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HETEROLOGOUS ANTIGENS IN LIVE CELL VACCINE STRAINS

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(57) Claim

1. A bacterial chromosome containing a DNA sequence encoding a non-toxic and immunogenic heterologous antigen, said DNA sequence being functionally linked to an iron-regulated promoter.

42. A process for inducing in an animal an immune response against a heterologous antigen, comprising administering to said animal recombinant *V.cholerae* containing DNA encoding said heterologous antigen, said heterologous antigen being expressed from said DNA in said animal, wherein the sequence of said heterologous antigen does not comprise the sequence of a full length polypeptide expressed by a wild type *V. cholerae* and wherein said heterologous antigen (a) comprises an antigenic part or all, of a protein that is naturally expressed by an infectious organism other than wild type *V. cholerae*, and (b) induces an immune response in an animal.

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(54) Title: HETEROLOGOUS ANTIGENS IN LIVE CELL VACCINE STRAINS

(57) Abstract

A bacterial cell (preferably a gram-negative, enteric bacterium such as *V. cholerae*) the chromosome of which contains a DNA sequence encoding a heterologous antigen, which sequence is functionally linked to an iron-regulated promoter such as the *irgA* promoter of *V. cholerae*.

HETEROLOGOUS ANTIGENS IN LIVE CELL VACCINE STRAINS

The field of the invention is genetically engineered live bacterial cell vaccine strains.

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Background of the Invention

V. cholerae is a gram-negative bacterium that causes a severe, dehydrating and occasionally fatal diarrhea in humans. There are an estimated 5.5 million cases of cholera each year, resulting in greater than 100,000 deaths (Bull. W.H.O. 68:303-312, 1990). Over the last several decades, cholera has been considered to occur primarily in developing countries of Asia and Africa, but recently it has reached epidemic proportions in regions of South and Central America, as well (Tauxe et al., J. Am. Med. Assn. 267:1388-1390, 1992; Swerdlow et al., J. Am. Med. Assn. 267:1495-1499, 1992).

Patients who recover from cholera infection have long-lasting, perhaps lifelong, immunity to reinfection (Levine et al., J. Infect. Dis. 143:818-820, 1981). The development of *V. cholerae* vaccines has focused on reproducing this naturally occurring immunity, but the currently available parenteral, killed whole-cell vaccine preparation provides less than 50% protection from disease, for a duration of only 3 to 6 months (Saroso et al., Bull. W.H.O. 56:619-627, 1978; Levine et al., Microbiol. Rev. 47:510-550, 1983). A genetically-engineered, live oral vaccine for *V. cholerae* has several theoretical advantages over the present parenteral killed whole-cell vaccine. As a mucosal pathogen, *V. cholerae*

adheres selectively to the M cells of the gastrointestinal tract (Owen et al., J. Infect. Dis. 153:1108-1118, 1986) and is a strong stimulus to the common mucosal immune system (Svennerholm et al., Lancet i:305-308, 1982); and oral cholera vaccination in humans produces a strong salivary gland IgA response to cholera toxin B subunit (Czerkinsky et al., Infect. Immun. 59:996-1001, 1991). Oral vaccines take advantage of the fact that oral administration of antigens appears to be the most efficient stimulus for the development of secretory IgA (Svennerholm, *supra*), and that secretory IgA by itself is sufficient to protect against intestinal disease from *V. cholerae* (Winner III, et al., Infect. Immun. 59:977-982, 1991). Oral, killed whole cell vaccines with or without the B subunit of cholera toxin have undergone extensive testing in volunteer and field trials over the past decade, and have been found to be more immunogenic and confer longer protection than the parenteral killed whole-cell vaccine (Svennerholm et al., J. Infect. Dis. 149:884-893, 1984; Black et al., Infect. Immun. 55:1116-1120, 1987; Clemens et al., Lancet i:1375-1378, 1988; Clemens et al., J. Infect. Dis. 158:60-69, 1988; Jertborn et al., J. Infect. Dis. 157:374-377, 1988; Sack et al., 164:407-11, 1991).

Such killed whole-cell vaccines were traditionally favored over live whole-cell vaccines because the latter, which can multiply in the gut of the vaccinated animal, were considered unsafe. However, unlike killed-cell vaccines, live-cell vaccines would not require multiple doses, and in a rabbit model, live bacteria are more effective immunogens for secretory IgA than dead organisms (Keren et al., J. Immunol. 128:475-479, 1982). Live vaccines have the further advantage of potentially being transmitted from recipients to others in the community, leading to herd immunity.

The most important virulence factor for *V. cholerae* in causing clinical disease is cholera toxin, a protein complex consisting of one A subunit and 5 B subunits. Live, oral vaccine strains currently being tested bear mutations in either the A subunit or in both subunits of cholera toxin (Mekalanos et al., Nature 306:551-557, 1983; Herrington et al., J. Exp. Med. 168:1487-1492, 1988; Levine et al., Lancet ii:467-470, 1988). An internal deletion of the gene encoding the A subunit of cholera toxin (*ctxA*) in the classical strain 0395 produces a strain (0395-N1) which is highly immunogenic in humans, but produces non-specific symptoms in about half of the recipients (Mekalanos, *supra*; Herrington, *supra*; Mekalanos, U.S. Patent No. 4,882,278, herein incorporated by reference), an indication that the strain is still virulent.

Summary of the Invention

As described in detail below, it has now been found that a *V. cholerae* gene, such as the *irgA* locus of *V. cholerae*, can function as a site for the integration and high-level expression of sequences encoding heterologous antigens in vaccine strains of *V. cholerae*. IrgA, the major iron-regulated outer membrane protein of *V. cholerae*, is a virulence factor for this organism that is independent of cholera toxin (Goldberg et al., USSN 07/629,102, herein incorporated by reference; Goldberg et al., Infect. Immun. 58:55-60, 1990). *In vivo*-grown *V. cholerae* expresses iron-regulated proteins that are not seen following growth in normal *in vitro* conditions (Sciortino et al., 42:990-996, 1983), suggesting that the organisms sense low-iron conditions in the intestine. A mutation in *irgA* produces a 100-fold defect in the virulence of *V. cholerae* in a suckling mouse model. Regulation of *irgA* expression by iron is

exceptionally tight, with a 1000-fold induction ratio in low- compared with high-iron conditions (Goldberg et al., Infect. Immun. 58:55-60, 1990). The entire structural gene of *irgA* has been cloned from the classical *V. cholerae* strain 0395 (Goldberg et al., Mol. Microbiol. 6:2407-2418, 1992). Use of such an iron-regulated promoter to control expression of a heterologous antigen in a live vaccine strain has a number of distinct advantages. A high induction ratio ensures that the gene encoding the heterologous antigen (1) will be expressed in the low-iron environment of the vaccinee's gut at a level high enough to ensure that it induces an immune response, and yet (2) will be expressed minimally when the cells are cultured *in vitro*, where high-level expression would potentially provide selection pressure favoring inactivation of the gene and complicate large-scale culturing of the cells necessary for vaccine production. Where, as in the case of *irgA*, the protein encoded by the naturally-occurring gene is, for at least some *V. cholerae* strains, a virulence factor that is not essential for growth of the bacterium, insertion of the heterologous antigen coding sequence next to the promoter can be readily accomplished in such a way as to delete or otherwise inactivate the virulence factor coding sequence, thereby decreasing the virulence of the engineered strain without affecting its viability.

The invention thus includes a genetically engineered *V. cholerae* chromosome containing a DNA sequence encoding a heterologous antigen, the DNA sequence being functionally linked to a naturally-occurring *V. cholerae* promoter. The heterologous antigen, defined as a polypeptide which is not expressed by the wildtype host species, is preferably a nontoxic polypeptide which is part or all of a protein that is naturally expressed by an infectious organism, and which

induces an antigenic response in an animal (preferably a mammal such as a human, non-human primate, cow, horse, sheep, goat, pig, dog, cat, rabbit, rat, mouse, guinea pig, or hamster). The infectious organism from which the heterologous antigen is derived may be, for example, a bacterium, a virus, or a eukaryotic parasite, and the heterologous antigen may be, e.g., an OSP (Outer Surface Protein) of *Borelia burgdorferai*; animmunogenic, nontoxic subunit or fragment of a bacterial toxin such as Shiga toxin, diphtheria toxin, *Pseudomonas* exotoxin A, pertussis toxin, tetanus toxin, anthrax toxin, one of the *E. coli* heat-labile toxins (LTs), one of the *E. coli* heat-stable toxins (STs), or one of the *E. coli* Shiga-like toxins; an immunogenic portion of a viral capsid from a virus such as human immunodeficiency virus (HIV), any of the Herpes viruses (e.g., Herpes simplex virus or Epstein-Barr virus), influenza virus, poliomyelitis virus, measles virus, mumps virus, or rubella virus; or an immunogenic polypeptide derived from a eukaryotic parasite, such as the causative agent for malaria, pneumocystis pneumonia, or toxoplasmosis. (One preferred example of such a polypeptide is a malarial circumsporozoite protein.) By "functionally linked to a naturally-occurring *V. cholerae* promoter" is meant that expression of the sequence encoding the heterologous antigen is controlled by a promoter which is found in wild-type *V. cholerae*, such as the *ctxA* promoter, or an iron-regulated promoter such as that of *irgA*. Construction of such a functional linkage can be accomplished as described in detail below, or generally, using standard methods, by locating the desired promoter sequence sufficiently near to (and typically, though not necessarily, just upstream of) the promoterless heterologous antigen-encoding sequence to permit the desired promoter sequence to control expression of the

latter sequence. Functional siting of promoter sequences is well within the abilities of one of ordinary skill in the art of prokaryotic gene expression. Where the promoter naturally controls the expression of a *V. cholerae* virulence factor that is nonessential for growth of the cell, the sequence encoding that virulence factor will preferably be deleted or otherwise mutated to prevent expression of a biologically active form of that virulence factor. Preferably, the *ctxA* locus on the chromosome will also be deleted or otherwise inactivated, so that biologically active cholera toxin cannot be expressed from the chromosome. Such deletions, mutations and insertions can readily be carried out by one of ordinary skill using the methods described herein, or other well-known, standard techniques. In preferred embodiments, the *ctxA* deletion is identical to that of strain 0395-N1 (Mekalanos, U.S. Patent No. 4,882,278).

