50 amino acids and comprising amino acids 140-149 of SEQ ID NO:26 or a homolog thereof. The

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vaccine vector is administered to the subject in an amount effective to enhance the immune response of the subject to the vaccine.

In a further aspect, methods of enhancing the immune response against Influenza A in a subject by administering to the subject a bacterium comprising a polynucleotide encoding a polypeptide of Influenza A M2e protein in an amount effective to enhance the immune response of the subject to Influenza A are provided.

In yet another aspect, methods of reducing the morbidity associated with Influenza A infection in a subject by administering to the subject a bacterium comprising a polynucleotide encoding a polypeptide of Influenza A M2e protein in an amount effective to reduce the morbidity associated with a subsequent infection with Influenza A are provided.

In still another aspect, methods of generating site-specific mutations in a bacterium are provided. A first polynucleotide comprising a counter-selection marker and an antibiotic resistance marker flanked by polynucleotides homologous to the sequences flanking a mutation site in the chromosome of the bacterium is generated. The first polynucleotide is then introduced into the bacterium and after homologous recombination and antibiotic selection an intermediate is isolated. A second polynucleotide comprising the mutation flanked by polynucleotides homologous to sequences flanking the mutation site is generated. The second polynucleotide is then introduced into the intermediate and the site-specific mutant is isolated by counter-selecting for loss of the counter-selection marker.

In a still further aspect, methods for developing bacterial vaccine vectors are provided. A bacterium capable of colonizing a subject is selected. The bacterium is attenuated and a polynucleotide comprising a sequence encoding a polypeptide of CD154 capable of binding to CD40 is incorporated into the bacterium.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 depicts the scheme for making site-directed mutations in *Salmonella enteritidis*.

Figure 2 depicts the design scheme of the overlapping extension PCR method used to generate the M2e and M2e-CD154 insertions into loop 9 of the *lamB* polynucleotide.

Figure 3 is a bar graph showing the relative amount of serum antibody generated at the time points indicated in response to administration of the indicated treatment.

Figure 4 is a line graph showing the amount of serum antibody over time after administration of the indicated treatments.

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Figure 5 is a graph showing the morbidity of chickens after vaccination with SE HM at day-of-hatch, boost at day 21 and challenge infection with a low pathogenicity Influenza A at 32 days post-hatch.

Figure 6 is a graph showing viral shedding at days 2 and 4 post-challenge with a low pathogenicity Influenza A after vaccination with SE HM at day-of-hatch, boost at day 21 and challenge infection at day 32 post-hatch.

Figure 7 is a graph showing the morbidity of chickens after vaccination with SE HM at day-of-hatch, boost at day 21 and challenge infection with a high pathogenicity Influenza A at 32 days post-hatch.

Figure 8 is a graph showing viral shedding at days 2 and 4 post-challenge with a high pathogenicity Influenza A after vaccination with SE HM at day-of-hatch, boost at day 21 and challenge infection at day 32 post-hatch.

DETAILED DESCRIPTION

Recombinant DNA technologies enable relatively easy manipulation of many bacterial and viral species. Some bacteria and viruses are mildly or non-pathogenic, but are capable of generating a robust immune response. These bacteria and viruses make attractive vaccine vectors for eliciting an immune response to a heterologous or foreign antigen. Bacterial or viral vaccine vectors may mimic the natural infection and produce robust and long lasting immunity. Vaccine vectors are often relatively inexpensive to produce and administer. In addition, such vectors can often carry more than one antigen and may provide protection against multiple infectious agents.

In one aspect, this invention relates to the use of Salmonella vectors in vaccination and generation of immune responses against Salmonella and other pathogenic agents. Salmonella strains make suitable vaccine vectors because of the ability to make bacteria capable of expressing heterologous polypeptides. In addition, bacterial genes may be mutated or attenuated to create bacteria with low to no pathogenesis to the infected or immunized subject, while maintaining immunogenicity.

The ability of the Salmonella to survive the gastrointestinal tract of the host and give rise to a mucosal immune response is documented. Oral vaccines using a Salmonella vector produce a robust mucosal immune response and are relatively easy to administer to both animals and humans. Many of the current Salmonella vaccine strains are not as effective in generating a strong protective immune response as compared to their more virulent

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counterparts. A *Salmonella* strain that could be used for effective mucosal, e.g., oral, vaccination would provide a vector that could be used to readily vaccinate a subject against one or more pathogenic agents, such as H5N1 influenza.

A *Salmonella enteritidis* strain useful as a vaccine vector, and various recombinant vaccine vectors made using this strain, are described. Specifically, a vaccine vector carrying the M2e epitope of Influenza A virus is provided. In addition, methods of developing vaccine vectors and methods of enhancing an immune response in a subject by administering a vaccine vector comprising a polynucleotide encoding a polypeptide of CD154 or a homolog thereof that is capable of binding to CD40 are disclosed. The vaccine vectors may be used to enhance an immune response against Influenza A or to reduce the morbidity associated with Influenza A infection. Finally, a method of generating site-specific mutations in a bacterium using the Red recombination system in conjunction with overlapping extension PCR to generate mutants containing no extraneous DNA is provided.

A wild-type isolate of *Salmonella*, *Salmonella enteritidis* 13A (SE13A) (deposited with the American Type Culture Collection (ATCC) on September 13, 2006, deposit number PTA-7871), was selected based upon its unusual ability to cause mucosal colonization and submucosal translocation in chickens, permitting robust presentation of associated antigens or epitopes in commercial chickens. Importantly, this wild-type *Salmonella* isolate causes no clinically detectable disease or loss of performance in commercial chickens, indicating little disease-causing potential of the wild-type *Salmonella* in vertebrate animals. The ability of an organism to colonize a subject, such as a chicken, is indicated by the ability of the organism to replicate at the site of infection. Optimally, a vaccine candidate can also invade and spread to tissues beyond the infection site. As demonstrated in Example 4, SE13A is capable of replication in the cecal tonsils after oral infection and can be isolated from the tonsils for weeks after infection. In addition, SE13A can invade other tissues, and is found in the liver and the spleen up to a month after infection.

The SE13A isolate may be further attenuated by inactivating at least one gene necessary for sustained replication of the bacteria outside of laboratory or manufacturing conditions. Attenuated *Salmonella* strains that can be used as vaccine vectors are described below. SE13A was used to generate attenuated *Salmonella* strains to develop vaccines and generate enhanced immune responses. As demonstrated in the Examples, SE13A is invasive, non-pathogenic for poultry and causes no measurable morbidity. These features result in an enhanced immune response as compared to non-invasive bacterial vectors. Attenuation of

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SE13A by mutation of genes that limit the ability of the bacterium to spread may increase the safety of the vaccine. As demonstrated in the Examples at Table 4, SE13A strains with mutations in *aroA* or *htrA* retain the ability to generate an immune response, but have limited replication in the host. Thus, the attenuation increases the safety of the vaccine vector
5 without compromising the immunogenicity.

Mutations may be made in a variety of other Salmonella genes including, but not limited to, *cya*, *crp*, *asd*, *cdt*, *phoP*, *phoQ*, *ompR*, outer membrane proteins, *dam*, *htrA* or other stress related genes, *aro*, *pur* and *gua*. As shown in the Examples, mutations in *aroA* and *htrA* were found to attenuate SE13A. The *aro* genes are enzymes involved in the
10 shikimate biosynthesis pathway or the aromatase pathway and *aro* mutants are auxotrophic for the aromatic amino acids tryptophan, tyrosine and phenylalanine. *htrA* is a stress response gene that encodes a periplasmic protease that degrades aberrant proteins. Mutants in *htrA* are also attenuated and display increased sensitivity to hydrogen peroxide.

The mutations in *aroA* and *htrA* described in the Examples are deletion mutations, but
15 the mutations can be made in a variety of ways. Suitably, the mutations are non-reverting mutations that cannot be repaired in a single step. Suitable mutations include deletions, inversions, insertions and substitutions. A vaccine vector may include more than one mutation, for example a vaccine vector may contain mutations in both *aroA* and *htrA*. Methods of making such mutations are well known in the art.

SE13A or the attenuated recombinant SE13A derivatives may be used as vaccine
20 vectors. Polynucleotides encoding polypeptide epitopes from any number of pathogenic organisms may be inserted into the bacteria and expressed by the bacteria to generate antigenic polypeptides. The polynucleotides may be inserted into the chromosome of the bacteria or encoded on plasmids or other extrachromosomal DNA. Suitably, polynucleotides
25 encoding epitopes are inserted into a bacterial polynucleotide that is expressed. Suitably, the bacterial polynucleotide encodes a transmembrane protein, and the polynucleotide encoding the epitope is inserted into the bacterial polynucleotide sequence to allow expression of the epitope on the surface of the bacteria. For example, the polynucleotide encoding the epitope may be inserted in frame into the bacterial polynucleotide in a region encoding an external
30 loop region of a transmembrane protein such that the bacterial polynucleotide sequence remains in frame. See Example 1.

