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(54) **BACTERIES ATTENUÉES PAR MUTATION IRREVERSIBLE
DE CHACUN DES GENES AROC, OMPF ET OMPC, UTILES
DANS DES VACCINS**

(54) **BACTERIA ATTENUATED BY A NON-REVERTING
MUTATION IN EACH OF THE AROC, OMPF AND OMPC
GENES, USEFUL AS VACCINES**

(57) L'invention concerne une bactérie atténuée par mutation irréversible de chacun des gènes aroC, ompF et ompC. Cette bactérie est utile comme vaccin. Elle peut, par exemple, être une souche atténuée de E. coli utile comme vaccin contre la diarrhée.

(57) The invention provides a bacterium attenuated by a non-reverting mutation in each of the aroC gene, the ompF gene and the ompC gene. The bacterium is useful as a vaccine. The bacterium may, for example, be an attenuated strain of E.coli useful in vaccination against diarrhoea.



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(54) Title: BACTERIA ATTENUATED BY A NON-REVERTING MUTATION IN EACH OF THE AROC, OMPF AND OMPC GENES, USEFUL AS VACCINES		
(57) Abstract The invention provides a bacterium attenuated by a non-reverting mutation in each of the aroC gene, the ompF gene and the ompC gene. The bacterium is useful as a vaccine. The bacterium may, for example, be an attenuated strain of E.coli useful in vaccination against diarrhoea.		

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BACTERIA ATTENUATED BY A NON-REVERTING MUTATION IN EACH OF THE AROC, OMPF AND OMPC GENES, USEFUL AS VACCINES

The invention relates to attenuated bacteria useful in vaccines.

5

Background to the invention

The principle behind vaccination is to induce an immune response in the host thus providing protection against subsequent challenge with a pathogen. This may be
10 achieved by inoculation with a live attenuated strain of the pathogen, i.e. a strain having reduced virulence such that it does not cause the disease caused by the virulent pathogen.

15 Clasically, live attenuated vaccine strains of bacteria and viruses have been selected using one of two different methodologies. Mutants have been created either by treatment of the organism using mutagenic chemical compounds or by repeated passage of the organism *in*
20 *vitro*. However, use of either method gives rise to attenuated strains in which the mode of attenuation is unclear. These strains are particularly difficult to characterise in terms of possible reversion to the wild type strain as attenuation may reflect single (easily
25 reversible) or multiple mutation events. Furthermore, it is difficult to obtain such strains having optimum immunogenic properties because of multiple mutation events, and multiple strains may need to be used to provide protection against the pathogen.

30

Using modern genetic techniques, it is now possible to construct genetiially defined attenuated bacterial strains in which stable attenuating deletions can be created. A number of site directed mutants of Salmonella have been
35 created using this type of technology (2, 4, 5, 9, 12,

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16, 17, 18). Mutations in a large number of genes have been reported to be attenuating, including the *aro* genes (e.g. *aroA*, *aroC*, *aroD* and *aroE*), *pur*, *htrA*, *ompR*, *ompF*, *ompC*, *galE*, *cya*, *crp* and *phoP*.

5

Salmonella *aroA* mutants have now been well characterised and have been shown to be excellent live vaccines against salmonellosis in several animal species. In addition, in order to reduce the chances of a reversion to virulence
10 by a recombination event, mutations have been introduced into two independent genes such as *aroA/purA* and *aroA/aroC*. Identical mutations in host adapted strains of Salmonella such as *S.typhi* (man) and *S.dublin* (cattle) has also resulted in the creation of a number of
15 candidate single dose vaccines which have proved successful in clinical (8, 11) and field trials (10).

A *Salmonella typhimurium* strain harboring stable mutations in both *ompC* and *ompF* is described in Chatfield
20 et al (1991, ref. 21). When administered orally to BALB/c mice the strain was attenuated, with the 50% lethal dose (LD50) reduced by approximately 1,000-fold. However, the intravenous LD50 was reduced only by approximately 10-fold, demonstrating the importance of the porins in
25 conferring on the bacteria the ability to infect by the oral route.

Expression of the *ompC* and *ompF* genes is regulated by *ompR*. Pickard et al (1994, ref. 13) describes the cloning
30 of the *ompB* operon, comprising the *ompR* and *envZ* genes, from a *Salmonella typhi* Ty2 cosmid bank and characterisation by DNA sequence analysis. The DNA sequence data were used to identify appropriate restriction sites for generating a defined deletion of

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517 bp within the open reading frame of the *ompR* gene. This deletion was introduced by homologous recombination into the chromosomes of two *S.typhi* strains which already harbored defined deletions in both the *aroC* and *aroD* genes. The *S.typhi ompR* mutants displayed a marked decrease in *ompC* and *ompF* porin expression as demonstrated by examination of outer membrane preparations. It was also shown that the *ompR-envZ* two component regulatory system plays an important role in the regulation of Vi polysaccharide synthesis in *S.typhi*.