Also within the invention is a bacterial chromosome (preferably from a gram-negative, enteric bacterium such as *V. cholerae*), containing a DNA sequence encoding a heterologous antigen, which sequence is functionally linked to an iron-regulated promoter which functions in the host bacterium to permit significantly (i.e., at least ten-fold and preferably 100-fold) higher expression of the heterologous antigen in a low-iron environment, such as in an animal's intestine, than in a high-iron environment, such as under typical *in vitro* culture conditions. An example of such a promoter is the naturally-occurring promoter of *V cholerae irgA*, which includes at a minimum a sequence substantially identical to nucleotides 1000 through 1041 (SEQ ID NO: 2), inclusive, of the sequence shown in Fig. 5 (SEQ ID NO: 1). The promoter sequence used is preferably nucleotides 922 to 1041 (SEQ ID NO: 3), more preferably 922 to 1079 (SEQ ID NO: 4) or 1000 to 1079 (SEQ ID

NO: 5), still more preferably 905 to 1041 (SEQ ID NO: 6) or 905 to 1079 (SEQ ID NO: 7), and most preferably 905 to 1438 (SEQ ID NO: 8), 922 to 1438 (SEQ ID NO: 9), or 1000 to 1438 (SEQ ID NO: 10) (all inclusive). Examples of other iron-regulated promoters which would be useful in the invention are those derived from the fatA gene of *V. anguillarum* (Koster et al. J. Biol. Chem. 266:23829-23833, 1991); *E. coli slt-IA* (or other *E. coli* Fur-binding promoter sequences, as discussed by Calderwood et al., J. Bacteriol. 169:4759-4764, 1987; De Grandis et al., J. Bacteriol. 169:4313-4319, 1987; and DeLorenzo et al., J. Bacteriol. 169:2624-2630, 1987); the iron-regulated outer membrane proteins of *Salmonella typhi* (Fernandez et al., Infect. Immun. 57:1271-1275, 1989), the iron-regulated hemolysin promoter of *Serratia* (Poole et al., Infect. Immun. 56:2967-2971, 1988); the *Yersenia* iron-regulated promoters (Carniel et al., Molecular Microbiol. 6:379-388, 1992; Staggs et al., J. Bacteriol. 173:417-425, 1991; and Staggs et al., Molecular Microbiol. 6:2507-2516, 1992); the *V. vulnificus* iron-regulated promoters; the *Pseudomonas* exotoxin A iron-regulated promoter (Bjorn et al., Infect. Immun. 19:785-791, 1978); and *Plesiomonas* iron-regulated genes involved in heme-iron uptake (Daskaleros et al., Infect. Immun. 59:2706-2711, 1991). It is believed that most if not all enteric, gram-negative bacterial species, including *E. coli, Salmonella, Shigella, Yersenia, Citrobacter, Enterobacter, Klebsiella, Morganella, Proteus, Providencia, Serratia, Vibrios, Plesiomonas, and Aeromonas*, utilize highly similar fur-binding, iron-regulated promoter sequences, and it is likely that they also utilize secondary iron-regulated promoter sequences similar to that of *irgA*. Such promoter sequences are well-known to those of ordinary skill, or can be readily determined from current information regarding iron-

regulated promoters. Construction of such promoter sequences adjacent to a given heterologous antigen-encoding sequence, and insertion of the resulting construct into a *V. cholerae* genome, is readily accomplished by one of ordinary skill; the ability of such a promoter to function as predicted can then be tested in low- and high-iron conditions as described below, without undue experimentation.

Also within the invention is a *V. cholerae* cell, or a homogeneous population of such cells, which contains the genetically engineered chromosome described above. Such cells can be said to define a vaccine strain useful, when combined with a pharmaceutically acceptable diluent suitable for oral administration, as a live-cell vaccine. Administration of such a vaccine to an animal (e.g., a human or other mammal) will provoke immunity not only to *V. cholerae*, but also to an antigen derived from a second organism; it thus serves as a bivalent vaccine. An example of such a vaccine utilizes a genetically engineered *V. cholerae* strain in which the *ctxA* and *irgA* coding sequences are largely deleted and a sequence encoding Shiga-like toxin B subunit is functionally linked to the *irgA* promoter. This strain is described in detail below. Of course, the bacterial strain of the invention could be engineered to encode several heterologous antigens, each linked to an identical or different iron-regulated promoter, to produce a multivalent vaccine effective for simultaneously inducing immunity against a number of infectious diseases.

Other features and advantages will be apparent from the detailed description provided below, and from the claims.

Brief Description of the Drawings

Fig. 1 is a schematic diagram illustrating the construction of plasmids used in this study. A partial restriction map of 0395 chromosomal DNA is shown with relevant restriction enzyme sites, using base-pair numbering as in Goldberg et al., Mol. Microbiol. 6:2407-2418, 1992; and Goldberg et al., Proc. Natl. Acad. Sci. USA 88:1125-1129, 1991. The location of *irgA*, the location of fragments cloned in the construction of vaccine strains and the locations of fragments used as probes in Southern blot analysis are indicated. The upstream *irgA* fragment is indicated by a solid bar; the downstream *irgA* fragment by a hatched bar; and the *slt*-IB subunit fragment by a stippled bar. Plasmids and chromosomal fragments are not drawn to scale.

Figs. 2A-2B is a set of Southern blots illustrating hybridization of chromosomal DNA from wild-type and mutant *V. cholerae* strains, digested with *Hin*dIII, separated by agarose electrophoresis and probed as follows: (A) *Sma*I - *Hinc*II fragment (region deleted in vaccine strains); (B) *Hinc*II - *Hinc*II fragment (downstream probe); (C) *Hin*dIII - *Sma*I fragment (upstream probe); (D) *Eco*RV - *Hin*dIII fragment from pSBC52 (*slt*-IB subunit probe). Lanes: 1, 0395-N1; 2, SBC20; 3, BO14-1; 4, BO24-1; 5, VAC1; 6, VAC2; 7, 0395-N1. The genomic location of the fragments used as probes is indicated in Fig. 1. The numbers to the left of the blot indicate the sizes (in kbp) of DNA standards.

Fig. 3 is a photograph of an SDS-PAGE analysis of the outer membrane proteins expressed by certain *V. cholerae* strains when grown in high- or low-iron medium. Lanes: 1, 0395-N1 grown in high-iron medium; 2, 0395-N1 grown in low-iron medium; 3, SBC20 grown in low-iron medium; 4, VAC1 grown in low-iron medium; 5, VAC2 grown in low-iron medium; 6, 0395-N1 grown in low-iron medium.

The numbers to the left of the gel indicate the molecular masses (in kDa) of the protein standards.

Fig. 4 is a schematic diagram of the construction of the pSBC52 plasmid utilized in these experiments. pSBC32 (Calderwood et al., Infect. Immun. 58:2977-2982, 1990) was subjected to PCR using primer No. 1: 5'-CCGAATTCTCTAGAGATATCGTGTGGAATTGTGAGCGGATAA-3' (SEQ ID NO: 11), which introduces restriction sites for *Eco*RI, *Xba*I, and *Eco*RV, and primer No. 2: 5'-CCAAGCTTCTGCAGCCCGGGATTTAACATTTATGAATCTCCGCCT-3' (SEQ ID NO: 12), which introduces restriction sites for *Hin*dIII, *Pst*I, and *Sma*I. The PCR product was then digested with *Eco*RI and *Hin*dIII, and cloned into *Eco*RI/*Hin*dIII-digested pUC19, to produce pSBC52.

Fig. 5 shows the nucleotide sequence of a portion of the *irgA* cDNA (SEQ ID NO: 1), including the promoter sequence. A 19-bp interrupted dyad symmetric element homologous to the Fur box of *E. coli* is indicated by inverted horizontal arrows below the sequence. Vertical lines mark the margins of what is believed to be regions important for *irgA* promoter function.

Detailed Description

In the experiments described below, the non-toxic B subunit of Shiga toxin was used as a model heterologous antigen, because of the easily available assays for this protein (Donohue-Rolfe et al., J. Clin. Microbiol. 24:65-68, 1986), as well as the possible role that antibodies against the B subunit play in protecting against severe Shigellosis and hemolytic uremic syndrome. Shiga toxin is a heterodimeric protein consisting of one A subunit (MW 32 kDa) and five B subunits (MW 7.7 kDa) (Seidah et al., J. Biol. Chem. 261:13928-13931, 1986); the B subunit of Shiga toxin is identical in amino acid sequence to the B subunit of Shiga-like toxin I produced by

enterohemorrhagic strains of *E. coli* (Calderwood et al., Proc. Natl. Acad. Sci. USA 84:4364-4368, 1987). This identical protein product is referred to as StxB throughout this study. Immune response to Shiga toxin is primarily directed against the B subunit, and antibodies directed against this subunit, or against synthetic peptides from regions of the subunit, provide protective immunity against holotoxin (Donohue-Rolfe et al., J. Exp. Med. 160:1767-1781, 1984; Harari et al. Infect. Immun. 56:1618-1624, 1988; Harari et al., Mol. Immunol. 27:613-621, 1990; Boyd et al., Infect. Immun. 59:750-757, 1991).

Described below are the insertion of a promoterless gene for the Shiga-like toxin I B subunit (*slt*-IB) into an *irgA* deletion, and the introduction of this construct into the chromosome of the *V. cholerae* *ctxA* deletion strain 0395-N1, thus producing a live, attenuated vaccine strain of *V. cholerae* that contains StxB under the transcriptional control of the iron-regulated *irgA* promoter.

MATERIALS AND METHODS

Bacterial strains and plasmids.