Alternatively, the polynucleotide encoding the epitope may be inserted into a secreted polypeptide. Those of skill in the art will appreciate that the polynucleotide encoding the

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epitope could be inserted in a wide variety of bacterial polynucleotides to provide expression and presentation of the epitope to the immune cells of a subject treated with the bacterial vaccine vector. In the Examples, an Influenza A virus M2e epitope was inserted into loop 9 of the *lamB* gene of SE13A and surface expression of the epitope was confirmed by antibody-mediated precipitation. The polynucleotide encoding an epitope may be included in a single copy or more than one copy. In the Examples, a bacterial vaccine vector containing multiple copies of the M2e epitope inserted into loop 9 of *lamB* is described. Alternatively, multiple copies of an epitope may be inserted into the bacterial vaccine vector at more than one location.

Polynucleotides encoding polypeptides that are homologous to proteins of the subject and capable of stimulating the immune system to respond to the foreign epitope may also be inserted into a vaccine vector. As described in more detail below, a vaccine vector may include a CD154 polypeptide that is capable of binding CD40 in the subject and stimulating the subject to respond to the vaccine vector and its associated foreign epitope. As described above with regard to epitopes, these polynucleotides may be inserted into the chromosome of the vaccine vector or maintained extrachromosomally. One of skill in the art will appreciate that these polypeptides can be inserted in a variety of polynucleotides and expressed in different parts of the vaccine vector or may be secreted. The polynucleotide encoding a CD154 polypeptide capable of enhancing the immune response to a foreign epitope may also encode the foreign epitope. The polynucleotide encoding a CD154 polypeptide may be linked to the polynucleotide encoding the epitope, such that in the vaccine vector the CD154 polypeptide and the foreign epitope are present on the same polynucleotide. In the Examples, a polynucleotide encoding a polypeptide of CD154 that is capable of binding to CD40 also encodes the M2e epitope of Influenza A. See SEQ ID NOS: 8 and 9 in the attached sequence listing. In the Examples, the polynucleotide encoding the M2e epitope and the polynucleotide encoding the CD154 polypeptide are both inserted in loop 9 of the *lamB* gene. Those of skill in the art will appreciate that bacterial polynucleotides encoding other transmembrane proteins and other loops of the *lamB* gene may also be used.

The SE13A bacteria may include a polynucleotide encoding a polypeptide of the influenza M2 protein. The ectodomain of the Influenza A virus M2 protein, known as M2e, protrudes from the surface of the virus. The M2e portion of the M2 protein contains about 24 amino acids. The M2e polypeptide varies little from one isolate to the next within a given species. In fact, only a few naturally occurring mutations in M2e have been isolated from

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infected humans since the 1918 flu epidemic. In addition, influenza viruses isolated from avian and swine hosts have different, yet still conserved, M2e sequences. For reviews of the M2e polypeptide sequences isolated from human, avian and swine hosts see Liu et al., *Microbes and Infection* 7:171-177 (2005) and Reid et al., *J. Virol.* 76:10717-10723 (2002) each of which are incorporated herein by reference in its entirety. See also SEQ ID NO: 1-4 in the attached sequence listing.

Suitably a polynucleotide encoding the entire M2e polypeptide may be inserted into the vaccine vector or only a portion may be used. In the Examples, an eight amino acid polypeptide (LM2 having amino acid sequence: EVETPIRN, SEQ ID NO:5 or its variant M2eA having amino acid sequence EVETPTRN, SEQ ID NO:20) was incorporated into SE13A and demonstrated to produce an antibody response after administration to chickens. Suitably, the portion of the M2e polypeptide inserted into the vaccine vector is immunogenic. An immunogenic fragment is a peptide or polypeptide capable of eliciting a cellular or humoral immune response. Suitably, an immunogenic fragment of M2e may be the full-length M2e polypeptide, or suitably may be 20 or more amino acids, 15 or more amino acids, 10 or more amino acids or 8 or more amino acids of the full-length sequence.

Other suitable epitopes for inclusion in an Influenza A vaccine vector include, but are not limited to, polynucleotides encoding polypeptides of the hemagglutinin or the nuclear protein of Influenza A. For example, polynucleotides encoding SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, or SEQ ID NO:24 may be included in a vaccine vector. One of skill in the art will appreciate that any of these sequences may be used in combination with any other epitope and may also be used in conjunction with polypeptides encoding immune stimulatory peptides such as a polypeptide of CD154.

As discussed above, a polynucleotide encoding a polypeptide homologous to a protein of the subject that is capable of enhancing the immune response to the epitope may be included in the vaccine vector. In the Examples, SE13A strains including a polynucleotide encoding a CD154 polypeptide capable of binding to CD40 were demonstrated to enhance the immune response to the M2e epitope as measured by increased antibody production in response to vaccination. Suitably, the CD154 polypeptide is fewer than 50 amino acids long, more suitably fewer than 40, fewer than 30 or fewer than 20 amino acids in length. The polypeptide may be between 10 and 15 amino acids, between 10 and 20 amino acids or between 10 and 25 amino acids in length. The CD154 sequence and CD40 binding region

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are not highly conserved among the various species. The CD154 sequences of chicken and human are provided in SEQ ID NO: 25 and SEQ ID NO: 26, respectively.

The CD40 binding regions of CD154 have been determined for a number of species, including human chicken, duck, mouse and cattle and are shown in SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, respectively. Although there is variability in the sequences in the CD40 binding region between species, the Examples below indicate that the human CD154 polypeptide was able to enhance the immune response in chickens. Therefore, one may practice the invention using species specific CD154 polypeptides or a heterologous CD 154 polypeptide.

10 In the Examples, several SE13A recombinant bacteria were generated. In each of the SE13A strains the M2e polypeptide and the CD154 polypeptide were encoded on the same polynucleotide and were in frame with each other and the Salmonella polynucleotide in which they were inserted. In alternative embodiments, the CD154 polypeptide and the M2e polypeptide may be encoded by distinct polynucleotides. SE13A *aroA* M2e contains a deletion in *aroA* and the LM2-M2e epitope (SEQ ID NO:5) inserted into loop 9 of *lamB*. SE13A *aroA* M2e-CD154 is the same as SE13A *aroA* M2e, but also contains the CD154 peptide (SEQ ID NO:6) inserted in loop 9 of *lamB* with the M2e epitope (See SEQ ID NO:8). This strain is deposited with the ATCC as deposit number PTA-7872.

20 SE13A *htrA* M2E contains a deletion in *htrA* and has the M2e-LM2 epitope inserted in loop 9 of *lamB*. SE13A *htrA* M2E-CD154 has the CD154 peptide inserted in loop 9 of *lamB* with the M2e epitope (SEQ ID NO:8) and is deposited with the ATCC as strain PTA-7873.

The strain designated as SE13A HM contains SEQ ID NO:9 inserted in loop 9 of *lamB*. This strain contains multiple copies of two epitopes of M2e, referred to as M2e-LM2 (SEQ ID NO:5) and M2eA (SEQ ID NO:20) and the CD154 polypeptide (SEQ ID NO:6).

25 In the Examples, the above-described recombinant Salmonella strains were demonstrated to produce high, putatively protective antibody titers against the M2e epitope of influenza viruses. Furthermore, expression of the immune-stimulating molecule was shown to further increase antibody titers, confirming functionality of this concept and these particular bacterial vaccine vectors.

30 Compositions comprising an attenuated Salmonella strain and a pharmaceutically acceptable carrier are also provided. A pharmaceutically acceptable carrier is any carrier suitable for *in vivo* administration. The pharmaceutically acceptable carrier may include

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water, buffered solutions, glucose solutions or bacterial culture fluids. Additional components of the compositions may suitably include excipients such as stabilizers, preservatives, diluents, emulsifiers and lubricants. Examples of pharmaceutically acceptable carriers or diluents include stabilizers such as carbohydrates (e.g., sorbitol, mannitol, starch, sucrose, glucose, dextran), proteins such as albumin or casein, protein-containing agents such as bovine serum or skimmed milk and buffers (e.g., phosphate buffer). Especially when such stabilizers are added to the compositions, the composition is suitable for freeze-drying or spray-drying.

Methods of enhancing immune responses in a subject by administering a vaccine vector containing a CD154 polypeptide capable of binding to CD40 and activating CD40 are also provided. The vaccine vector comprising the polynucleotide encoding a polypeptide of CD154 capable of binding to CD40 is administered to a subject in an amount effective to enhance the immune response of the subject to the vaccine. Suitably, the vaccine vector contains a polynucleotide encoding a polypeptide including amino acids 140-149 of the human CD154 polypeptide (SEQ ID NO: 26) or a homolog thereof. Several suitable polypeptides are identified herein. Suitably, the polynucleotide encodes a CD154 polypeptide from the same species as the subject. Suitably, a polynucleotide encoding the polypeptide of SEQ ID NO: 6 is used in human subjects, a polynucleotide encoding the polypeptide of SEQ ID NO: 7 is used in chickens, a polynucleotide encoding the polypeptide of SEQ ID NO: 27 is used in ducks, a polynucleotide encoding the polypeptide of SEQ ID NO: 28 is used in mice, and a polynucleotide encoding the polypeptide of SEQ ID NO: 29 is used in cows. In the Examples, the human CD154 polypeptide (SEQ ID NO: 6) is used in a chicken vaccine vector and is demonstrated to enhance the immune response to a foreign antigen. Thus other heterologous combinations of CD154 polypeptides and subjects may be useful in the methods of the invention. The CD154 polypeptide may be used to enhance the immune response in the subject to any foreign antigen or antigenic polypeptide present in the vaccine vector. One of skill in the art will appreciate that the CD154 polypeptide could be used to enhance the immune response to more than one antigenic polypeptide present in a vaccine vector.