In animal studies, attenuated *S.typhimurium* has been used as a vehicle for the delivery of heterologous antigens to the immune system (3, 6, 15). This raises the potential of the development of multivalent vaccines for use in man (7).

Summary of the Invention

The invention provides a bacterium attenuated by a non-reverting mutation in each of the *aroC* gene, the *ompF* gene and the *ompC* gene. The invention also provides a vaccine containing the bacterium.

It is believed that the *aroC/ompF/ompC* combination of mutations gives a vaccine having superior properties. For example, it is believed that the *aroC/ompF/ompC* combination may be superior to a *aroC/ompR* combination for two reasons:

1. The *ompR* mutation may cause higher levels of attenuation than the *ompF/ompC* combination of mutations because *ompR* may regulate a number of genes other than *ompF* and *ompC* which are important for survival of the bacterium *in vivo*. Thus, the

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ompF/ompC combination may allow the bacterium to survive in the vaccinated host for a longer time and at higher levels, resulting in better protection.

5

2. The *ompR* mutation may cause reduced immunogenicity compared to the *ompF/ompC* combination of mutations because *ompR* may regulate the expression of antigens important for immunogenicity.

10

Detailed Description of the Invention

Bacteria useful in the Invention

The bacteria that are used to make the vaccines of the invention are generally those that infect by the oral route. The bacteria may be those that invade and grow within eukaryotic cells and/or colonise mucosal surfaces. The bacteria are generally Gram-negative.

- 20 The bacteria may be from the genera *Escherichia*, *Salmonella*, *Vibrio*, *Haemophilus*, *Neisseria*, *Yersinia*, *Bordetella* or *Brucella*. Examples of such bacteria are *Escherichia coli* - a cause of diarrhoea in humans; *Salmonella typhimurium* - the cause of salmonellosis in
25 several animal species; *Salmonella typhi* - the cause of human typhoid; *Salmonella enteritidis* - a cause of food poisoning in humans; *Salmonella choleraesuis* - a cause of salmonellosis in pigs; *Salmonella dublin* - a cause of both a systemic and diarrhoeal disease in cattle,
30 especially of new-born calves; *Haemophilus influenza* - a cause of meningitis; *Neisseria gonorrhoeae* - a cause of gonorrhoeae; *Yersinia enterocolitica* - the cause of a spectrum of diseases in humans ranging from gastroenteritis to fatal septicemic disease; *Bordetella*

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pertussis - the cause of whooping cough; and *Brucella abortus* - a cause of abortion and infertility in cattle and a condition known as undulant fever in humans.

5 Strains of *E.coli* and *Salmonella* are particularly useful in the invention. As well as being vaccines in their own right against infection by *Salmonella*, attenuated *Salmonella* can be used as carriers of heterologous antigens from other organisms to the immune system via
10 the oral route. *Salmonella* are potent immunogens and are able to stimulate systemic and local cellular and antibody responses. Systems for driving expression of heterologous antigens in *Salmonella in vivo* are known; for example the *nirB* and *htrA* promoters are known to be
15 effective drivers of antigen expression *in vivo*.

The invention may be applied to enterotoxigenic *E.coli* ("ETEC"). ETEC is a class of *E.coli* that cause diarrhoea. They colonise the proximal small intestine.
20 A standard ETEC strain is ATCC H10407.

Infections of ETEC are the single most frequent cause of travellers diarrhoea, causing 3-9 million cases per year amongst visitors to developing countries. In endemic
25 areas, ETEC infections are an important cause of dehydrating diarrhoea in infants and young children, resulting in 800,000 deaths a year in the under fives world-wide. In developing countries, the incidence of ETEC infections leading to clinical disease decreases
30 with age, indicating that immunity to ETEC infection can be acquired. In contrast, naive adults from industrialized countries who visit endemic areas are highly susceptible to ETEC infections. However, with prolonged or repeated visits to endemic areas
35 susceptibility to ETEC infections diminishes, suggesting

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that a live attenuated approach to ETEC vaccination may prove successful.