The bacterial strains and plasmids used in this study are described in Table 1, with the exception of plasmids pMBG126, pSAB18, pSAB12, pSAB19, pSAB14, and pSAB24, which are described in detail below and are depicted in Fig. 1; and plasmid pSBC52, which is described in the description of Fig. 4 provided above. Standard plasmid cloning vectors pUC18, pUC19, and pBR322 are commercially available (e.g., Pharmacia).

Media.

All strains were maintained at -70°C in Luria broth (LB) media (Sambrook et al., A Laboratory Manual, 2nd ed. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), containing 15% glycerol. LB media,

with or without the addition of the iron chelator 2,2-dipyridyl (final concentration, 0.2 mM), was used for growth in low- and high-iron conditions, respectively. Ampicillin (100 μg/ml), kanamycin (45 μg/ml), and streptomycin (100 μg/ml) were added as appropriate.

Genetic methods.

Isolation of plasmid and bacterial chromosomal DNA, restriction enzyme digests, agarose gel electrophoresis, and Southern hybridization of DNA separated by electrophoresis were performed according to standard molecular biologic techniques (Sambrook, *supra*). GeneScreen Plus hybridization transfer membranes (DuPont Biotechnology Systems, NEN Research Products, Boston, MA) were used according to the manufacturer's protocols for Southern hybridization. DNA sequencing was performed using the Sequenase DNA Sequencing Kit (United States Biochemical Corporation, Cleveland, OH).

Plasmids were transformed into *E. coli* strains by standard techniques, or were electroplated into *V. cholerae* using a Gene Pulser (Bio-Rad Laboratories, Richmond, CA), following the manufacturer's protocol, and modified for electroporation into *V. cholerae* as previously described (Goldberg et al., Proc. Natl. Acad. Sci. USA 88:1125-1129, 1991). Electroporation conditions were 2,500 V at 25-μF capacitance, producing time constants of 4.7-4.9 ms.

DNA restriction endonucleases, T_4 DNA ligase, calf intestinal alkaline phosphatase, and the Klenow fragment of DNA polymerase I were used according to the manufacturers' specifications. Restriction enzyme-digested chromosomal and plasmid DNA fragments were separated on 1% agarose gels; required fragments were cut from the gel under ultraviolet illumination and purified by electroelution (Sambrook et al, 1989, *supra*). DNA fragments used as probes were radiolabeled with α-^{32}P-dCTP

using a random priming labeling kit (Prime Time "C" Oligonucleotide Labeling Biosystem, International Biotechnologies, Inc., New Haven, CT).

Construction of plasmids.

DNA was recovered upstream and at the 5′ terminus of *irgA* as a *Hin*dIII-*Sma*I fragment from pMBG59, which contains the *irgA* promoter (*irgP*) (Goldberg et al., J. Bacteriol. 172:6863-6870, 1990) (Fig. 1). This fragment was cloned into the *Hin*dIII and *Sph*I sites of pUC18 to yield plasmid pMBG126; the *Sph*I site of pUC18 had first been made blunt-ended by treatment with mung bean nuclease. DNA sequence analysis of pMBG126 revealed that the *Sph*I site was unexpectedly preserved at the junction with *Sma*I; the sequence was otherwise as predicted. DNA was then recovered at the 3′ terminus and downstream of *irgA* as a 1.5 kilobase-pair (kbp) *Hinc*II fragment from plasmid pSAB25. *Sac*I linkers were added to this fragment and it was ligated into the unique *Sac*I site of pMBG126, in the same orientation as the upstream *irgA* fragment, to yield plasmid pSAB18. The internal *Sal*I site in the pUC polylinker of pSAB18 was removed by digesting with *Sal*I, treating with the Klenow fragment of DNA polymerase I, and religating the blunt ends, to create pSAB12. A DNA segment encoding the promoterless B subunit of Shiga-like toxin I (*slt*-IB) was recovered as an *Eco*RV-*Sma*I fragment from plasmid pSBC52. This fragment was introduced into the unique *Eco*RV and *Sma*I sites of pSAB18, such that *slt*-IB was under the transcriptional control of *irgP* on the upstream *irgA* fragment, yielding plasmid pSAB19. The construction of plasmids pMBG126, pSAB18, pSAB12, and pSAB19 was verified by restriction enzyme digestion and double-stranded DNA sequencing.

The desired fragments were then introduced into the suicide vector pCVD442 as follows. pSAB12 and pSAB19 were digested with *Hin*dIII and *Eco*RI and the DNA fragment

containing either the *irgA* deletion (from pSAB12) or the *irgA* deletion-*slt*-IB-substitution (from pSAB19) were made blunt-ended by the Klenow fragment of DNA polymerase I. Following ligation to *Sal*I linkers, the fragments were ligated into the unique *Sal*I site of pCVD442, yielding plasmids pSAB14 and pSAB24 respectively, and propagated in the permissive strain SM10 λ *pir*. Plasmid pCVD442 is a recently described suicide vector containing the *pir*-dependent R6K replicon, ampicillin resistance, and the *sacB* gene from *Bacillus subtilis* (Donnenberg et al., Infect. Immun. 59:4310-4317, 1991).

Construction of VAC1 and VAC2

V. cholerae strain SBC20 is an *irgA*::Tn*phoA* derivative of 0395-N1 (Pearson et al., Res. Microbiol. 141:893-899, 1990). The kanamycin resistance marker in Tn*phoA* allowed screening of mutants for deletion of *irgA* (and hence Tn*phoA*) by assessing susceptibility to kanamycin. The *irgA* allele of SBC20 was replaced with either the previously constructed *irgA* deletion, or the *irgA* deletion containing *slt*-IB, as follows. Plasmids pSAB14 and pSAB24 were electroporated into SBC20, with selection for ampicillin and streptomycin resistance. Doubly-resistant colonies contained the respective plasmids integrated into the chromosome by homologous recombination involving either the upstream or downstream fragments of *irgA* on pSAB14 or pSAB24, with creation of a merodiploid state. One such colony from the integration of pSAB14 into the chromosome of SBC20 was selected and named BO14-1; one from the integration of pSAB24 into the chromosome of SBC20 was named BO24-1. BO14-1 and BO24-1 were grown overnight in LB media without ampicillin selection, then plated on LB media with 10% sucrose but without NaCl, and grown at 30°C for 30 hours, thereby selecting for clones that had deleted the integrated *sacB* gene (Blomfield et al., Mol. Microbiol. 5: 1447-1457,

1991). Sucrose-resistant colonies that are ampicillin susceptible but kanamycin resistant have re-excised the plasmid (yielding the parent SBC20, which contains the kanamycin resistance marker in Tn*phoA*); those that are both ampicillin and kanamycin susceptible have resolved the merodiploid state to replace the *irgA* locus in SBC20 with either the *irgA* deletion from pSAB14 or the *irgA* deletion-*slt*-IB fragment from pSAB24. Approximately 10% of sucrose-resistant colonies that were ampicillin-susceptible were also kanamycin-susceptible. One of these colonies which had replaced the *irgA*::Tn*phoA* locus with the *irgA* deletion was further purified and named VAC1; one which had replaced the *irgA*::Tn*phoA* locus with *irgA*::*irgP-slt*-IB was named VAC2. Confirmation of the proper constructions in VAC1 and VAC2 was obtained by Southern hybridization of restriction enzyme-digested chromosomal DNA that was probed with several different DNA fragments to verify the expected deletion in *irgA*, as well as the introduction of the *slt*-IB within the deleted *irgA* segment.

Preparation of outer-membrane proteins, whole cell proteins, and periplasmic extracts.

Enriched outer membrane proteins were prepared from strains following growth in low- and high-iron media as previously described (Goldberg, Infect. Immun. 58:55-60, 1990). Proteins were separated by electrophoresis on a sodium dodecyl sulfate/10% polyacrylamide (SDS-PAGE) gel and visualized by staining with Coomassie brilliant blue. Whole cell proteins and periplasmic extracts were prepared from exponentially growing cells as previously described (Hovde et al., Proc. Natl. Acad. Sci. USA 85:2568-2572, 1988).

Immunodetection of StxB production.

Whole cell proteins and periplasmic extracts were separated on a SDS-15% PAGE gel as described above, then

transferred to a NitroBind Transfer Membrane (Micron Separations Inc., Westboro, MA) with a semidry blotting apparatus (Hoefer Scientific Instruments, San Francisco, CA). Immunoreactive proteins were visualized after sequential incubation with polyclonal rabbit anti-Shiga toxin antiserum and goat anti-rabbit IgG-conjugated alkaline phosphatase (Sigma Chemical Co., St. Louis, MO), followed by staining for phosphatase activity as described previously (Hovde, *supra*). The amount of StxB present in periplasmic extracts or culture supernatants was quantitated with an enzyme-linked immunosorbent assay (ELISA) developed for the detection of Shiga toxin and modified for detection of purified StxB (Donohue-Rolfe et al., J. Clin. Microbiol. 24:65-68, 1986; Calderwood et al., Infect. Immun. 58:2977-2982, 1990).

HeLa cell cytotoxicity.

The cytotoxicity of periplasmic extracts or culture supernatants for HeLa cells was assayed in a quantitative cytotoxicity assay by determining the extent of HeLa cell detachment from microtiter plates (Gentry et al., J. Clin. Microbiol. 12:361-366, 1980). HeLa cells were grown at 37°C in a 5% CO_2 atmosphere in McCoy 5a (modified) medium containing 10% fetal calf serum and 100 μg of penicillin and streptomycin per ml. Freshly trypsinized cells were suspended in 0.1 ml of growth medium and allowed to attach to the wells of microtiter plates overnight. Serial dilutions of samples were added and the plates were again incubated overnight. The cells were fixed and then stained with crystal violet in a 5% ethanol - 2% formaldehyde solution. Stained cell monolayers were dissolved in ethanol and the A_{595} read with a microtiter plate colorimeter.

Evaluation of virulence of vaccine strains.