The polypeptide from CD154 stimulates an immune response at least in part by binding to its receptor, CD40. In the Examples, a polypeptide homologous to the CD154 expressed on immune cells of the subject and which is capable of binding to the CD40 receptor on macrophages and other antigen presenting cells was utilized. Binding of this

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ligand-receptor complex stimulates macrophage (and macrophage lineage cells such as dendritic cells) to enhance phagocytosis and antigen presentation while increasing cytokine secretions known to activate other local immune cells (such as B-lymphocytes). As such, molecules associated with the CD154 peptide are preferentially targeted for immune response
5 and expanded antibody production.

Potential vaccine vectors for use in the methods include, but are not limited to, *Salmonella* (*Salmonella enteritidis*), *Shigella*, *Escherichia* (*E. coli*), *Yersinia*, *Bordetella*, *Lactococcus*, *Streptococcus*, *Vibrio* (*Vibrio cholerae*), *Listeria*, adenovirus, poxvirus, herpesvirus, alphavirus, and adeno-associated virus.

10 In addition, methods of enhancing an immune response against influenza A and methods of reducing morbidity associated with subsequent Influenza A infection are disclosed. Briefly, the methods comprise administering to a subject a bacterium comprising an Influenza A M2e polynucleotide sequence encoding a polypeptide of Influenza A M2e in an effective amount. The M2e polypeptides include SEQ ID NO:1-5 and 20. The insertion
15 of the M2e polypeptides into the bacterium may be accomplished in a variety of ways known to those of skill in the art, including but not limited to the scarless site-directed mutation system described herein. The bacterium may also be engineered to express the M2e polypeptides in conjunction with polynucleotides capable of enhancing the immune response as discussed above, such as in SEQ ID NO:8 and SEQ ID NO:9. In particular, a polypeptide
20 of CD154 capable of binding CD40 may be expressed by the bacterium to enhance the immune response of the subject to the M2e polypeptide.

The useful dosage to be administered will vary depending on the age, weight and species of the subject, the mode and route of administration and the type of pathogen against which an immune response is sought. The composition may be administered in any dose of
25 bacteria sufficient to evoke an immune response. It is envisioned that doses ranging from 10^3 to 10^{10} bacteria, from 10^4 to 10^9 bacteria, or from 10^5 to 10^7 bacteria are suitable. The composition may be administered only once or may be administered two or more times to increase the immune response. For example, the composition may be administered two or more times separated by one week, two weeks, or by three or more weeks. The bacteria are
30 suitably viable prior to administration, but in some embodiments the bacteria may be killed prior to administration. In some embodiments, the bacteria may be able to replicate in the subject, while in other embodiments the bacteria may not be capable of replicating in the subject.

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For administration to animals or humans, the compositions may be administered by a variety of means including, but not limited to, intranasally, mucosally, by spraying, intradermally, parenterally, subcutaneously, orally, by aerosol or intramuscularly. Eye-drop administration or addition to drinking water or food are additionally suitable. For chickens,
5 the compositions may be administered in ovo.

Some embodiments of the invention provide methods of enhancing immune responses in a subject. A subject includes, but is not limited to, a vertebrate, suitably a mammal, suitably a human, or birds, suitably poultry such as chickens. Other animal models of infection may also be used. Enhancing an immune response includes, but is not limited to,
10 inducing a therapeutic or prophylactic effect that is mediated by the immune system of the subject. Specifically, enhancing an immune response may include enhanced production of antibodies, such as demonstrated in Figure 3 and Figure 4, enhanced class switching of antibody heavy chains, maturation of antigen presenting cells, stimulation of helper T cells, stimulation of cytolytic T cells or induction of T and B cell memory.

15 It is envisioned that several epitopes or antigens from the same or different pathogens may be administered in combination in a single vaccine vector to generate an enhanced immune response against multiple antigens. Recombinant vaccine vectors may encode antigens from multiple pathogenic microorganisms, viruses or tumor associated antigens. Administration of vaccine vectors capable of expressing multiple antigens has the advantage
20 of inducing immunity against two or more diseases at the same time. For example, live attenuated bacteria, such as *Salmonella enteritidis* 13A, provide a suitable vaccine vector for eliciting an immune response against multiple antigens.

Heterologous polynucleotides encoding antigens can be inserted in the bacterial genome at any non-essential site or alternatively may be carried on a plasmid using methods
25 well known in the art. One suitable site for insertion of polynucleotides is within external portions of transmembrane proteins or coupled to sequences which target the heterologous polynucleotide for secretory pathways. One example of a suitable transmembrane protein for insertion of polynucleotides is the *lamB* gene. In the Examples, M2e and CD154 polynucleotides were inserted into loop 9 of the *lamB* sequence.

30 Heterologous polynucleotides include, but are not limited to, polynucleotides encoding antigens selected from pathogenic microorganisms or viruses other than the vaccine vector. Such polynucleotides may be derived from pathogenic viruses such as influenza (e.g., M2e, hemagglutinin, or neuraminidase), herpesviruses (e.g., the genes encoding the structural

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proteins of herpesviruses), retroviruses (e.g., the gp160 envelope protein), adenoviruses, paramyxoviruses, coronaviruses and the like. Heterologous polynucleotides can also be obtained from pathogenic bacteria, e.g., genes encoding bacterial proteins such as toxins, and outer membrane proteins. Further, heterologous polynucleotides from parasites, such as
5 Eimeria are attractive candidates for use of a vector vaccine.

Polynucleotides encoding polypeptides involved in triggering the immune system may also be included in a vaccine vector, such as a live attenuated Salmonella vaccine. The polynucleotides may encode immune system molecules known for their stimulatory effects, such as an interleukin, Tumor Necrosis Factor or an interferon, or another polynucleotide
10 involved in immune-regulation. The vaccine vector may also include polynucleotides encoding peptides known to stimulate an immune response, such as the CD154 polypeptide described herein.

A method of generating site-specific mutations in a bacterium that is a member of the Enterobacteriaceae family is provided. The method as exemplified makes use of overlapping
15 extension PCR, the Red recombinase system, and an intermediary insertion of the I-SceI endonuclease recognition site as a counter-selection marker. Alternatively, *sacB* may also be used as a counter-selection marker. The overall strategy is shown in Figure 1. Overlapping extension PCR was used to produce linear DNA with long flanking homology to the genome of SE13A. The Red recombinase system was used to mediate recombination between
20 incoming linear, PCR-generated DNA with the bacterial genome. In the two-step mutation process, the I-SceI site/ *Km^r* cassette was first inserted into the chromosome in the *lamB* gene by homologous recombination. Then, this mutation was replaced with the desired insertion sequences (LM2-M2e, CD154s or combination sequences). To make the replacement, a PCR product carrying the desired insertion sequence was added simultaneously with a plasmid
25 encoding the I-SceI endonuclease enzyme used for counter-selection between the first and second mutations.

The procedure for generating site-directed mutants may be used in any member of the Enterobacteriaceae family. The Enterobacteriaceae family includes, but is not limited to, members of the Salmonella, Shigella, Escherichia and Yersinia genera. A site-directed
30 mutant includes but is not limited to insertion, deletion, substitution and replacement mutations targeted to a specific location in the chromosome of the bacteria. The advantage of the current system is that it results in a "scarless" mutation or a mutation that does not contain any extraneous sequences. Thus, the site-directed mutagenesis disclosed herein can be used

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to generate autologous bacteria which are deleted for a single gene or even a single amino acid or nucleotide.

In the Examples, the polynucleotides were generated by overlapping extension PCR, but one of skill in the art will appreciate that other methods of generating linear polynucleotides are available and could be utilized. The linear first and second polynucleotides must contain some sequence homologous to the sequence flanking the mutation site to allow for Red mediated recombination. The amount of homologous sequence may comprise less than 300 base pairs on either side of the mutation site. Suitable the homologous sequence is less than 200 base pairs. The polynucleotides may be introduced into the bacteria by any method known to those of skill in the art. In the Examples, the linear polynucleotides were electroporated into the bacteria.