The inventors chose to work on a non-toxigenic strain of ETEC called E1392/75/2A. E1392/75/2A arose spontaneously from a toxic mutant by deletion of toxin genes. In human studies, oral vaccination with live E1392/75/2A gave 75% protection against challenge with toxin-expressing ETEC from a different serotype. However, approximately 15% of vaccinees experienced diarrhoea as a side effect of the vaccine. The strain needs further attenuation to reduce the side effects before it can be considered as a potential vaccine and the invention gives a means of achieving such attenuation.

15

Seq Id No. 1 shows the sequence of the *E.coli aroC* gene, Seq Id No. 3 shows the sequence of the *E.coli ompC* gene and Seq. Id No. 5 shows the sequence of the *E.coli ompF* gene.

20

Further mutations

One or more further mutations may be introduced into the bacteria of the invention to generate strains containing mutations in addition to those in *aroC*, *ompC* and *ompF*. Such a further mutation may be (i) an attenuating mutation in a gene other than *aroC*, *ompC* and *ompF*, (ii) a mutation to provide *in vivo* selection for cells maintaining a plasmid (e.g. a plasmid expressing a heterologous antigen), or (iii) a mutation to prevent expression of a toxin gene.

30

The further attenuating mutation may be a mutation that is already known to be attenuating. Such mutations

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include mutations in *aro* genes (e.g. *aroA*, *aroD* and *aroE*), *pur*, *htrA*, *ompR*, *galE*, *cya*, *crp*, *phoP* and *surA* (see e.g. refs 2, 4, 5, 9, 12, 13, 16, 17 and 18).

- 5 A mutation to provide selection for maintenance of a plasmid may be made by mutating a gene that is essential for the bacterium to survive. A plasmid carrying the essential gene is then introduced into the bacterium, so that only cells carrying the plasmid can survive. This
10 may be useful where the plasmid contains, for example, a heterologous antigen to be expressed by the bacterium.

A mutation to prevent expression of a toxin gene may be made to reduce any side-effects caused by vaccination
15 with the bacterium. For example, in the case of vaccination with *E.coli* strains such as ETEC it may be desirable to mutate the heat labile toxin (LT) or heat stable toxin (ST) genes so that they are not expressed.

20 **The nature of the mutations**

The mutations introduced into the bacterial vaccine generally knock-out the function of the gene completely. This may be achieved either by abolishing synthesis of
25 any polypeptide at all from the gene or by making a mutation that results in synthesis of non-functional polypeptide. In order to abolish synthesis of polypeptide, either the entire gene or its 5'-end may be deleted. A deletion or insertion within the coding
30 sequence of a gene may be used to create a gene that synthesises only non-functional polypeptide (e.g. polypeptide that contains only the N-terminal sequence of the wild-type protein).

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The mutations are non-reverting mutations. These are mutations that show essentially no reversion back to the wild-type when the bacterium is used as a vaccine. Such mutations include insertions and deletions. Insertions
5 and deletions are preferably large, typically at least 10 nucleotides in length, for example from 10 to 600 nucleotides. Preferably, the whole coding sequence is deleted.

- 10 The bacterium used in the vaccine preferably contains only defined mutations, i.e. mutations which are characterised. It is clearly undesirable to use a bacterium which has uncharacterised mutations in its genome as a vaccine because there would be a risk that
15 the uncharacterised mutations may confer properties on the bacterium that cause undesirable side-effects.

- The attenuating mutations may be introduced by methods well known to those skilled in the art (see ref. 14).
- 20 Appropriate methods include cloning the DNA sequence of the wild-type gene into a vector, e.g. a plasmid, and inserting a selectable marker into the cloned DNA sequence or deleting a part of the DNA sequence, resulting in its inactivation. A deletion may be
25 introduced by, for example, cutting the DNA sequence using restriction enzymes that cut at two points in or just outside the coding sequence and ligating together the two ends in the remaining sequence. A plasmid carrying the inactivated DNA sequence can be transformed
30 into the bacterium by known techniques such as electroporation and conjugation. It is then possible by suitable selection to identify a mutant wherein the inactivated DNA sequence has recombined into the chromosome of the bacterium and the wild-type DNA
35 sequence has been rendered non-functional by homologous

recombination.

Expression of heterologous antigens

The attenuated bacterium of the invention may be
5 genetically engineered to express an antigen that is not
expressed by the native bacterium (a "heterologous
antigen"), so that the attenuated bacterium acts as a
carrier of the heterologous antigen. The antigen may be
from another organism, so that the vaccine provides
10 protection against the other organism. A multivalent
vaccine may be produced which not only provides immunity
against the virulent parent of the attenuated bacterium
but also provides immunity against the other organism.
Furthermore, the attenuated bacterium may be engineered
15 to express more than one heterologous antigen, in which
case the heterologous antigens may be from the same or
different organisms.