50% lethal dose (LD_{50}) assays were performed by oral inoculation of 3- to 4-day old CD1 suckling mice

with either the parent *V. cholerae* strain 0395, an *irgA* mutant strain MBG40 (Goldberg et al., Infect. Immun. 58:55-60, 1990), the *ctxA* mutant strain 0395-N1, or VAC2. Cholera strains were grown overnight in LB medium at 30°C, pelleted, and resuspended in 0.5M $NaHCO_3$ (pH 8.5). Mice were orally inoculated with serial dilutions of organisms, then kept at 30°C. Four or more mice were used per dose of bacteria. Survivial was determined at 40 h (Taylor et al., Proc. Natl. Acad. Sci. USA 84:2833-2837, 1987).

RESULTS

Confirmation of vaccine strain construction.

(i) Southern hybridization analysis. To confirm the construction of the vaccine strains, chromosomal DNA was purified from *V. cholerae* parent strains 0395-N1 and SBC20, the merodiploid strains BO14-1 and BO24-1, and the vaccine strains VAC1 and VAC2. The chromosomal DNAs were digested with *Hin*dIII, separated on agarose gels, and transferred to membranes for Southern hybridizations. The Southern hybridizations of these digests, probed with four different fragment probes, are shown in Fig. 2. The location of the fragment probes within the *irgA* gene is shown in Fig. 1. The presence and size of the recognized fragments is consistent with the constructions depicted in Fig. 1, confirming the deletion of *irgA* in VAC1 and the deletion-replacement of the *irgA* locus with *irgA*::*irgP-slt*IB in VAC2.

ii. Outer membrane protein analysis. Outer membrane proteins were prepared from strain 0395-N1 grown in low- and high-iron media and from strains SBC20, VAC1 and VAC2 following growth in low-iron media, then separated by electrophoresis on a SDS-PAGE gel (Fig. 3). IrgA, the 77 kilodalton (kDa) major iron-regulated outer membrane protein (Goldberg et al., Infect. Immun. 58:55-60, 1990), is present in 0395-N1 grown in low iron but is

absent in SBC20 (an *irgA* mutant) and the vaccine strains, confirming the deletion of *irgA* in VAC1 and VAC2.

Iron-regulated expression of the Shiga toxin B subunit in VAC2.

(i) Western blot analysis of StxB production in VAC2. Western blot analysis of whole cell proteins and periplasmic extracts of VAC2 grown in high- and low-iron media demonstrated the production of a 7.7 kDa protein recognized by polyclonal rabbit anti-Shiga toxin antiserum in both whole cell proteins and periplasmic extracts prepared from VAC2 grown in low-iron media; no such protein was recognized in proteins prepared from the vaccine strain grown in high-iron media, demonstrating that the production of StxB is tightly iron-regulated (data not shown).

(ii) Quantitation of StxB production from irgP-slt-IB in plasmid pSAB19 and VAC2. To verify iron-regulated production of StxB by *irgP-slt*-IB in plasmid pSAB19, and compare it with StxB production by VAC2, we first had to return pSAB19 to the *V. cholerae* background because *irgP* is not active in *E. coli* (Goldberg et al., Proc. Natl. Acad. Sci. USA 88:1125-1129, 1991). The production of StxB by strains 0395-N1(pSAB19) and VAC2 was quantitated using a sandwich ELISA, with a monoclonal antibody specific for StxB as the capture molecule. Purified StxB, in measured amounts, was used as the standard. As shown in Table 2, both 0395-N1(pSAB19) and VAC2 express StxB in a tightly iron-regulated fashion, as expected, and produce five times the amount of B subunit made by the reference strain, *Shigella dysenteriae* 60R, under low-iron conditions.

Virulence of vaccine strains.

(i) Cytotoxicity to HeLa cells. The cytotoxicity of periplasmic extracts or culture supernatants of strains 0395-N1(pSAB19) and VAC2, grown in low-iron

media, was assayed as described (Gentry et al., J. Clin. Microbiol. 12:361-366, 1980), and compared to the *S. dysenteriae* strain 60R. Neither 0395-N1(pSAB19) or VAC2 had detectable cytotoxicity in periplasmic extracts or supernatants, in contrast to periplasmic extracts of *S. dysenteriae* 60R, which were cytotoxic to at least a 10^5-fold dilution (data not shown).

(ii) LD_{50} assays. The results of LD_{50} assays for the wild-type *V. cholerae* strain 0395, *ctxA* mutant strain 0395-N1, *irgA* mutant strain MBG40, and vaccine strain VAC2 in the suckling mouse model are shown in Table 3. *V. cholerae* strain MBG40, an *irgA*::Tn*phoA* mutant of strain 0395, had an LD_{50} in suckling mice that was 2 orders of magnitude higher than that for the parental strain 0395, as previously demonstrated (Goldberg et al., Infect. Immun. 58:55-60, 1990). Strain 0395-N1, deleted for the A subunit of cholera toxin, was avirulent at an inoculum of 2 x 10^9 organisms in this model. The vaccine strain VAC2, despite expressing StxB at high level, remains avirulent in this model at an inoculum of 2 x 10^9 organisms, similar to its parent strain 0395-N1.

USE

The *V. cholerae* strains of the invention are useful as bivalent vaccines capable of inducing immunity to *V. cholerae* and to an antigen derived from a second infectious organism. Because the strains are attenuated (i.e., do not induce a significant toxic reaction in the vaccinee), they can be used as live-cell vaccines, permitting effective immunity to result from administration of a single dose of the vaccine. An effective oral dose of the vaccine would contain approximately 10^6 to 10^8 bacteria in a volume of approximately 150 ml liquid. The diluent used would typically be water or an aqueous solution, such as

2 grams of sodium bicarbonate dissolved in 150 ml distilled water, which may be ingested by the vaccinee at one sitting, either all at once or over any convenient period of time.

Other Embodiments

Other embodiments are within the claims set forth below. For example, the host bacterium (the bacterium the chromosome of which is engineered to encode a heterologous antigen) can be *E. coli* or any other enteric bacterium, including *Salmonella, Shigella, Yersenia, Citrobacter, Enterobacter, Klebsiella, Morganella, Proteus, Providencia, Serratia, Plesiomonas, and Aeromonas*, all of which are known or believed to have iron-regulated promoters similar to the Fur-binding promoters of *E. coli*, and which may have other iron-regulated promoters analogous to that of *irgA*. Also potentially useful would be a bacille Calmette-Guerin (BCG) vaccine strain engineered to encode a heterologous antigen linked to an iron-regulated promoter. The promoter used can be native to the species of the host bacterium, or can be a heterologous promoter (i.e., from a species other than that of the host bacterium) engineered into the host bacterium along with the heterologous antigen coding sequence, using standard genetic engineering techniques. Multiple heterologous antigen coding sequences linked to the same or different iron-regulated promoter sequences can be inserted into a given chromosome, using techniques analogous to those set forth above, to produce a multivalent vaccine strain.

Those who practice in the field of prokaryotic gene expression will realize that, while naturally-occurring promoter sequences are preferred, synthetic sequences such as a consensus Fur-binding sequence or a hybrid of two or more Fur-binding sequences would also be

expected to be useful in the chromosomes of the invention. Alteration, addition or deletion of one or a few nucleotides within a naturally-occurring promoter sequence such as the *irgA* promoter would generally not affect its usefulness. The invention therefore encompasses iron regulated promoters having such inconsequential changes.

Table 1. Bacterial strains and plasmids used in this study

Strain or plasmid	Relevant genotype or phenotype	Ref. or source
V. cholerae strains		
0395	Sm^r	1
0395-N1	0395 *ctxA*, Sm^r	1
SBC20	0395-N1 *irgA*::Tn*phoA*, Sm^r, Km^r	2
MBG40	0395 *irgA*::Tn*phoA*, Sm^r, Km^r	3
BO14-1	SBC20 with pSAB14 integrated into *irgA*, Sm^r, Km^r, Ap^r	4
BO24-1	SBC20 with pSAB24 integrated into *irgA*, Sm^r, Km^r, Ap^r	4
VAC1	0395-N1 Δ*irgA*, Sm^r	4
VAC2	0395-N1 Δ*irgA*::*irgP-slt*-IB, Sm^r	4
***E. coli* strains**		
SM10 λ pir	*thi thr leu tonA lacY supE recA*::RP4-2-Tc::Mu *λ pir*R6K, Km^r	5
Plasmids		
pMBG59	pBR322 with 4.7-kbp of *V. cholerae* MBG40 chromosome, containing DNA upstream and at the 5' terminus of *irgA*, as well as the *irgA*::Tn*phoA* fusion joint from this strain.	6
pSAB25	3.0 kbp *Sma*I - *Mlu*I fragment of *V. cholerae* 0395 chromosome, containing DNA at the 3'terminus and downstream of *irgA*, made blunt-ended at the *Mlu*I site and ligated into *Sma*I-digested pUC19.	4
pSBC52	pUC19 with a promoterless gene for the B subunit of SLT-I (identical to StxB) cloned between the *Eco*RI and *Hin*dIII sites.	4
pCVD442	Suicide vector composed of the *mob*, *ori*, and *bla* regions from pGP704 and the *sacB* gene of *Bacillus subtilis*.	7

Ap^r, ampicillin resistance; Km^r, kanamycin resistance; Sm^r, streptomycin resistance.

Ref. or source:

1. Mekalanos et al., Nature 306:551-557, 1983.
2. Pearson et al., Res. Microbiol. 141:893-899, 1990.
3. Goldberg et al., Infect. Immun. 58:55-60, 1990.
4. This study.
5. Miller et al., J. Bacteriol. 170:2575-2583, 1988.
6. Goldberg et al., J. acteriol. 172:6863-6870, 1990.
7. Donnenberg and Kaper, Infect. Immun. 59:4310-4317, 1991.