Methods of developing a bacterial vaccine vector are also provided. First, a bacterium capable of colonizing a subject is selected. Then, the bacterium is attenuated to generate an attenuated bacterium. Attenuation may be performed by a variety of methods known to those of skill in the art. Finally, a CD154 polynucleotide sequence encoding a CD154 polypeptide capable of binding CD40 is incorporated into the attenuated bacterium to generate a vaccine vector. The CD154 polypeptide may be fewer than 50 amino acids long and will comprise amino acids 140-149 of CD154 SEQ ID NO: 26 or a homolog thereof. The bacterial vaccine vector may also incorporate a second polynucleotide sequence encoding an antigenic polypeptide. In one embodiment, the CD154 polypeptide and the antigenic polypeptide are encoded on the same polynucleotide sequence.

The following examples are meant only to be illustrative and are not meant as limitations on the scope of the invention or of the appended claims.

EXAMPLES

25 Example 1. Construction of M2e and M2e/CD154 inserts.

Strains and Culture Conditions

All plasmids were first maintained in TOP10 *E. coli* cells (Invitrogen, Carlsbad, CA, USA) unless described otherwise. *Salmonella enteritidis* 13A was used for introduction of mutations. *Salmonella enteritidis* strain 13A was a field isolate available from USDA/APHIS/NVSL and deposited with the ATCC as deposit number PTA-7871. Bacteria

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carrying plasmid pKD46 were grown at 30°C. Other bacteria were grown at 37°C. Plasmid curing was conducted at 37°C.

Luria-Bertani (LB) media was used for routine growth of cells, and SOC media (Invitrogen, Carlsbad, CA, USA) was used for phenotypic expression after electroporation.

5 When appropriate, the following antibiotics were added to the media: ampicillin (Amp) at 100µg/ml, kanamycin (Km) at 50µg/ml, and chloramphenicol (Cm) at 25µg/ml.

Plasmids

Plasmids pKD46, pKD13, and pBC-I-SceI were described previously (Datsenko and Wanner, PNAS 2000, 97:6640-6645 and Kang et al., J Bacteriol 2004, 186:4921-4930, both
10 of which are incorporated herein by reference in their entireties). Plasmid pKD46 encodes Red recombinase enzymes which mediate homologous recombination of incoming linear DNA with chromosomal DNA. This plasmid also contains the Ampicillin resistance gene and is temperature-sensitive so that it requires 30°C for maintenance in the cell. Plasmid pKD13 served as a template for amplification of the Km resistance (Km^r) gene used in
15 overlapping PCR. Plasmid pBC-I-SceI, which is maintained in the cell at 37°C, produces the I-SceI enzyme, which cleaves the following 18 base pair, rare recognition sequence: 5'-TAGGGATAACAGGGTAAT-3' (SEQ ID NO:30). Plasmid pBC-I-SceI also contains the chloramphenicol resistance (Cm^r) gene.

PCR

20 All primers used for PCR are listed in Table 1. Typically, PCR was performed using approximately 0.1µg of purified genomic, plasmid or PCR-generated DNA (Qiagen, Valencia, CA, USA), 1x cloned *Pfu* polymerase buffer, 5U *Pfu* polymerase (Stratagene La Jolla, CA, USA), 1mM dNTPs (GE Healthcare Bio-Sciences Corp., Piscataway, NJ), and 1.2µM of each primer in a total volume of 50 µL. The DNA engine thermal cycler (Bio-Rad,
25 Hercules, CA, USA) was used with the following amplification conditions: 94°C for 2 minutes; 30 cycles of 94°C for 30 sec, 58°C for 60 sec, 72°C for 90 sec per 1 kb; and 72°C for 10 minutes for final extension. Each PCR product was gel purified (Qiagen, Valencia, CA, USA) and either eluted in 25µL EB buffer for preparation of templates used in overlapping extension PCR or in 50µL EB buffer, ethanol precipitated and suspended in 5µL
30 of ddH₂O for electroporation into *S. enteritidis*.

Table 1. Primer sequences

Primer	Amplified region	Primer sequence
lam-up-f	loop 9 up	5'TGTACAAGTGGACGCCAATC 3'
lam-up-r		5' <i>GTTATCGCCGTC</i> TTTGATATAGCC 3'
lam-dn-f	loop 9 dn	5' <i>ATTTCCCGTTATGCCG</i> CAGC 3'
lam-dn-r		5'GTTAAACAGAGGGCGACGAG 3'
Km-f	I-SceI/Km ^r gene	5' <i>GCTATATCAAAGACGGCGATAAC</i> TAACTATAACGGTCCTAAGGTAGCGAAT
Km-r		TTCCGGGGATCCGTCGA 3'
Kan4f	inside Km ^r gene: sequencing	5'CAAAAGCGCTCTGAAGTTCC 3'
Kan4r		5'GCGTGAGGGGATCTTGAAGT 3'
lam-il	M2e/ loop 9 dn	5' <i>GCTATATCAAAGACGGCGATAAC</i> GAAGTTGAAACCCCGATT CGTAAC <i>ATTTC</i> <i>CGTTATGCCGCAGC</i> 3'
lam-i2	CD154s/ loop 9 dn	5' <i>GCTATATCAAAGACGGCGATAAC</i> TGGGCAGAAAAAGTTATTATACCATGTCT <i>ATTTC</i> CGTTATGCCGCAGC 3'
i2-ilh-f	CD154s-(Gly) ₃ -LM2-(Gly) ₃ -loop 9 dn	5' TGGGCAGAAAAAGTTATTATACCATGTCTGGTGGTGGTGAAGTTGAAACCC CGATT CGTAACGGTGGTGGT <i>ATTTC</i> CGTTATGCCGCAGC 3'
i2-il-r	CD154s-(Gly) ₃ -loop 9 up	5' AGACATGGTATAATAACCTTTTCTGCCCAACCACCACC GGTTATGCCGCCTT <i>TGATATAGCC</i> 3'
TJ1-f	CD154-(Ser) ₄ -LM2-(Ser) ₄ -LM2-(Ser) ₄ -loop 9 dn	5' TGGGCAGAAAAAGTTATTATACCATGTCTTCTCCTCCTCCGAAAGTTGAAA CCCCGATT CGTAAC TCTCCTCCTCCGAAAGTTGAAACCCCGATT CGTAAC TCTC CCTCCTCCATT TCGGTTATGCCGCAGC 3'
TJ1-r	CD154-(Ser) ₄ -M2eA-(Ser) ₄ -M2eA-(Ser) ₄ -loop 9 up	5' AGACATGGTATAATAACCTTTTCTGCCCAGGAGGAGGAGGAGTTACGGGTC GGGGTTTCAACTTCGGAGGAGGAGGAGTTACGGGTCGGGGTTTCAACTTCGGA GGAGGAGGAGTTATCGCCGCTTTGATATAGCC 3'
lam 3f	outer regions of loop 9: sequencing	5'GCCATCTCGCTTGGTGATAA 3'
lam 3r		5'CGCTGGTATTTGCGGTACA 3'

In Table 1, italicized nucleotides are complementary to either side of the *lamB* gene loop 9 insertion site, which corresponds to nucleotide 1257 using *S. typhimurium* as an annotated reference genome. Bold font nucleotides represent the I-SceI recognition site in the Km-f primer. All other insertion sequences are shown as underlined.

Electroporation

Transformation of pKD46 into *S. enteritidis* was the first step carried out so that Red recombinase enzymes could be used for mediating recombination of subsequent mutations. Plasmid pKD46 was harvested from *E. coli* BW25113 (Datsenko and Wanner, PNAS 2000, 97:6640-6645) using a plasmid preparation kit (Qiagen Valencia, CA, USA). Then 0.5μL of pKD46 DNA was used for transformation into *S. enteritidis* 13A which had been prepared for electroporation. (Datsenko and Wanner, PNAS 2000, 97:6640-6645). Briefly, cells were inoculated into 10-15mL of 2X YT broth and grown at 37°C overnight. Then 100μL of overnight culture was re-inoculated into 10mL fresh 2X YT broth at 37°C for 3-4 hours. Cells to be transformed with pKD46 plasmid were heated at 50°C for 25 minutes to help

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inactivate host restriction. Cells were washed five times in ddH₂O water and resuspended in 60μL of 10% glycerol. Cells were then pulsed at 2400-2450kV for 1-6ms, incubated in SOC for 2-3 hours at 30°C and plated on LB media with appropriate antibiotics. *S. enteritidis* transformants with pKD46 were maintained at 30°C. When these transformants were prepared for additional electroporation reactions, all steps were the same except that 15% arabinose was added to induce Red recombinase enzymes one hour prior to washing, and cells did not undergo the 50°C heat step.