The heterologous antigen may be a complete protein or a
20 part of a protein containing an epitope. The antigen may
be from another bacterium, a virus, a yeast or a fungus.
More especially, the antigenic sequence may be from
E.coli (e.g. ETEC), tetanus, hepatitis A, B or C virus,
human rhinovirus such as type 2 or type 14, herpes
25 simplex virus, poliovirus type 2 or 3, foot-and-mouth
disease virus, influenza virus, coxsackie virus or
Chlamydia trachomatis. Useful antigens include non-toxic
components of *E.coli* heat labile toxin, *E.coli* K88
antigens, ETEC colonization factor antigens, P.69 protein
30 from *B.pertussis* and tetanus toxin fragment C.

The ETEC colonization factors and components thereof are
prime candidates for expression as heterologous antigens.
To instigate diarrhoeal disease, pathogenic strains of
35 ETEC must be able to colonize the intestine and elaborate

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- enterotoxins. For most strains of ETEC colonization factors (CF) that are required for adhesion to the intestinal mucosa have been identified. In almost all cases CFs are expressed as fimbriae on the outer surface of the bacteria. A large number of CFs have been identified, the most prevalent being CFAI, CRAII (includes CS1, CS2, CS3) and CFAIV (includes CS4, CS5, CS6).
- 10 A vaccine to ETEC will ideally give protection against a range of colonization factor antigens to ensure that protection against different strains is obtained. In order to achieve this, it would be possible to express several colonization factors in one strain.
- 15 Alternatively, the same attenuations could be made in a range of different ETEC strains, each with a different colonization factor. This would involve deleting the toxins from such strains.
- 20 The DNA encoding the heterologous antigen is expressed from a promoter that is active *in vivo*. Two promoters that have been shown to work well in *Salmonella* are the *nirB* promoter (19, 20) and the *htrA* promoter (20). For expression of the ETEC colonization factor antigens, the wild-type promoters could be used.
- 25

A DNA construct comprising the promoter operably linked to DNA encoding the heterologous antigen may be made and transformed into the attenuated bacterium using conventional techniques. Transformants containing the DNA construct may be selected, for example by screening for a selectable marker on the construct. Bacteria containing the construct may be grown *in vitro* before being formulated for administration to the host for vaccination purposes.

35

Formulation of the vaccine

The vaccine may be formulated using known techniques for formulating attenuated bacterial vaccines. The vaccine is advantageously presented for oral administration, for example in a lyophilised encapsulated form. Such capsules may be provided with an enteric coating comprising, for example, Eudragate "S" (Trade Mark), Eudragate "L" (Trade Mark), cellulose acetate, cellulose phthalate or hydroxypropylmethyl cellulose. These capsules may be used as such, or alternatively, the lyophilised material may be reconstituted prior to administration, e.g. as a suspension. Reconstitution is advantageously effected in a buffer at a suitable pH to ensure the viability of the bacteria. In order to protect the attenuated bacteria and the vaccine from gastric acidity, a sodium bicarbonate preparation is advantageously administered before each administration of the vaccine. Alternatively, the vaccine may be prepared for parenteral administration, intranasal administration or intramuscular administration.

The vaccine may be used in the vaccination of a mammalian host, particularly a human host but also an animal host. An infection caused by a microorganism, especially a pathogen, may therefore be prevented by administering an effective dose of a vaccine prepared according to the invention. The dosage employed will ultimately be at the discretion of the physician, but will be dependent on various factors including the size and weight of the host and the type of vaccine formulated. However, a dosage comprising the oral administration of from 10^7 to 10^{11} bacteria per dose may be convenient for a 70 kg adult human host.

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Examples

The Examples described in this section serve to illustrate the invention.

5 Brief description of the drawings

Figure 1 shows a system for constructing defined deletions in target genes using splicing by overlay extension PCR mutagenesis.

10

Figure 2 shows the expected sequences of target genes after recombination and selection for deletions.

Figure 3 shows the cloning of deletion cassettes into
15 plasmid pCVD442.