Table 2. Production of Shiga toxin B subunit by various strains following growth in high- and-low iron conditions

Strain	Periplasmic extract[a]		Supernatant[a]	
	High-iron	Low-iron	High-iron	Low-iron
0395-N1	--[b]	--	--	--
0395-N1 (pSAB19)	15.5	3,620	0.16	3.5
VAC2	0.87	4,130	--	0.73
S.dysenteriae 60R	238	674	0.8	16.4

[a] ng/50 OD_{600} of original culture

[b] < 0.1 ng

Table 3. Virulence assays of wild-type and mutant strains of *Vibrio cholerae* in suckling mice

Strain	LD_{50} (no. of bacteria)
0395	1×10^5
MBG40	1×10^7
0395-N1	$> 2 \times 10^9$
VAC2	$> 2 \times 10^9$

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Calderwood, Stephen B.
Butterton, Joan R.
Mekalanos, John J.

(ii) TITLE OF INVENTION: HETEROLOGOUS ANTIGENS IN LIVE CELL VACCINE STRAINS

(iii) NUMBER OF SEQUENCES: 12

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
(B) COMPUTER: IBM PS/2 Model 50Z or 55SX
(C) OPERATING SYSTEM: MS-DOS (Version 5.0)
(D) SOFTWARE: WordPerfect (Version 5.1)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/020,501
(B) FILING DATE: February 22, 1993
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Clark, Paul T.
(B) REGISTRATION NUMBER: 30,162
(C) REFERENCE/DOCKET NUMBER: 00786/136001

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(C) TELEX: 200154

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1535
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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ATCGATGATA AAAAATCCCG CTGCGGCGGG ATTTTTTATT GCCACTCATC GGGCCTTGCT      60

TGGCGGAGCG CATCAATAAA TAGGCGCAGC CGAAGTGGGT GACGACCGAG CGGATAGAAG     120

CAGTTGATTT CTGTTGGCTG TGATTGCCAT CCGTTGACGC AAGGAATGAG GCTGCCCGGA     180

TGCGCCGTTT CAAAACCATT GGCAAACCAA GTGGGAAGCA AACCAATACC ACGACCTTTA     240

GCAATCGCAT CGGCTTGCAT GGCAAGATTA TCGCTTTGTA AACGACTCTC TAGTGCTGGC     300

AGTGAATAAC TGCCGAACTC TGGATGGTGC AGTTCAAGCT CCGCGCGCCG ACAAGCAATA     360

AAATCAATCC ATGGGTGATG AATCAGCTCA CGAGGATGGG TCGGTTTATC TCGATGGGCC     420

AAATATTTGG GAGAGGCGTA AGTGGCATAG CGCCAATAGC CTAAGCGTTC TTTGCGATAA     480

CCCATGGGGG CGGCGTGTTC AATCCAAATG ATCAAATCGG GCTCAAACAC CTCATCACTG     540

TGTTGAAACT GGCTGAGTAG ACGGATCTTC AATGTCGAAT GCTGCTGCAT AAACTCATCC     600

AATACTTGGC TGAGCCAGCC GCGGATCAAA TTGGGGTGTA CCACCAGCGT GAGTTCGCCA     660

GTCACTTGAT TGTTCAATTC TTGCAACGCT TCCTGACTTT TATTGGCCAG TTCAAGTAGT     720

TGCTCCGAGT AAACCGCAAA CACTTCTCCT GCTTTGGTGA GCGTTAAGCG GTTGCCTTGA     780

CGCATCAACA AGCTTTGTCC CAAGTCCTCT TCAAGTTGCG CCAAACGGCG ACTCAGGGTG     840

GATTTAGGCT GTTCAAGCGC TTTGGCAGCG GCAGTCAGGC TCTTATGTTG GCAAAGCGCA     900

TGGAAAGCTT TTACGGCGCT GAGATCTTGC ATAGGTATTT GACCCTTAAA GAATAATTAC     960

CACAGACGTT CCATATTTGG ACCGAACTAT TCCATGTGTC GATCTATCTC CAGTACAGAA    1020

TATATGAATA ATCCGCTTCT GAAATTAAGA ATAATTATCA TTTAAAGGAG TGGTAA       1076

ATG TCC AGA TTC AAT CCA TCC CCC GTC AGT TTA TCT GTG ACA CTA GGC      1124
Met Ser Arg Phe Asn Pro Ser Pro Val Ser Leu Ser Val Thr Leu Gly
1               5                  10                  15

TTA ATG TTT TCG GCT AGC GCT TTT GCT CAA GAC GCG ACG AAA ACG GAT      1172
Leu Met Phe Ser Ala Ser Ala Phe Ala Gln Asp Ala Thr Lys Thr Asp
            20                  25                  30

GAA ACC ATG GTG GTC ACT GCG GCG GGA TAC GCG CAA GTG ATT CAA AAT      1220
Glu Thr Met Val Val Thr Ala Ala Gly Tyr Ala Gln Val Ile Gln Asn
        35                  40                  45

GCA CCA GCC AGT ATC AGT GTG ATT TCA AGA GAA GAT CTG GAA TCT CGC      1268
Ala Pro Ala Ser Ile Ser Val Ile Ser Arg Glu Asp Leu Glu Ser Arg
    50                  55                  60

TAT TAC CGT GAT GTG ACC GAT GCG CTA AAA AGC GTA CCG GGT GTG ACA      1316
Tyr Tyr Arg Asp Val Thr Asp Ala Leu Lys Ser Val Pro Gly Val Thr
65                  70                  75                  80

GTC ACC GGA GGG GGC GAT ACT ACC GAT ATC AGC ATT CGT GGT ATG GGA      1364
Val Thr Gly Gly Gly Asp Thr Thr Asp Ile Ser Ile Arg Gly Met Gly
                85                  90                  95

TCA AAC TAT ACT CTT ATC TTG GTG GAT GGT AAG CGC CAA ACC TCA CGC      1412
Ser Asn Tyr Thr Leu Ile Leu Val Asp Gly Lys Arg Gln Thr Ser Arg
            100                 105                 110
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CAG ACC CGT CCA AAC AGC GAT GGC CCG GGC ATT GAG CAA GGT TGG TTA          1460
Gln Thr Arg Pro Asn Ser Asp Gly Pro Gly Ile Glu Gln Gly Trp Leu
        115                 120                 125

CCG CCA CTG CAA GCG ATT GAA CGT ATC GAG GTG ATC CGT GGC CCG ATG          1508
Pro Pro Leu Gln Ala Ile Glu Arg Ile Glu Val Ile Arg Gly Pro Met
    130                 135                 140

TCT ACG CTG TAC GGC TCG GAT GCT GAC                                      1535
Ser Thr Leu Tyr Gly Ser Asp Ala Asp
145                 150
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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	51
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	both
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TCCATGTGTC GATCTATCTC CAGTACAGAA TATATGAATA ATCCGCTTCT G 51

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	120
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	both
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AGATCTTGCA TAGGTATTTG ACCCTTAAAG AATAATTACC ACAGACGTTC CATATTTGGA 60

CCGAACTATT CCATGTGTCG ATCTATCTCC AGTACAGAAT ATATGAATAA TCCGCTTCTG 120

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	158
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	both
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AGATCTTGCA TAGGTATTTG ACCCTTAAAG AATAATTACC ACAGACGTTC CATATTTGGA 60

CCGAACTATT CCATGTGTCG ATCTATCTCC AGTACAGAAT ATATGAATAA TCCGCTTCTG 120

AAATTAAGAA TAATTATCAT TTAAAGGAGT GGTAAATG 158

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	80
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	both
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CGATCTATCT CCAGTACAGA ATATATGAAT AATCCGCTTC TGAAATTAAG AATAATTATC 60

ATTTAAAGGA GTGGTAAATG 80

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	137
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	both
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AAGCTTTTAC GGCGCTGAGA TCTTGCATAG GTATTTGACC CTTAAAGAAT AATTACCACA 60

GACGTTCCAT ATTTGGACCG AACTATTCCA TGTGTCGATC TATCTCCAGT ACAGAATATA 120

TGAATAATCC GCTTCTG 137

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	175
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	both
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AAGCTTTTAC GGCGCTGAGA TCTTGCATAG GTATTTGACC CTTAAAGAAT AATTACCACA 60

GACGTTCCAT ATTTGGACCG AACTATTCCA TGTGTCGATC TATCTCCAGT ACAGAATATA 120

TGAATAATCC GCTTCTGAAA TTAAGAATAA TTATCATTTA AAGGAGTGGT AAATG 175

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	534
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	both
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

AAGCTTTTAC GGCGCTGAGA TCTTGCATAG GTATTTGACC CTTAAAGAAT AATTACCACA 60

GACGTTCCAT ATTTGGACCG AACTATTCCA TGTGTCGATC TATCTCCAGT ACAGAATATA 120

TGAATAATCC GCTTCTGAAA TTAAGAATAA TTATCATTTA AAGGAGTGGT AAATGTCCAG 180

ATTCAATCCA TCCCCCGTCA GTTTATCTGT GACACTAGGC TTAATGTTTT CGGCTAGCGC 240

TTTTGCTCAA GACGCGACGA AAACGGATGA AACCATGGTG GTCACTGCGG CGGGATACGC 300

GCAAGTGATT CAAAATGCAC CAGCCAGTAT CAGTGTGATT TCAAGAGAAG ATCTGGAATC 360

TCGCTATTAC CGTGATGTGA CCGATGCGCT AAAAAGCGTA CCGGGTGTGA CAGTCACCGG 420

AGGGGGCGAT ACTACCGATA TCAGCATTCG TGGTATGGGA TCAAACTATA CTCTTATCTT 480

GGTGGATGGT AAGCGCCAAA CCTCACGCCA GACCCGTCCA AACAGCGATG GCCC 534

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	517
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	both
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