Loop 9 up- I-SceI/ Km^r- Loop 9 down Construct

Introduction of I-SceI enzyme recognition site along with the Km^r gene into loop 9 of the *lamB* gene was done by combining the Red recombinase system (Datsenko and Wanner, PNAS 2000, 97:6640-6645, which is incorporated herein by reference in its entirety) and overlapping PCR (Horton et al., BioTechniques 1990, 8:528-535, which is incorporated herein by reference in its entirety). The insertion site corresponds to nucleotide 1257 of the *lamB* gene using *Salmonella typhimurium* LT2 (*S. typhimurium*) as an annotated reference genome. First, the upstream and downstream regions immediately flanking the loop 9 insertion site (loop 9 up and loop 9 down, respectively) were amplified separately. Primers used were lam-up-f and lam-up-r for loop 9 up and lam-dn-f and lam-dn-r for loop 9 down. Then the Km^r gene from pKD13 plasmid was amplified using primers Km-f and Km-r. Here, the I-SceI enzyme site was synthetically added to the 5' end of Km-f primer then preceded by a region complimentary to the loop-up-r primer. Likewise, a region complimentary to the loop-dn-f primer was added to the 5' end of Km-r primer. The complimentary regions allow all 3 PCR products to anneal when used as templates in one PCR reaction. Figure 2a represents this design scheme. PCR fragments consisting of loop 9 up- I-SceI/ Km^r- loop 9 down sequence (PCR-A) were electroporated into *S. enteritidis* cells, which harbored pKD46 and were induced by arabinose, and then plated on LB with Km plates. To verify the correct sequence orientation of the mutation, we performed colony PCR with primer pairs Kan4F/lam3f and Kan4R/lam3r, where Kan4F and Kan4R are Km^r gene-specific primers and lam3f and lam3r are primers located outside the *lamB* loop 9 region. These PCR fragments were gel purified (Qiagen, Valencia, CA, USA) and used for DNA sequencing.

Loop 9 up- LM2 or CD154s or combination sequence- Loop 9 down Construct

The final overlapping PCR fragment, PCR-B, contained the added LM2 (or CD154s or combination sequences flanked by loop 9 up and down regions (Figure 2b). Combination

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sequences consisted of LM2 or an alternate M2e epitope associated with avian species (M2eA) and CD154 along with spacers such as Glycine (Gly) or Serine (Ser) residues. Inserted sequences were as follows: LM2 (SEQ ID NO:37); M2eA (SEQ ID NO:38); combination sequence no. 1 (Gly)₃-CD154s-(Gly)₃-LM2-(Gly)₃ (SEQ ID NO:39); and
5 combination sequence no.2 (Ser)₄-M2eA-(Ser)₄-M2eA-(Ser)₄-CD154-(Ser)₄-LM2-(Ser)₄-LM2-(Ser)₄ (SEQ ID NO:40).

To shorten the amount of steps for construction of the next fragment, the LM2 or CD154 sequence was synthetically added to the 5' end of the lam-dn-f primer and preceded by the complimentary region to the loop-up-r primer. The previously used PCR product for
10 loop 9 up could be used together with the newly constructed PCR product in which LM2 or CD154s were incorporated at the 5' end of loop 9 down to perform the final PCR reaction. However, for other insert sequences (referred to as combination sequences), an extra PCR step was needed, due to the longer lengths of insert sequences, to amplify loop 9 up with added nucleotides specific to insertion sequences connected to loop-up-r primer. The coding
15 sequence for Gly (GGT) and Serine (TCC) as well as all other amino acids were chosen based on compiled data of the most frequently used codons in *E. coli* and *Salmonella typhimurium* proteins. See Table 1 for further details of primer design.

Genomic Replacement of I-SceI/ Km^r with LM2 or CD154s or Combination Sequences

PCR-B products were electroporated into *S. enteritidis* cells along with plasmid pBC-I-SceI at a molar ratio of approximately 40:1 (Kang et al., J Bacteriol 2004, 186:4921-4930,
20 which is incorporated herein by reference in its entirety). Clones for each PCR-B recombination mutation were chosen according to the ability to grow on Cm plates but not on Km plates, due to the replacement of PCR-B for the Km^r encoding PCR-A sequence. Modified regions in the selected clones were PCR-amplified, and DNA sequences were
25 determined using primers lam3f and lam3r located outside the loop 9 down and up amplified regions.

I-SceI site/ Km^r insertion mutation

The first mutation step involved designing a PCR fragment, PCR-A, which would serve as the carrier of the I-SceI site/ Km^r cassette to be inserted into the *lamB* site. PCR-A
30 consisted of the I-SceI enzyme recognition site adjacent to the Km^r gene with approximately 200- 300bp of flanking DNA on each end homologous to the upstream and downstream regions of *lamB* loop 9 insertion site (loop 9 up and loop 9 down, respectively). The

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fragment was introduced into *S. enteritidis* cells expressing Red recombinase enzymes and Km^r colonies were selected. After screening a few colonies by colony PCR, positive clones were sequenced for the desired inserted I-SceI site/ Km^r sequence, and the identified mutant was designated SE164.

5 Genomic Replacement of I-SceI/ Km^r with LM2 or CD154s or combination sequences

The second mutation step required constructing a PCR fragment, referred to as PCR-B and shown in Figure 2B, consisting of the final insertion sequence, LM2 or CD154 or combination sequences, flanked by *lamB* homologous fragments. PCR-B amplicons have no selection marker and must be counter-selected after replacement for the previous I-SceI site/ Km^r mutation in SE164. Plasmid pBC-I-SceI encodes the Cm^r gene and the I-SceI enzyme, which will cut the genome at the I-SceI site of SE164. Therefore, pBC-I-SceI was electroporated into SE164 along with PCR-B. After recombination of PCR-B to replace PCR-A, positive clones were chosen based on the ability to grow on Cm but not on Km. After DNA sequencing of mutants to confirm successful recombination of PCR-B, the strains were designated SE172, SE173, SE180, and SE189 for insert sequences LM2, CD154s, (Gly)₃-CD154s-(Gly)₃-LM2-(Gly)₃, and (Ser)₄-M2eA-(Ser)₄-M2eA-(Ser)₄-CD154-(Ser)₄-LM2-(Ser)₄-LM2-(Ser)₄, respectively. Ten random clones for each the LM2 and CD154s insertion were used for PCR with *lam* 3f and *lam* 3r then digested using unique restriction enzymes sites for each insertion sequence and 100% of clones tested by digestion were positive for the desired mutation sequence. Sequencing results demonstrated that the insertion of LM2 or CD154s or combination sequences was exactly into the loop 9 region without the addition of extraneous nucleotides.

Example 2. Attenuation of M2e or M2e/CD154 mutants/inserts.

Attenuation of SE13A was achieved by deletion mutation of the *aroA* gene and/or the *htrA* gene. Mutation of the *aroA* gene, a key gene in the chorismic acid pathway of bacteria, results in a severe metabolic deficiency which affects seven separate biochemical pathways. Mutation of the *htrA* gene reduces the cell's ability to withstand exposure to low and high temperatures, low pH, and oxidative and DNA damaging agents and reduces the bacteria's virulence.

To achieve deletion mutations in SE13A, the target gene sequence in the bacterial genome of *S. enteritidis* was replaced with the Km resistant gene sequence. This was completed using overlapping extension PCR and electroporation of the PCR products as

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described above. The Km resistance gene was targeted into the genomic region containing the genes of interest (*aroA* or *htrA*) by flanking the Km resistance gene with 200-300 base pairs of sequences homologous to the genes of interest. Once Km resistant mutants were obtained, the *aroA* or *htrA* deletion mutations were confirmed by DNA sequencing. The resulting *aroA*- and *htrA*- Salmonella strains were deposited with the American Type Culture Collection on September 13, 2006 (Deposit No.PTA-7872 and Deposit No. PTA-7873, respectively). The attenuated strains were also tested *in vivo* with regards to clearance time. Both of the attenuated strains had quicker clearance times than did the wildtype 13A strain, but both were able to colonize the liver, spleen, and cecal tonsils of chickens after oral infection. In addition, an attenuated strain lacking both *aroA* and *htrA* was also isolated.

Example 3. Confirmation of cell surface expression of M2e and CD154.

Cell surface expression of the M2e and CD154 inserts was confirmed with a simple antibody/antigen precipitation reaction. In short, polyclonal antibodies were made against the amino acid sequences of both M2E-LM2 (EVETPIRN; SEQ ID NO:5) and CD154 (WAEKGYTMS; SEQ ID NO:6) conjugated to a carrier protein (KLH). The resulting antibodies were then incubated with SE13A wildtype (no inserts) or SE13A with either the M2e-LM2, the CD154 or the M2e-LM2 and CD154 combined insert on a glass plate at room temperature and allowed to incubate for 30 seconds. Cell surface expression was determined by the presence of a precipitate. Results are shown in Table 2. A positive precipitation reaction is indicated by a (+) sign and a negative precipitation reaction is indicated by a (–) sign. The results demonstrate that the SE13A wildtype did not react with the M2e and CD154 peptide antibodies, while the strains expressing M2e, CD154 or M2e and CD154 reacted with the appropriate antibodies. Thus, M2e and CD154 peptides are being expressed on the surface of the bacteria.

Table 2. Precipitation reaction

	SE13A	SE13A-M2E	SE13A-CD154	SE13A-M2E-CD154
M2E antibody	-	+	Not tested	+
CD154 antibody	-	Not tested	+	+

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Example 4. Vaccination Study.