Figure 4 shows an SDS-PAGE analysis of outer membranes prepared from ETEC strains under conditions of low (no salt L-broth) and high (no salt L-broth + 15% sucrose) osmolarity. M = markers; Sample 1 = PTL010; Sample 2 = PTL002; Sample 3 = PTL003; Sample 4 = Δ aroC Δ ompC; Sample 5 = Δ ompF.
20

Figure 5 shows expression of CS1 and CS3 in deletion strains after growth on CFA agar. Equal numbers of cells from each strain were loaded on a 15% SDS-PAGE gel and Western blotted with monospecific anti-CS1 or anti-CS3 polyclonal antibodies. Controls for antibody specificity were whole ces11 lysates of TG1 cells expressing the majore pilin protein of CS1, or purified major pilin protein from CS3. Lane M, rainbow low molecular mass markers; lane 1, induced TG1 cells harbouring pKK223; lane 2, induced TG1 cells harbouring pKKCs1; lane 3, CS1-ETEC strain; lane 4, PTL010; lane 5, PTL001; lane 6, PTL002; lane 7, PTL003; lane 8, purified CS3 major pilin
25
30
35

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protein.

Figure 6 shows a Southern blot of mutant loci.

Chromosomal DNA was extracted from the wild-type ETEC
5 (E1392/75-2A), PTL001 (htrA aroC), PTL002 (aroC ompR) and
PTL003 (aroC ompC ompF) as indicated, digested with
restriction endonuclease EcoRV, and pulsed field
electrophoresed through 1% agarose. DNA was blotted from
the gel onto Hybond N+ nylon membranes (Amersham) and
10 hybridised with DNA probes derived from the aroC, htrA,
ompR, ompC, or ompF loci as shown. The banding patterns
are consistent with the mutant loci being deletions.

Figure 7 shows the IgA responses in volunteers
15 administered a vaccine according to the invention.

**EXAMPLE 1: CONSTRUCTION AND CHARACTERISATION OF STRAIN
ACCORDING TO THE INVENTION**

20 **Design of deletions and construction of plasmids**
pCVD Δ AroC, pCVD Δ OmpC and pCVD Δ OmpF

Deletions were designated to remove the entire open
reading frame of the target gene. Using the *E.coli* genome
sequence as a template, PCR primers were designed to
25 amplify fragments of 500-600 base pairs flanking the
target open reading frame (see Table 1 for primer
sequences). Splicing by overlap extension using PCR was
used to fuse the two flanking sequences, creating a PCR
product with the entire gene deleted (Figure 1). The
30 wild-type sequences around the deletion site and the
predicted sequences after deletion are depicted in Figure
2.

For each gene two different restriction sites were

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introduced into the splice region (see Table 2 below). These were used for identification of deletion clones. The PCR primers at either end of the PCR fragment introduced unique restriction sites that were used to
5 clone the fragment into the multiple cloning site of pCVD442 (Figure 3).

PCR products were gel purified using a Qiagen (Trade Name) gel extraction kit and digested with the relevant
10 restriction enzymes prior to ligation to the suicide plasmid pCVD442(22) digested with the same enzyme and treated with alkaline phosphatase to prevent vector self-ligation (Figure 3). The ligation mix was transformed into SY327 λ pir and plated on L-Ampicillin (100 μ g/ml)
15 plates. Plasmids from Ampicillin resistant transformants were screened for the presence of the deletion cassettes by restriction digestion. The following plasmids were generated:

20 pCVD Δ AroC
pCVD Δ OmpC
pCVD Δ OmpF

The suicide plasmid pCVD442 can only replicate in cells
25 harboring the *pir* gene. On introduction into *non-pir* strains, pCVD442 is unable to replicate, and the Ampicillin resistance conferred by the plasmid can only be maintained if the plasmid is integrated in the chromosome by a single homologous recombination event.
30 The plasmid also has a *sacB* gene, encoding levan sucrase, which is toxic to gram negative bacteria in the presence of sucrose. This can be used to select clones that have undergone a second recombination event, in which the suicide plasmid is excised. Such cells will be resistant
35 to sucrose, but Ampicillin sensitive.

Construction and characterisation of Δ AroC Δ OmpC Δ OmpF strain

This section outlines the chronology of construction and history of a Δ AroC Δ OmpC Δ OmpF strain. In the section,
 5 "ETEC" refers specifically to strain E1392/75/2A or its derivatives.