AGATCTTGCA TAGGTATTTG ACCCTTAAAG AATAATTACC ACAGACGTTC CATATTTGGA 60

CCGAACTATT CCATGTGTCG ATCTATCTCC AGTACAGAAT ATATGAATAA TCCGCTTCTG 120

AAATTAAGAA TAATTATCAT TTAAAGGAGT GGTAAATGTC CAGATTCAAT CCATCCCCCG 180

TCAGTTTATC TGTGACACTA GGCTTAATGT TTTCGGCTAG CGCTTTTGCT CAAGACGCGA 240

CGAAAACGGA TGAAACCATG GTGGTCACTG CGGCGGGATA CGCGCAAGTG ATTCAAAATG 300

CACCAGCCAG TATCAGTGTG ATTTCAAGAG AAGATCTGGA ATCTCGCTAT TACCGTGATG 360

TGACCGATGC GCTAAAAAGC GTACCGGGTG TGACAGTCAC CGGAGGGGGC GATACTACCG 420

ATATCAGCAT TCGTGGTATG GGATCAAACT ATACTCTTAT CTTGGTGGAT GGTAAGCGCC 480

AAACCTCACC CCAGACCCGT CCAAACAGCG ATGGCCC 517

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	439
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	both
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CGATCTATCT CCAGTACAGA ATATATGAAT AATCCGCTTC TGAAATTAAG AATAATTATC 60

ATTTAAAGGA GTGGTAAATG TCCAGATTCA ATCCATCCCC CGTCAGTTTA TCTGTGACAC 120

TAGGCTTAAT GTTTTCGGCT AGCGCTTTTG CTCAAGACGC GACGAAAACG GATGAAACCA 180

TGGTGGTCAC TGCGGCGGGA TACGCGCAAG TGATTCAAAA TGCACCAGCC AGTATCAGTG 240

TGATTTCAAG AGAAGATCTG GAATCTCGCT ATTACCGTGA TGTGACCGAT GCGCTAAAAA 300

GCGTACCGGG TGTGACAGTC ACCGGAGGGG GCGATACTAC CGATATCAGC ATTCGTGGTA 360

TGGGATCAAA CTATACTCTT ATCTTGGTGG ATGGTAAGCG CCAAACCTCA CGCCAGACCC 420

GTCCAAACAG CGATGGCCC 439

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	42
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CCGAATTCTC TAGAGATATC GTGTGGAATT GTGAGCGGAT AA 42

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	45
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCAAGCTTCT GCAGCCCGGG ATTTAACATT TATGAATCTC CGCCT 45

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A bacterial chromosome containing a DNA sequence encoding a non-toxic and immunogenic heterologous antigen, said DNA sequence being functionally linked to an iron-regulated promoter.

2. The chromosome of claim 1, wherein said chromosome is a *Vibrio cholerae* chromosome.

3. The chromosome of claim 1, wherein said chromosome is a chromosome of an *E. coli* bacterium, a *Shigella* bacterium, a *Salmonella* bacterium, a *Yersinia* bacterium, a *Citrobacter* bacterium, an *Enterobacter* bacterium, a *Klebsiella* bacterium, a *Proteus* bacterium, a *Providencia* bacterium, a *Serratia* bacterium, a *Vibrio* bacterium, a *Plesiomonas* bacterium, an *Aeromonas* bacterium, or a bacille Calmette-Guerin (BCG).

4. The chromosome of claim 1, wherein said promoter is the promoter of a naturally-occurring *V. cholerae* gene.

5. The chromosome of claim 4, wherein said promote is the *V. cholerae* irgA promoter, and said chromosome lacks part or all of the irgA coding sequence.

6. The chromosome of claim 5, wherein said promoter comprises a nucleotide sequence substantially identical to SEQ ID NO: 2.

7. The chromosome of claim 1, wherein said heterologous antigen is a non-toxic polypeptide which induces an antigenic response in an animal.

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8. The chromosome of claim 7, wherein said polypeptide is a portion or all of a protein naturally expressed by an infectious organism.

9. The chromosome of claim 8, wherein said infectious organism is a bacterium.

10. The chromosome of claim 9, wherein said polypeptide is an immunogenic, nontoxic subunit or fragment of a bacterial toxin.

11. The chromosome of claim 10, wherein said toxin is Shiga toxin, diphtheria toxin, *Pseudomonas* exotoxin A, cholera toxin, pertussis toxin, tetanus toxin, anthrax toxin, *E. coli* heat-labile toxin (LT), *E. coli* heat-stable toxin (ST), or *E. coli* Shiga-like toxin.

12. The chromosome of claim 9, wherein said protein is an OSP (Outer Surface Protein) of *Borrelia burgdorferi*.

13. The chromosome of claim 8, wherein said infectious organism is a virus and said polypeptide is an immunogenic portion of a viral capsid.

14. The chromosome of claim 13, wherein said virus is a human immunodeficiency virus (HIV), one of the Herpes viruses, an influenza virus, a poliomyelitis virus, a measles virus, a mumps virus, or a rubella virus.

15. The chromosome of claim 8, wherein said infectious organism is a eukaryotic parasite.

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16. The chromosome of claim 15, wherein said parasite is the causative agent for malaria, pneumocystis pneumonia, or toxoplasmosis.

17. The chromosome of claim 16, wherein said protein does not encode biologically active cholera toxin A subunit.

18. The chromosome of claim 2, wherein said chromosome does not encode biologically active cholera toxin A subunit.

19. The chromosome of claim 5, wherein said chromosome does not encode biologically active cholera toxin A subunit.

20. A *V. cholerae* chromosome containing a DNA sequence encoding a non-toxic and immunogenic heterologous antigen, said DNA sequence being functionally linked to a naturally-occurring *V. cholerae* promoter.

21. The chromosome of claim 20, wherein said promoter is the promoter of a naturally-occurring gene encoding a *V. cholerae* virulence factor that is non-essential for growth of said cell, the coding sequence encoding said virulence factor being mutated or deleted so that said chromosome cannot express a biologically active form of said virulence factor.

22. The chromosome of claim 20, wherein said promoter is the *irgA* promoter.

23. The chromosome of claim 20, wherein said heterologous antigen is part or all of a non-toxic polypeptide which is naturally expressed by an infectious

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organism, which antigen induces an antigenic response in an animal.

24. The chromosome of claim 23, wherein said infectious organism is a bacterium.

25. The chromosome of claim 24, wherein said antigen is an immunogenic, nontoxic subunit or fragment of a bacterial toxin.

26. The chromosome of claim 25, wherein said toxin is Shiga toxin, diphtheria toxin, *Pseudomonas* exotoxin A, cholera toxin, pertussis toxin, tetanus toxin, anthrax toxin, *E. coli* LT, *E. coli* ST, or *E. coli* Shiga-like toxin.

27. The chromosome of claim 23, wherein said infectious organism is a virus and said antigen is an immunogenic portion of a viral capsid.

28. The chromosome of claim 27, wherein said virus is a human immunodeficiency virus (HIV), one of the Herpes viruses, an influenza virus, a poliomyelitis virus, a measles virus, a mumps virus, or a rubella virus.

29. The chromosome of claim 23, wherein said infectious organism is a eukaryotic parasite.

30. The chromosome of claim 29, wherein said parasite is the causative agent for malaria, pneumocystis pneumonia, or toxoplasmosis.

31. The chromosome of claim 20, wherein said chromosome does not encode biologically active cholera toxin A subunit.

32. A *V. cholerae* cell, the chromosome of which is the chromosome of claim 1.

33. A *V. cholerae* strain, the chromosome of which is the chromosome of claim 1.

34. A homogeneous population of *V. cholerae* cells, each of which comprises the chromosome of claim 1.

35. A live-cell vaccine comprising the cell of claim 32 in a pharmaceutically acceptable diluent suitable for oral administration.

36. The vaccine of claim 35, wherein said chromosome does not encode biologically active cholera toxin A subunit.

37. The vaccine of claim 36, wherein said chromosome does not encode biologically active IrgA.

38. The vaccine of claim 37, wherein said heterologous antigen is Shiga-like toxin B subunit.

39. A method of vaccinating an animal comprising orally administering to said animal the vaccine of claim 35.

40. The method of claim 39, wherein said animal is a human.

41. A process for inducing in an animal an immune response against a heterologous antigen, comprising administering to said animal recombinant *V. cholerae* containing DNA encoding said heterologous antigen, said heterologous antigen being expressed from said DNA in said animal, and is non-toxic and immunogenic.

42. A process for inducing in an animal an immune response against a heterologous antigen, comprising administering to said animal recombinant *V.cholerae* containing DNA encoding said heterologous antigen, said heterologous antigen being expressed from said DNA in said animal, wherein the sequence of said heterologous antigen does not comprise the sequence of a full length polypeptide expressed by a wild type *V. cholerae* and wherein said heterologous antigen (a) comprises an antigenic part or all, of a protein that is naturally expressed by an infectious organism other than wild type *V. cholerae*, and (b) induces an immune response in an animal.

43. The process of claim 41 or claim 42, wherein said DNA encoding said heterologous antigen is functionally linked to a promoter of a naturally-occurring *V.cholerae* gene.

44. The process of claim 41 or claim 42, wherein said heterologous antigen is a non-toxic polypeptide.

45. The process of claim 41, wherein said polypeptide is a portion or all of a protein naturally expressed by an infectious organism.

46. The process of claim 42 or claim 45, wherein said infectious organism is a bacterium.

47. The process of claim 46, wherein said polypeptide is an immunogenic, non-toxic subunit or fragment of a bacterial toxin.

48. The process of claim 47 wherein said toxin is Shiga toxin, diphtheria toxin, *Pseudomonas* exotoxin A, cholera toxin, pertussis toxin, tetanus toxin, anthrax toxin, *E.coli* heat-labile toxin (LT), *E. coli* heat-stable

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toxin (ST), or *E. coli* Shiga-like toxin.

49. The process of claim 42 or claim 45, wherein said protein is an OSP (Outer Surface Protein) of *Borrelia burgdorferi*.

50. The process of claim 42 or claim 45, wherein said infectious organism is a virus and said polypeptide is an immunogenic portion of a viral capsid.

51. The process of claim 50, wherein said virus is a human immunodeficiency virus (HIV), one of the herpes viruses, an influenza virus, a poliomyelitis virus, a measles virus, a mumps virus, or a rubella virus.