Day-of-hatch (day 0) chicks were obtained from a local commercial hatchery and randomly distributed into treatment groups (n=55/treatment group). Fifteen chicks out of the possible 55 in each treatment group were tagged and numbered. The chicks were orally
 5 infected by gavage with 0.25 ml of 10^4 , 10^5 , or 10^7 (data not shown) cfu/ml of the various SE13A treatments as indicated in Table 3.

Table 3. Challenge Dose for each treatment group.

Treatment Group	Challenge Dose
SE13A-M2E	10^5 cfu/ml
SE13A-M2E-CD154	10^5 cfu/ml
SE13A-M2E aroA	10^4 cfu/ml
SE13A-M2E-CD154 aroA	10^4 cfu/ml
SE13A-M2E htrA	10^5 cfu/ml
SE13A-M2E-CD154 htrA	10^5 cfu/ml

Each treatment group was housed in an individual floor pen on fresh pine litter and
 10 provided water and feed *ad libitum*. On days 7, 14, 21 and 28 post-hatch, approximately 1 ml of blood was collected from each of the fifteen tagged birds and the serum was removed for later use in determining antibody titers. On the same days, ten birds from each treatment group were euthanized, their liver, spleen and ceca tonsils aseptically removed for determination of bacterial colonization (ceca tonsils) and bacterial invasion (liver and spleen).
 15 Individual liver, spleen and ceca tonsil samples were pre-enriched in tetrathionate broth overnight at 37°C. The next day loopfuls of each broth culture were streaked onto XLD agar plates supplemented with Novabycin and Naladixic Acid and incubated overnight at 37°C. The following morning the plates were read for the presence or absence of Salmonella colonies. Bacterial colonization and invasion data are presented in Table 4 by treatment
 20 group. Each ratio presented in Table 4 represents the number of birds from which Salmonella positive isolates were recovered out of the possible ten birds that were cultured on days 7, 14, 21, and 28 post-challenge.

Table 4. Bacterial Colonization and Invasion.

Treatment Groups	Colonization (Ceca Tonsils)				Invasion (Liver/Spleen)			
	D7	D14	D21	D28	D7	D14	D21	D28
SE13A	9/10	3/10	5/10	2/10	8/10	8/10	2/10	4/10
SE13A-M2E-CD154	9/10	7/10	6/10	9/10	8/10	1/10	5/10	4/10

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SE13A-M2E aroA	10/10	4/10	0/10	3/10	9/10	4/10	0/10	3/10
SE13A-M2E-CD154 aroA	4/10	1/10	1/10	3/10	4/10	0/10	0/10	3/10
SE13A-M2E htrA	5/10	1/10	0/10	1/10	4/10	2/10	0/10	2/10
SE13A-M2E-CD154 htrA	4/10	1/10	0/10	0/10	6/10	0/10	0/10	0/10

Positive Salmonella bacterial isolates recovered from birds in each treatment group were subjected to analysis by polymerase chain reaction (PCR) using the primers specific to each insert disclosed in Table 1 to verify the M2e- and or CD154 insert. This technique was utilized to ensure that the strain that the birds were originally given was equivalent to the strain recovered. In each treatment group, PCR confirmed that the recovered strains were the same as the strains with which the birds were infected. The results indicated acceptable colonization of tissues with the various Salmonella strains tested.

Example 5. M2e antibody production.

Serum collected from the tagged birds in each treatment group was used in an antigen capture ELISA to calculate M2e antibody levels. In brief, individual wells of a 96-well plate were coated with 5 µg/ml of the M2e-LM2 epitope (EVETPIRN: SEQ ID NO:5) conjugated to BSA. Antigen adhesion was allowed to proceed overnight at 4°C. Plates were rinsed with PBS + 0.05% Tween 20 and incubated for 2 hours with the serum previously collected from the birds in each of the 6 treatment groups described above. The plates were rinsed with PBS + 0.05% Tween 20 followed by incubation with peroxidase conjugated Goat-anti-Chicken IgY secondary antibody (1:10,000 dilution) obtained from Jackson ImmunoResearch Laboratories (West Grove, PA) for an additional hour. After subsequent rinsing, the plates were developed using a peroxidase substrate kit obtained from Fisher Scientific and absorbances read on a spectrophotometer at 450nm and 405nm.

Each plate also contained a positive control and negative control where the M2e polyclonal antibody described above and chicken serum from an untreated bird respectively replace the serum from the treatment groups. The absorbances obtained for the positive control, negative control and experimental samples were used to calculate Sample to Positive control ratios (S/P ratios) using the following calculation:

$$\text{S/P ratio calculation: } \frac{\text{sample mean} - \text{negative control mean}}{\text{positive control mean} - \text{negative control mean}}$$

The calculated S/P ratios for each group are shown in Figure 3 and 4. As is shown, M2e-specific antibody levels for each group expressing M2e-CD154 produced an ELISA signal

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that was on average over 30% higher when compared with their respective group that only expresses M2e. The data demonstrate that SE13A-M2e and SE13A-M2e-CD154 are both capable of eliciting a robust antibody response to M2e. This response was clearly augmented by addition of the CD154 peptide. In addition, similar responses were generated when either the *aroA* or *htrA* auxotrophic SE13A strains were utilized. These strains may provide vaccine vectors with higher safety for clinical use without sacrificing generation of a robust immune response.

Example 6. Virus Neutralization.

Antisera (collected 2 weeks after the booster immunization in each experiment) generated against the recombinant SE vectors described above were subjected to virus neutralization testing using H9N2 Influenza (Charles River Laboratories, Franklin, CT) using standard protocols (Charles River Laboratories). See Table 5. Neutralizing indices indicate that the antisera from vaccinated chickens were effective in neutralizing Avian Influenza and thus in protecting embryos from the virus (VN titers ranged from 6.3 to 8.8 in two studies). Hyperimmune serum raised against synthetic M2e peptide was used as a positive control.

Table 5. Virus Neutralization

SE strain	Neutralization Index
SE <i>aroA</i> M2E	7.5
SE <i>aroA</i> M2E-CD154	8.3
SE <i>aroA</i> M2E (multi-copy)-CD154	8.3
Positive control	8.3

Example 7. Challenge Study.

Viruses.

The influenza viruses used in these studies were A/Turkey/Virginia/158512/2002 (TV/02) H7N2 LP Avian Influenza (LPAI H7N2) and A/Egret/Hong Kong/757.2/2002 (Eg/02) H5N1 HP avian influenza (HPAI H5N1). Viruses were grown and titered in 9-11 day old embryonated SPF (specific pathogen free) chicken eggs as previously described (Suarez et al., J Virol. 1998 Aug; 72(8):6678-88.).

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Chickens and housing.

For LP and HPAI challenge chickens were transferred into negative-pressure-stainless steel Horsfall units containing HEPA filters in a USDA-certified biosafety level 3 agriculture facility. Feed and water were provided *ad libitum*.

5 Serology and virus isolation.

Hemagglutination inhibition test was performed with BPL-inactivated homologous H5N1 antigen with sera collected at day 0 in Expt. I and Day 0 and 14 in Expt. II as previously described (Suarez et al., 1998). Titers greater ≥ 3 ($\log_2$) were considered positive. Virus isolation from oral and cloacal swabs on days 2 and 4 post-challenge was performed in
10 9-11 day of embryonation SPF chicken eggs as previously described (Tumpey et al., Avian Dis. 2004 Jan-Mar;48(1):167-76). Briefly, swabs were collected into 2 ml brain-heart infusion (BHI) broth with antibiotics (1000 units/ml penicillin G, 200 μ g/ml gentamicin sulfate, and 4 μ g/ml amphotericin B; Sigma Chemical Company, St. Louis, MO) from each bird on day 0, 2, 4, days post challenge for virus isolation.

15 Western blot.

Purified AIV proteins from whole virus (H5N1 and H7N2) were separated by SDS-PAGE in a 10 % polyacrylamide gel and transferred as previously described (Kapczynski and Tumpey, Avian Dis. 2003 Jul-Sep;47(3):578-87). Briefly, anti-M2e serum from birds previously immunized with Δ SE M2e-HM (1:1000) was incubated with the membrane
20 containing AIV antigen for 1 hour at room temperature. Following three washes in PBS-Tween 20 (0.05%) the membrane was reacted with horseradish peroxidase-labeled goat anti-chicken IgG secondary antibody (Southern Biotech Associates, Inc, Birmingham, AL) at a 1:2000 dilution for 1 hour. After washing as above, the membrane was reacted with ECL Western Blotting Detection Reagents (Amersham Biosciences, Piscataway, NJ) according to
25 the manufacturers' recommendations, and exposed to Hyperfilm ECL (Amersham Biosciences). The film was developed using Kodak GBX developing reagents (Eastman Kodak Company) according to the manufacturers' recommendations.

Protection studies.