Δ AroC Δ OmpC Δ OmpF deletions were introduced into E1392/75/2A in the following order:

10 Δ AroC- Δ AroC Δ OmpC- Δ AroC Δ OmpC Δ OmpF

Construction of ETEC Δ AroC

- 1) E1392/75/2A from original microbanked stock was plated onto L-Agar.
- 15 2) Electroporation competent cells were prepared from these cells. 100 μ l aliquots were frozen.
- 3) pCVD Δ AroC was purified from SY327pir cells using a Qiagen Qiafilter (Trade Name) midiprep. The plasmid was concentrated about 10-fold by ethanol
 20 precipitation. The construction of pCVD Δ AroC is described above.
- 4) 5 μ l of concentrated plasmid was mixed with 100 μ l defrosted cells and electroporated. The whole transformation was plated on an L-Ampicillin plate
 25 (50 μ g/ml) and incubated overnight at 37°C.
- 5) A single Ampicillin resistant colony grew.
- 6) The colony was streaked onto an L-Ampicillin plate (100 μ g/ml) and grown overnight at 37°C ("merodiploid plate").
- 30 7) PCR using primers TT19 and TT20 (specific for the aroC gene) and a colony picked from the merodiploid plate amplified two bands, with sizes corresponding to that of the wild-type and Δ aroC genes. The sequences of the primers are shown in Table 1

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below.

- 8) A colony from the merodiploid plate was grown up for 7 hr in a) L-Ampicillin broth (100 µg/ml) and b) L-Broth. The colony grown on L-Ampicillin was microbanked.
- 9) Serial dilutions of the L-broth culture were set up on:
- a) No salt L-agar
 - b) No salt L-agar + 5% sucrose.
- 10) The plates were incubated overnight at 30°C.
- 10) Colony counts showed that 10⁴ more colonies grew on L-agar than on L-agar + 5% sucrose, showing sucrose selection worked.
- 11) Sucrose resistant colonies were screened for the presence of Δ aroC gene by PCR. Colonies chosen for screening were picked onto an L-agar plate and grown overnight at 37°C. This plate was stored at 4°C, whilst further tests were carried out.
- 12) 50% of 90 colonies tested had Δ aroC only.
- 13) Colonies were tested for growth on:
- a) M-9 minimal media plates
 - b) M-9 minimal media + Aromix plates
 - c) L-Amp (100 µg/ml)

Δ aroC colonies should not grow on M-9 minimal media without Aromix or on L-Amp.

Aromix is a mix of aromatic compounds as follows:

Substance	Final concentration (% w/v)
Phenylalanine	0.004
Tryptophan	0.004
Tyrosine	0.004
p-aminobenzoic acid	0.001
dihydroxybenzoic acid	0.001

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These compounds are made in wild-type bacteria, but the *aroC* mutation prevents their synthesis.

- 14) 13/14 putative Δ AroC colonies required Aromix for growth on M-9 minimal media and were susceptible to Ampicillin.
- 15) 3 colonies (No. 1,2,3) were tested for the presence of the CS1 major pilin protein gene by PCR using primers MGR169 and MGR170. All 3 colonies gave PCR products of the expected size (700 bp.). The sequences of the primers are shown in Table 1.
- 16) Colonies 1, 2 and 3 from screening master plate were streaked onto L-Agar and grown overnight at 37°C. Cells from these plates were used to inoculate microbank tubes.
- 17) Colony 1, stored in a microbank, was used for further work.
- 18) For permanent storage, a bead from the microbank tray was inoculated into 1 ml L-broth, grown for 4 hr with shaking at 37°C and used to make agar slopes which were used to make freeze dried stocks. The freeze dried stock of E1392/75/2A Δ AroC was designated PTL004. 20 ml of L-broth was added to the rest of the 1 ml culture and the culture was incubated overnight at 30°C. 1 ml of the overnight culture was transferred to each of three cryovials and stored in liquid nitrogen.

Construction of ETEC Δ AroC Δ Omp_r

- 1) Preparation of pCVD Δ OmpC plasmid DNA for electroporation:

A colony of SY327 Δ pir harbouring pCVD Δ OmpC was grown overnight at 37°C in 100 ml L-Ampicillin broth

(100 μ g/ml). Plasmid DNA was purified using 2 Qiagen Qiafilter (Trade Name) midipreps. DNA was

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further concentrated by ethanol precipitation. The construction of pCVD Δ OmpC is described above.

2) Preparation of electrocompetent cells:

ETEC Δ AroC cells from the microbank tray produced in step 17 of the preceding section were streaked on L-agar, grown at 37°C overnight and then stored at 4°C for no more than 1 week before being used to inoculate cultures for preparing electrocompetent cells.