52. The process of claim 42 or claim 45, wherein said infectious organism is a eukaryotic parasite.

53. The process of claim 52, wherein said parasite is the causative agent for malaria, pneumocystis pneumonia, or toxoplasmosis.

54. The process of claim 42 or claim 45, wherein said protein is a malarial circumsporozoite protein.

55. The process of claim 41, wherein the chromosome of said recombinant *V. cholerae* does not encode a biologically active cholera toxin A subunit.

56. A live vaccine comprising (A) recombinant *V. cholerae* containing DNA encoding a non-toxic and immunogenic heterologous antigen and (B) a pharmaceutically acceptable diluent.

57. The vaccine of claim 56, wherein said heterologous antigen is part or all of a protein that is naturally expressed by an infectious organism other than *V. cholerae*, and said DNA is functionally linked to a naturally-occurring *V. cholerae* promoter.

58. The vaccine of claim 57, wherein said promoter is the promoter of a naturally-occurring gene encoding a *V. cholerae* virulence factor that is non-essential for growth of said cell, the coding sequence encoding said virulence factor being mutated or deleted so that said *V. cholerae* cannot express a biologically active form of said virulence factor.

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59. The vaccine of claim 56, wherein said heterologous antigen is part or all of a non toxic polypeptide which is naturally expressed by an infectious organism, which antigen induces an antigenic response in an animal.

60. The vaccine of claim 59, wherein said infectious organism is a bacterium.

61. The vaccine of claim 59, wherein said antigen is an immunogenic, non-toxic subunit or fragment of a bacterial toxin.

62. The vaccine of claim 61, wherein said toxin is Shiga toxin, diphtheria toxin, *Pseudomonas* exotoxin A, cholera toxin, pertussis toxin, tetanus toxin, anthrax toxin, *E. coli* LT, *E. coli* ST, or *E. coli* Shiga-like toxin.

63. The vaccine of claim 59, wherein said infectious organism is a virus and said antigen is an immunogenic protion of a viral capsid.

64. The vaccine of claim 63, wherein said virus is a human immunodeficiency virus (HIV), one of the Herpes viruses, an influenza virus, a poliomyelitis virus, a measles virus, a mumps virus, or a rubella virus.

65. The vaccine of claim 59, wherein said infectious organism is a eukaryotic parasite.

66. The vaccine of claim 65, wherein said parasite is the causative agent for malaria, pneumocystis pneumonia, or toxoplasmosis.

67. The vaccine of claim 56, wherein said *V. cholerae* does not express biologically active cholera toxin A subunit.

68. The vaccine of claim 56, wherein the chromosome of said *V. cholerae* does not encode biologically active IrgA.

69. The vaccine of claim 56, wherein said heterologous antigen is Shiga-like toxin B subunit.

70. A method of vaccinating an animal comprising orally administering to said animal the vaccine of claim 56.

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71. The method of claim 70, wherein said animal is a human.

72. A composition comprising (A) recombinant *V. cholerae* containing DNA encoding a heterologous antigen, the sequence of which does not comprise the sequence of a full length polypeptide expressed by wildtype *V. cholerae*, and (B) a pharmaceutically acceptable diluent, wherein said heterologous antigen (1) comprises an antigenic part, or all, of a protein that is naturally expressed by an infectious organism other than wildtype *V. cholerae*, and (2) induces an immune response in an animal.

73. The composition of claim 72, wherein said DNA is functionally linked to a naturally-occurring *V. cholerae* promoter.

74. The composition of claim 73, wherein said promoter is the promoter of a naturally-occurring gene encoding a *V. cholerae* virulence factor that is non-essential for growth of said cell, the coding sequence encoding said virulence factor being mutated or deleted so that said *V. cholerae* cannot express a biologically active form of said virulence factor.

75. The composition of claim 72, wherein said heterologous antigen comprises an antigenic portion of a protein naturally expressed by a first infectious organism and an antigenic portion of a protein naturally expressed by a second infectious organism.

76. The composition of claim 72, wherein said infectious organism is a bacterium.

77. The composition of claim 72, wherein said heterologous antigen comprises an immunogenic, nontoxic subunit or fragment of a bacterial toxin.

78. The composition of claim 77, wherein said toxin is Shiga toxin, diphtheria toxin, *Pseudomonas* exotoxin A, cholera toxin, pertussis toxin, tetanus toxin, anthrax toxin, *E. coli* ST, or *E. coli* Shiga-like toxin.

79. The composition of claim 72, wherein said infectious organism is a virus and said protein is a viral

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protein.

80. The composition of claim 79, wherein said virus is a human immunodeficiency virus (HIV), one of the Herpes viruses, an influenza virus, a poliomyelitis virus, a measles virus, a mumps virus, or a rubella virus.

81. The composition of claim 72, wherein said infectious organism is a eukaryotic parasite.

82. The composition of claim 81, wherein said parasite is the causative agent for malaria, pneumocystic pneumonia, or toxoplasmosis.

83. The composition of claim 72, wherein said *V. cholerae* does not express biologically active cholera toxin A subunit.

84. The composition of claim 72, wherein said composition is a live-cell vaccine.

85. The composition of claim 72, wherein the chromosome of said *V. cholerae* does not encode biologically active IrgA.

86. The composition of claim 72, wherein said protein is Shiga-like toxin B subunit.

Dated this 15th day of August 1997
THE GENERAL HOSPITAL CORPORATION
PRESIDENT AND FELLOWS OF HARVARD COLLEGE
By their Patent Attorneys
GRIFFITH HACK
Fellows Institute of Patent
Attorneys of Australia