The initial experimentation was designed to assess protection of chickens receiving
30 vaccination with Δ SE M2e-HM (multi-copy M2e-CD154 with the SEQ ID NO:9 insertion sequence) Salmonella from challenge with LPAI TV/02 (10^6 EID₅₀ per bird (EID refers to

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embryo infectious dose)) to determine reduction of morbidity and viral shedding. Subsequently, protection from HPAI Eg/02 challenge was investigated using a sublethal (0.1 CLD₅₀ per bird (CLD refers to chick lethal dose)) and lethal dose (100 CLD₅₀ per bird), in terms of morbidity, mortality and viral shedding.

5 *Experiment I. Challenge with LPAI H7N2*

Groups of ten 1-day old SPF chickens were divided into 3 groups. Birds in groups 1 and 2 received sham vaccination with 100 µl of phosphate-buffered saline (PBS, pH 7.4). Birds in group 3 received vaccination with ΔSE M2e-HM. Three weeks later (Day 21) the three groups of SPF chickens received an identical second vaccination (boost) utilizing saline
10 (Groups 1 and 2) or the recombinant Salmonella vectored vaccine (Group 3). Three weeks after boost (Day 42), birds in group 2 and 3 were challenged intranasally (IN) with 10⁶ embryo infectious dose 50 (EID₅₀) / bird of TV/02 (LPAI H7N2). Unchallenged birds were sham-challenged with 100 µl PBS via intranasal route. Following challenge, birds were monitored daily for disease signs for 14 days post-infection (PI). The morbidity results
15 following challenge with LPAI H7N2 are shown in Figure 5 and demonstrate a significant reduction in morbidity after vaccination with SE13A expressing M2E and CD154. For determining incidence of viral shedding, oral and cloacal swabs were taken on day 2 and 4 PI. The amount of viral shedding following challenge with LPAI H7N2 at days 2 and 4 PI is shown in Figure 6 and demonstrated that vaccination with SE13A-HM also reduce the ability
20 of AI to replicate in the chicks.

Experiment II. Challenge with HPAI H5N1

Groups of ten 1-day old SPF chickens were divided into 5 groups. Birds in groups 1, 2 and 3 received sham vaccination with 100 µl of phosphate-buffered saline (PBS, pH 7.4). Birds in group 4 and 5 received vaccination with ΔSE M2e-HM as described in Expt. I. On
25 day 42, birds in group 1 receive sham challenge with 100 µl PBS via intranasal route. Birds in groups 2 and 3 received challenge with 0.1 and 100 CLD₅₀ Eg/02 (HPAI H5N1) per bird, respectively. Birds in groups 4 and 5 received challenge with 0.1 and 100 CLD₅₀ Eg/02 (HPAI H5N1) per bird, respectively. Following challenge, birds were monitored daily for morbidity and mortality for 14 days PI. Chickens displaying severe clinical signs of disease
30 were euthanized by overdose of sodium pentobarbital. The morbidity results following challenge with HPAI H5N1 are shown in Figure 7 and demonstrate a significant reduction in morbidity after vaccination with SE13A expressing M2E and CD154. For determining

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incidence of viral shedding, oral and cloacal swabs were taken on day 2 and 4 PI. The amount of viral shedding following challenge with HPAI H5N1 at days 2 and 4 PI is shown in Figure 8 and demonstrated that vaccination with SE13A-M2e also reduce the ability of AI to replicate in the chicks.

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We claim:

1. A *Salmonella enteritidis* 13A strain having ATCC deposit number PTA-7871.
2. The *Salmonella* strain of claim 1, wherein the strain is attenuated and wherein the strain is capable of colonizing a subject.
- 5 3. The *Salmonella* strain of claim 1 or 2, wherein the strain comprises a mutation in an aromatization pathway.
4. The *Salmonella* strain of claim 3, wherein the mutation is within *aroA*.
5. The *Salmonella* strain of any of claims 1-4, wherein the strain comprises a mutation in a stress response pathway.
- 10 6. The *Salmonella* strain of claim 5, wherein the mutation is within *htrA*.
7. The *Salmonella* strain of any of claims 1-6, further comprising an Influenza M2e polynucleotide sequence encoding an Influenza M2e polypeptide.
8. The *Salmonella* strain of claim 7, wherein the Influenza M2e polypeptide is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, an
15 immunogenic fragment of SEQ ID NO:1, an immunogenic fragment of SEQ ID NO:2, an immunogenic fragment of SEQ ID NO:3 and an immunogenic fragment of SEQ ID NO:4 or combinations thereof.
9. The *Salmonella* strain of claim 7, wherein the Influenza M2e polypeptide is SEQ ID NO:5 or SEQ ID NO:20.
- 20 10. The *Salmonella* strain of any of claims 7-9, wherein the Influenza M2e polynucleotide sequence is inserted into a *Salmonella* polynucleotide sequence encoding an external portion of a transmembrane protein.
11. The *Salmonella* strain of claim 10, wherein the transmembrane protein is *lamB*.
12. The *Salmonella* strain of any of claims 7-11, wherein the strain comprises more than
25 one copy of the Influenza M2e polynucleotide sequence.

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13. The *Salmonella* strain of any of claims 1-12, further comprising a CD154 polynucleotide sequence encoding a CD154 polypeptide capable of binding CD40.
14. The *Salmonella* strain of claim 13, wherein the CD154 polypeptide is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:27, SEQ ID NO:28 and
5 SEQ ID NO:29.
15. The *Salmonella* strain of claim 13 or 14, wherein the CD154 polynucleotide sequence is inserted into a *Salmonella* polynucleotide sequence encoding an external portion of a transmembrane protein.
16. The *Salmonella* strain of claim 15, wherein the transmembrane protein is *lamB*.
- 10 17. The *Salmonella* strain of any of claims 13-16, wherein the CD154 polynucleotide sequence is linked in frame to a polynucleotide sequence encoding an antigenic polypeptide.
18. The *Salmonella* strain of claim 17, wherein the antigenic polypeptide is an Influenza M2e polypeptide.
19. The *Salmonella* strain of claim 4, having ATCC deposit number PTA-7872.
- 15 20. The *Salmonella* strain of claim 6, having ATCC deposit number PTA-7873.
21. The *Salmonella* strain of any of claims 1-20, further comprising an Influenza A hemagglutinin polynucleotide sequence encoding an Influenza A hemagglutinin polypeptide.
22. The *Salmonella* strain of claim 21, wherein the Influenza A hemagglutinin polypeptide comprises SEQ ID NO:21 or SEQ ID NO:22.
- 20 23. The *Salmonella* strain of any of claims 1-22, further comprising an Influenza A nuclear protein polynucleotide sequence encoding an Influenza A nuclear protein polypeptide.
24. The *Salmonella* strain of claim 23, wherein the Influenza A nuclear protein polypeptide comprises SEQ ID NO:23 or SEQ ID NO:24.
- 25 25. A composition comprising a *Salmonella* strain according to any of claims 1-24, and a pharmaceutically acceptable carrier.

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26. A method of enhancing an immune response in a subject comprising administering to the subject a vaccine vector in an amount effective to enhance the immune response of the subject in response to vaccination, the vaccine vector comprising a CD154 polynucleotide sequence encoding a CD154 polypeptide capable of binding CD40, the CD154 polypeptide
5 having fewer than about 50 amino acids and comprising amino acids 140-149 of SEQ ID NO:26 or a homolog thereof.

27. The method of claim 26, wherein the CD154 polypeptide has fewer than 25 amino acids.

28. The method of claim 26, wherein the CD154 polypeptide is at least 10 amino acids
10 long.

29. The method of claim 26, wherein the CD154 polypeptide is from 10 to 20 amino acids long.

30. The method of claim 26, wherein the CD154 polypeptide is SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:27, SEQ ID NO:28, or SEQ ID NO:29.

15 31. The method of any of claims 26-30, wherein the CD154 polypeptide is expressed on the surface of the vaccine vector.

32. The method of any of claims 26-31, wherein the CD154 polynucleotide sequence is inserted within a sequence encoding an external portion of a transmembrane protein.

33. The method of any of claims 26-32, wherein the vaccine vector is a bacterium.

20 34. The method of claim 33, wherein the bacterium is *Salmonella*.

35. The method of claim 34, wherein the *Salmonella* is *Salmonella enteritidis*.

36. The method of claim 34, wherein the *Salmonella* is *Salmonella enteritidis* 13A, having ATCC deposit number PTA-7871.

25 37. The method of any of claims 34-36, wherein the CD154 polynucleotide sequence is inserted into a sequence encoding an external portion of *lamB*.