3) ETEC Δ AroC cells were electroporated with 5 μ l of concentrated pCVD Δ OmpC DNA, and each transformation plated on a single L-Ampicillin plate (50 μ g/ml) and grown overnight at 37°C.

4) 17 Ampicillin resistant colonies (putative ETEC Δ AroC/ pCVD Δ OmpC merodiploids) were obtained.

5) These colonies were spotted onto a master L-Ampicillin (100 μ g/ml) plate and used as templates for PCR with primers TT7/TT8. The master plate was grown at room temperature over the weekend. The sequences of the primers are given in Table 1 below.

6) A single colony (No. 7) had the Δ ompC gene.

7) The colony was grown for 5 hr in L-broth.

8) Serial dilutions of the L-broth culture were set up on:

a) No salt L-agar

b) No salt L-agar + 5% sucrose.

The plates were incubated overnight at 30°C.

9) Colony counts showed that 10⁴ more colonies grew on L-agar than on L-agar + 5% sucrose, showing sucrose selection worked.

10) 45 sucrose resistant colonies were screened for Δ ompC by PCR using primers TT7 and TT8. 9 colonies had the Δ ompC gene, but most had traces of w.t. ompC gene. The sequences of the primers are given

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in Table 1 below.

- 11) To further characterise putative ETEC Δ AroC Δ OmpC colonies, they were grown in 1 ml L-Broth for 5 hr and plated on:

- 5 a) L-Agar + 100 μ g/ml Ampicillin
 b) L-Agar
 c) L-Agar + 5% sucrose

Δ OmpC colonies should be resistant to sucrose and sensitive to Ampicillin.

- 10 12) Only 1 colony (No. 1) was Ampicillin sensitive and sucrose resistant.

- 13) Colony 1 was checked for the presence of Δ aroC, Δ ompC and CS1 genes by PCR with primers TT19/TT20, TT7/TT8 and MGR169 and 170. The sequences of the
15 primers are given in Table 1 below.

- 14) Colony 1 gave single PCR products of the expected size for Δ aroC, Δ ompC and CS1 genes.

- 15) The colony was microbanked.

- 16) For permanent storage, a bead from the microbank
20 was inoculated into 1 ml L-broth, grown for 4 hr with shaking at 37°C and used to make agar slopes which were freeze dried. The freeze dried stock of E1392/75/2A Δ AroC Δ OmpC was designated PTL008. 20 ml of L-broth was added to the rest of the 1 ml
25 culture and the culture was incubated overnight at 30°C. 1 ml of the overnight culture was transferred to each of three cryovials and stored in liquid nitrogen.

30 **Construction of ETEC Δ AroC Δ OmpC Δ OmpF**

Conjugation was used to introduce pCVD Δ OmpF into E1392/75/2A Δ AroC Δ OmpC.

- 1) Conjugation donor cells SM10 λ pir were transformed with pCVD Δ OmpF. The construction of plasmid

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pCVD Δ OmpF is described above.

- 2) ETEC Δ AroC Δ OmpC cells were conjugated with SM10 λ pir/
pCVD Δ OmpF cells. The pCVD442 plasmid includes a
transfer origin which allows the plasmid to be
transferred from a donor strain containing the RP4
transfer genes (e.g. SM10 λ pir) to a recipient
strain (e.g. ETEC). ETEC Δ aroC Δ ompC cells and
E.coli strain SM10 λ pir harbouring the Pcvd Δ ompF
recombinant were cross-streaked on L-agar plates so
as to cover an area of approximately 10 cm².
Plates were incubated at 37° C for 20 h, then the
growth washed off using 4 ml L-broth and the
suspension plated onto McConkey agar (Difco)
containing streptomycin at 20 μ g ml⁻¹ and ampicillin
at 300 μ g ml⁻¹. Plates were incubated overnight at
37°C and resulting colonies were checked for
merodiploidy by PCR using appropriate
oligonucleotides as primers.
- 3) Putative ETEC transconjugants were screened. 10
colonies were picked from McConkey agar plates and
grown overnight on L-Ampicillin (100 μ g/ml) agar.
The presence of Δ ompF gene was checked for by PCR
with primers TT1/TT2. The sequences of the primers
are given in Table 1 below.
- 4) The colonies were grown for 5 hr in L-broth.
- 5) Serial dilutions of the L-broth culture were set up
on:
 - a) No salt L-agar
 - b) No salt L-agar + 5% sucrose.
- 6) Colony counts showed 10⁵ more colonies grew on L-
agar than on L-agar + 5% sucrose, showing sucrose
selection worked.
- 7) Sucrose resistant colonies were screened for Δ ompF
gene by PCR with primers TT1/TT2. The sequences of

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the primers are given in Table 1 below. The screened colonies were grown overnight on L-Agar. 3 colonies out of 47 had the $\Delta ompF$ gene with no evidence of the wild-type *ompF* gene.