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WO 94/19482

FIG. 1

PCT/US94/01780

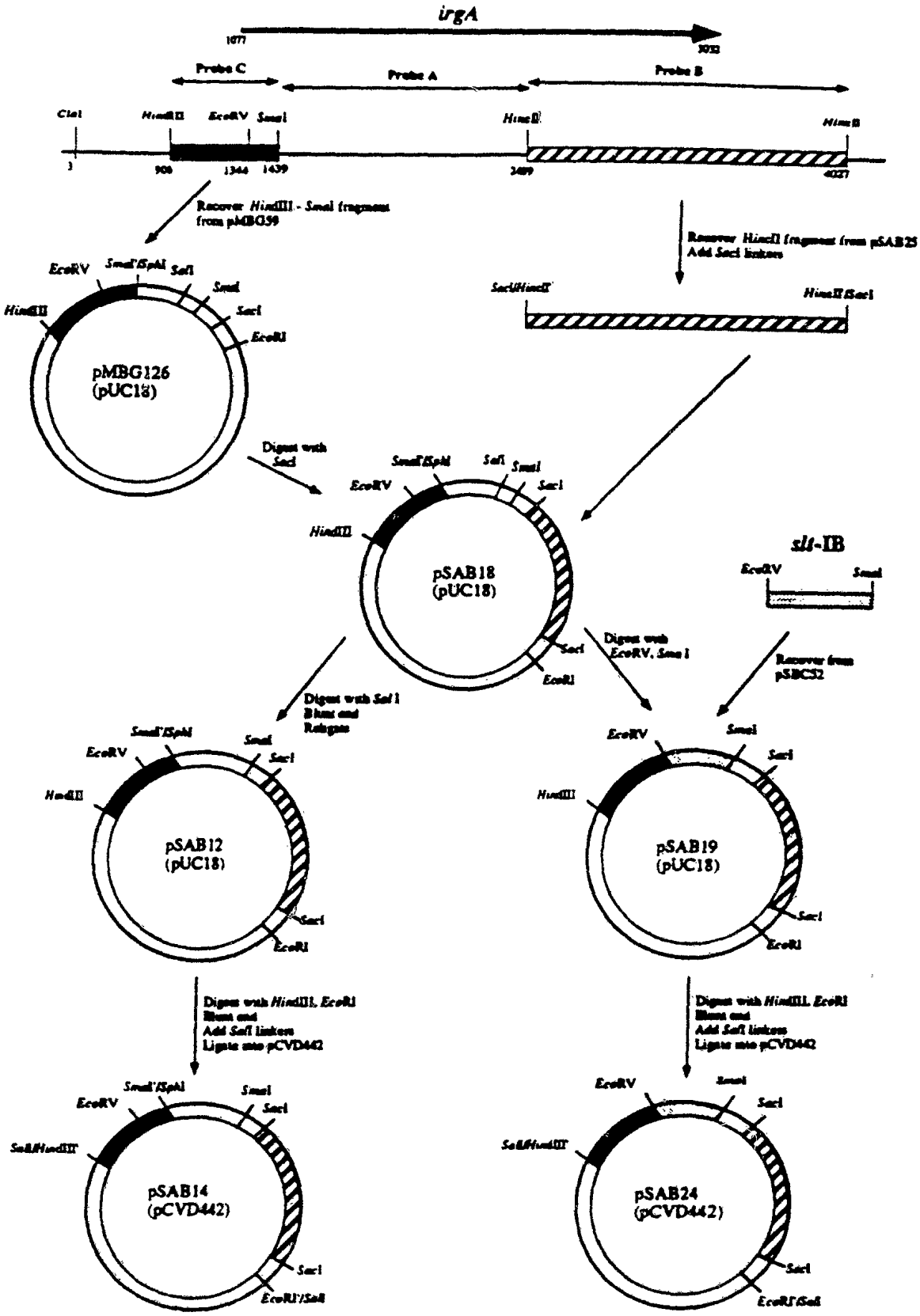


Fig. 2A

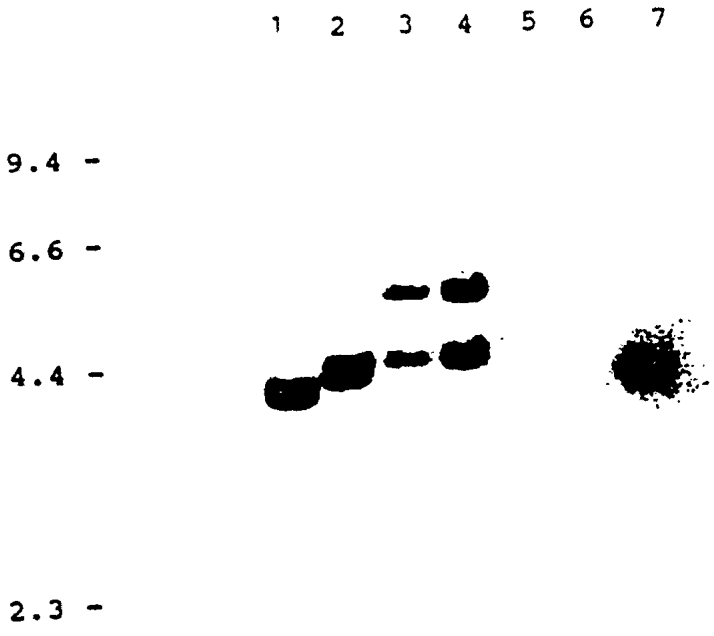


Fig. 2B



C



D



FIG. 3

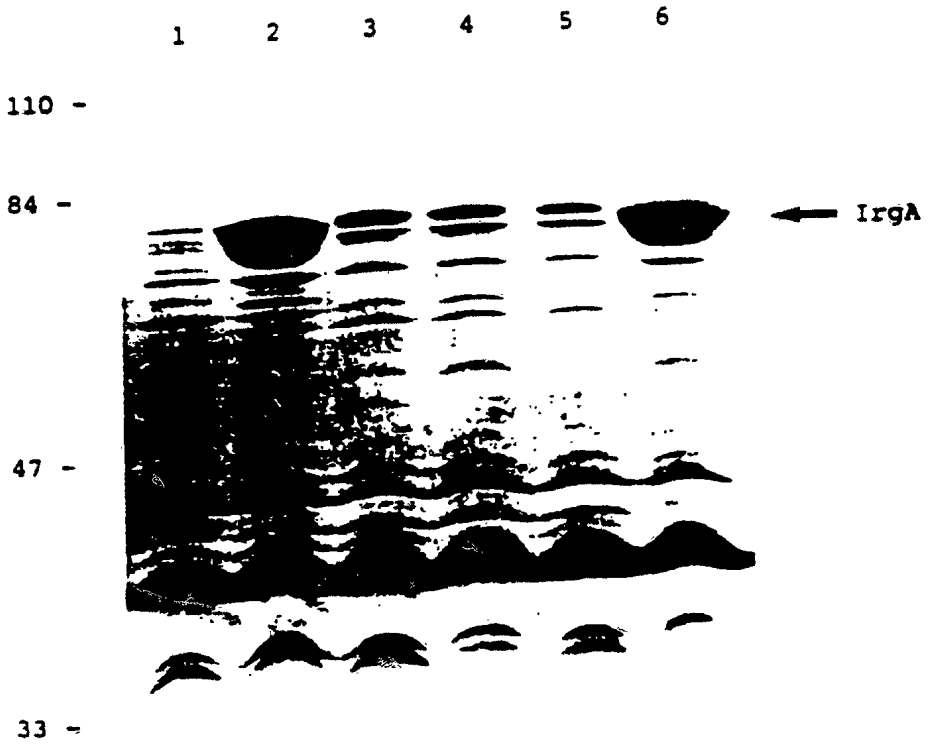
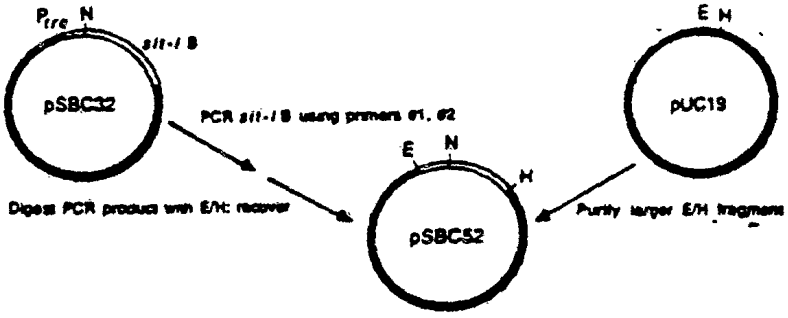


FIG. 4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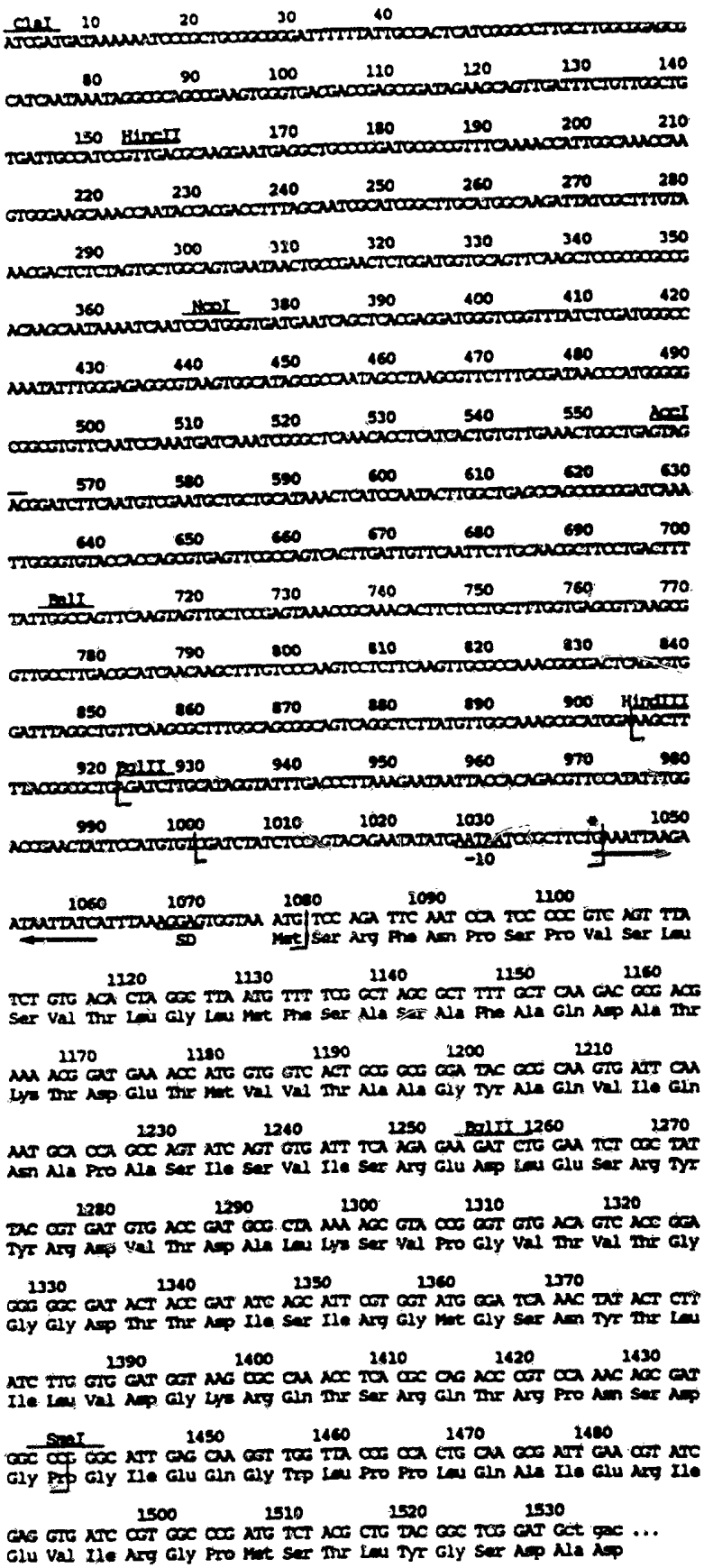
pSBC52
E H
pUC19
Purify larger E/H fragment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Lys Thr Asp Glu Thr Met Val Val Thr Ala Ala Gly Tyr Ala Gln Val Ile Gln
Asn Ala Pro Ala Ser Ile Ser Val Ile Ser Arg Glu Asp Leu Glu Ser Arg Tyr
Tyr Arg Asp Val Thr Asp Ala Leu Lys Ser Val Pro Gly Val Thr Val Thr Gly
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Ile Leu Val Asp Gly Lys Arg Gln Thr Ser Arg Gln Thr Arg Pro Asn Ser Asp
Gly Pro Gly Ile Glu Gln Gly Trp Leu Pro Pro Leu Gln Ala Ile Glu Arg Ile
Glu Val Ile Arg Gly Pro Met Ser Thr Leu Tyr Gly Ser Asp Ala Asp

INTERNATIONAL SEARCH REPORT

International application No
PCT/US94/01780

A. CLASSIFICATION OF SUBJECT MATTER

IPC(5) :C12P 21/06; C12N 1/20, 1/12; A01N 63/00
US CL :435/69.1, 252.3, 252.33, 253.1; 424/93A, 93P, 93D

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.1, 252.3, 252.33, 253.1; 424/93A, 93P, 93D

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, DIALOG

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO,A, 89/02924 (BREY ET AL.) 06 APRIL 1989, see entire document.	1-40
Y	US, A, 4,882,278 (MEKALANOS) 21 NOVEMBER 1989, see entire document.	1-40
Y	PNAS, USA, Volume 88, Number 4, issued 15 February 1991, Goldberg et al., "Positive transcriptional regulation of an iron-regulated virulence gene in Vibrio cholerae", pages 1125-1129, see entire document.	1-40

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be part of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search 31 March 1994	Date of mailing of the international search report APR 26 1994
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer GARY L. BROWN Jill Warden for Telephone No. (703) 308-0196

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C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	INFECTION AND IMMUNITY, Volume 58, No.1, issued January 1990, Goldberg et. al., "Identification of an Iron-regulated virulence determinant in Vibrio cholerae, using TnphoA mutants, pages 55-60, see entire document.	1-40
Y	NATURE, Volume 327, issued 11 JUNE 1987, Jacobs et al., "Introduction of foreign DNA into mycobacteria using a shuttle phasmid", pages 532-534, see entire document.	1-40