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38. The method of any of claims 26-37, wherein the subject is member of a poultry species.
39. The method of claim 38, wherein the poultry species is a chicken.
40. The method of any of claims 26-37, wherein the subject is a mammal.
- 5 41. The method of claim 40, wherein the mammal is a human.
42. The method of claim 40, wherein the mammal is a swine.
43. A method of enhancing the immune response against Influenza A in a subject comprising administering to the subject a bacterium comprising an Influenza A M2e polynucleotide sequence encoding an Influenza A M2e polypeptide in an amount effective to
10 enhance the immune response of the subject to Influenza A.
44. The method of claim 43, wherein the Influenza A M2e polypeptide is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, an immunogenic fragment of SEQ ID NO:1, an immunogenic fragment of SEQ ID NO:2, an immunogenic fragment of SEQ ID NO:3 and an immunogenic fragment of SEQ ID NO:4 or
15 a combination thereof.
45. The method of any of claims 43-45, wherein the Influenza A M2e polypeptide comprises SEQ ID NO:5 or SEQ ID NO:20.
46. The method of any of claims 43-45, wherein the Influenza A M2e polynucleotide sequence is inserted into a bacterial polynucleotide sequence encoding an external portion of
20 a transmembrane protein.
47. The method of any of claims 43-46, wherein the bacterium comprises more than one copy of the Influenza A M2e polynucleotide sequence.
48. The method of any of claims 43-47, wherein the bacterium is a member of the Enterobacteriaceae family.
- 25 49. The method of claim 48, wherein the bacterium is *Salmonella*.
50. The method of claim 48, wherein the bacterium is *Salmonella enteritidis* 13A.

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51. The method of claim 48, wherein the bacterium is an attenuated *Salmonella* strain of any of claims 1-5.

52. The method of any of claims 48-51, wherein the Influenza A M2e polynucleotide sequence is inserted in *lamB*.

5 53. The method of claim 48, wherein the bacterium is *Escherichia coli*.

54. The method of any of claims 43-47, wherein the bacterium is *Lactobacillus*.

55. The method of any of claims 43-54, wherein the bacterium further comprises a CD154 polynucleotide sequence encoding a CD154 polypeptide capable of binding CD40, the CD154 polypeptide having fewer than 50 amino acids and comprising amino acids 140-
10 149 of SEQ ID NO:26 or a homolog thereof.

56. The method of claim 55, wherein the CD154 polypeptide comprises SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:27, SEQ ID NO:28, or SEQ ID NO:29.

57. The method of claim 55 or 56, wherein the CD154 polynucleotide sequence is inserted into a bacterial polynucleotide sequence encoding an external portion of a
15 transmembrane protein.

58. The method of any of claims 43-57, wherein the bacterium is administered by a method selected from the group consisting of oral, intranasal, parenteral, and in ovo.

59. The method of any of claims 43-58, wherein the enhanced immune response comprises an enhanced antibody response.

20 60. The method of any of claims 43-58, wherein the enhanced immune response comprises an enhanced T cell response.

61. The method of any of claims 43-60, wherein the subject is member of a poultry species.

62. The method of claim 61, wherein the poultry species is a chicken.

25 63. The method of any of claims 43-60, wherein the subject is a mammal.

64. The method of claim 63, wherein the subject is a human.
65. The method of any of claims 43-64, wherein from about 10^4 to about 10^9 bacteria are administered to the subject.
66. The method of any of claims 43-64, wherein from about 10^5 to about 10^7 bacteria are administered to the subject.
67. The method of any of claims 43-66, wherein the bacterium is killed prior to administration to the subject.
68. The method of any of claims 43-66, wherein the bacterium is not capable of replicating in the subject.
69. A method of reducing the morbidity associated with Influenza A infection in a subject comprising administering to the subject a bacterium comprising an Influenza A M2e polynucleotide sequence encoding an Influenza A M2e polypeptide in an amount effective to reduce the morbidity associated with a subsequent Influenza A infection.
70. The method of claim 69, wherein the Influenza A M2e polypeptide is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, an immunogenic fragment of SEQ ID NO:1, an immunogenic fragment of SEQ ID NO:2, an immunogenic fragment of SEQ ID NO:3 and an immunogenic fragment of SEQ ID NO:4 or combinations thereof.
71. The method of any of claims 69-70, wherein the Influenza A M2e polypeptide is SEQ ID NO:5 or SEQ ID NO:20.
72. The method of any of claims 69-71, wherein the Influenza A M2e polynucleotide sequence is inserted into a bacterial polynucleotide sequence encoding an external portion of a transmembrane protein.
73. The method of any of claims 69-72, wherein the bacterium comprises more than one copy of the Influenza A M2e polynucleotide.
74. The method of any of claims 69-73, wherein the bacterium is a member of the Enterobacteriaceae family.

75. The method of claim 74 wherein the bacterium is *Salmonella enteritidis* 13A.
76. The method of claim 74, wherein the bacterium is an attenuated *Salmonella* strain of any of claims 1-5.
77. The method of claim 74, wherein the bacterium is *Escherichia coli*.
78. The method of any of claims 69-73, wherein the bacterium is *Lactobacillus*.
79. The method of any of claims 69-78, wherein the bacterium further comprises a CD154 polynucleotide sequence encoding a CD154 polypeptide capable of binding CD40, the CD154 polypeptide having fewer than 50 amino acids and comprising amino acids 140-149 of SEQ ID NO:26 or a homolog thereof.
80. The method of claim 79, wherein the CD154 polypeptide is SEQ ID NO:6 or SEQ ID NO:7, SEQ ID NO:27, SEQ ID NO:28, or SEQ ID NO:29.
81. The method of claim 79 or 80, wherein the CD154 polynucleotide sequence is inserted into a bacterial polynucleotide sequence encoding an external portion of a transmembrane protein.
82. The method of any of claims 69-81, wherein the bacterium is administered by a method selected from the group consisting of oral, intranasal, parenteral, and in ovo.
83. The method of any of claims 69-82, wherein the subject is a member of a poultry species.
84. The method of claim 83, wherein the poultry species is a chicken.
85. The method of any of claims 69-82, wherein the subject is a mammal.
86. The method of claim 85, wherein the subject is a human.
87. The method of any of claims 69-86, wherein from about 10^4 to about 10^9 bacteria are administered to the subject.
88. The method of any of claims 69-87, wherein the bacterium is killed prior to administration to the subject.

89. A method of generating site-specific mutations in a bacterium member of the Enterobacteriaceae family, comprising:

a) generating a first polynucleotide comprising a counter-selection marker and a first antibiotic resistance marker flanked by polynucleotides homologous to the sequences flanking a mutation site in the chromosome of the bacterium;

b) introducing the first polynucleotide into the chromosome of the bacterium by Red recombinase-mediated homologous recombination to generate an intermediate;

c) isolating the intermediate by selection for the first antibiotic resistance marker;

d) generating a second polynucleotide comprising the mutation flanked by polynucleotides homologous to the sequences flanking the mutation site;

e) introducing the second polynucleotide into the intermediate by Red recombinase-mediated homologous recombination to generate a site-specific mutant; and

f) isolating the site-specific mutant by counter-selecting for the loss of the counter-selection marker.

90. The method of claim 89, wherein the first polynucleotide is generated by overlapping extension polymerase chain reaction.

91. The method of claim 89 or 90, wherein the second polynucleotide is generated by overlapping extension polymerase chain reaction.

92. The method of any of claims 89-91, wherein the bacterium is selected from the group consisting of *Salmonella*, *Escherichia*, *Shigella* and *Yersinia*.

93. The method of claim 92, wherein the bacterium is *Salmonella*.

94. The method of claim 93, wherein the bacterium is *Salmonella enteritidis*.

95. The method of claim 92, wherein the bacterium is *Escherichia coli*.

96. The method of any of claims 89-95, wherein the polynucleotides homologous to the sequence flanking the mutation site in step (a) comprise less than 300 base pairs on each side of the mutation site.

97. The method of any of claims 89-95, wherein the polynucleotides homologous to the sequence flanking the mutation site in step (a) comprise less than 200 base pairs on each side of the mutation site.

98. The method of any of claims 89-97, wherein the counter-selection marker comprises a I-SceI recognition sequence.

99. The method of claim 98, wherein counter-selecting in step (f) comprises introducing a plasmid encoding the I-SceI endonuclease and selecting for loss of the I-SceI recognition sequence.

100. The method of any of claims 89-99, wherein the counter-selection marker comprises *sacB*.

101. The method of claim 100, wherein counter-selecting in step (f) comprises selecting for loss of sucrose sensitivity.

102. A method for developing a bacterial vaccine vector comprising:

- a) selecting a bacterium capable of colonizing a subject;
- b) attenuating the bacterium to generate an attenuated bacterium;
- c) incorporating a CD154 polynucleotide sequence encoding a CD154 polypeptide capable of binding CD40 into the attenuated bacterium to generate a vaccine vector, the CD154 polypeptide having fewer than 50 amino acids long and comprising amino acids 140-149 of CD154 SEQ ID NO:26 or a homolog thereof.

103. The method of claim 102, further comprising incorporating a second polynucleotide sequence encoding an antigenic polypeptide into the chromosome of the vaccine vector.

104. The method of claim 102 or 103, wherein the bacterial vaccine vector is *Salmonella*.

105. The method of claim 104, wherein the *Salmonella* is *Salmonella enteritidis* 13A.

106. The method of claim 103, wherein the CD154 polynucleotide sequence or its complement and the second polynucleotide sequence or its complement are on the same polynucleotide molecule.