- 5 8) To further characterise putative ETEC Δ AroC Δ OmpC Δ OmpF colonies, they were plated on:
- a) L-Agar + 100 μ g/ml Ampicillin
 - b) L-Agar
 - c) L-Agar + 5% sucrose
- 10 $\Delta ompF$ colonies should be resistant to sucrose and sensitive to Ampicillin.
- 9) All three $\Delta ompF$ colonies were Ampicillin sensitive and sucrose resistant.
- 10) The colonies were microbanked and one colony was
15 chosen as a master stock.
- 11) For permanent storage, a bead from the master stock was inoculated into 1 ml L-broth, grown for 4 hr with shaking at 37°C and used to make agar slopes which were used to make freeze dried stocks. The
20 freeze dried stock of E1392/75/ 2A Δ aroC Δ OmpC Δ OmpF was designated PTL003. 20 ml of L-broth was added to the rest of the 1 ml culture and the culture was incubated overnight at 30°C. 1 ml of the overnight culture was transferred to each of three cryovials
25 and stored in liquid nitrogen.

Characterisation of E1392/75/2A Δ aroC Δ OmpC Δ OmpF

- 1) Growth requirements:
- Cells taken from the master stock produced in step
30 10 of the preceding section were streaked on L-Agar plate. At the same time 8 ml L-broth was inoculated for a chromosomal DNA prep for Southern blots. Both plate and liquid culture were grown overnight at 37°C.
- 35 Cells from the grown plate were streaked onto the

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following media and grown overnight at 37oc.

	<u>Medium</u>	<u>Growth</u>
5	L-Amp	No
	M9 minimal media	No
	M9 minimal + Aromix	Yes
	M9 + sulfathiazole (100 µg/ml)	No
10	M9 + sulfathiazole (100 µg/ml) + Aromix	Yes
	L-Agar + 50 µg/ml streptomycin	Yes
	L-Agar + 5% sucrose	Yes

15 As expected, the cells were Amp sensitive. The cells were resistant to sucrose, streptomycin and sulfathiazole, but required Aromix to grow on minimal media.

2) LPS analysis of PTL003:

20 a) A freeze dried vial of PTL003 was broken open. The culture was resuspended in L-Broth and plated on L-Agar for growth. Some cells were scraped off and stored in microbank.

25 b) More cells were scraped off and the LPS profile was analysed. There was no visible difference between the LPS profile of PTL003 and original E1392/75/2A strain.

3) Confirmation of deletions by PCR:

30 a) A scrape of cells was taken from the plate made in in 2a and streaked onto L-Agar and grown overnight.

b) Freshly grown cells were used for PCR with primers that flank the following genes: *aroC*, *htrA*, *ompC*, *ompF*, *ompR*.

35 c) PTL003 was shown to have deletions in *aroC*,

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ompC and *ompF* genes, but not in *htrA* or *ompR*.

- 4) Analysis of outer membrane protein profile of PTL003:

Outer membrane protein fractions were prepared from strains PTL010 (E1392/75/2A) and the deletion strains PTL002 and PTL003. A strain with a single *ompF* deletion and a strain with both *aroC* and *ompC* deletion were also analysed. Strains were grown under conditions of low osmolarity (no salt L-broth) and high osmolarity (no salt L-broth+15% sucrose). The OmpF protein product is normally expressed at low osmolarity whereas the OmpC product is expressed at high osmolarity. The OmpC and OmpF proteins have similar electroporetic mobilities. At both high and low osmolarities, the strain PTL003 lacks proteins in the OmpC/OmpF region when compared to the wild-type E1392/75/2A strain or to the Δ AroC Δ OmpC or Δ OmpF deletion strains. The results are shown in Figure 4.

20

- 5) Expression of CS1 and CS3 pili on CFA agar:
The expression of CS1 and CS3 pili in the deletion strains was examined. Equal numbers (2 A_{600nm} units) of bacteria strains PTL010, PTL001, PTL002 and PTL003 grown overnight at 37°C on CFA agar were subjected to SDS PAGE and analysed by Western blotting with monospecific polyclonal antibodies against CS1 or CS3. CS1 and CS3 pili were expressed equally well in four strains (Figure 5).

25

30

A CFAII-negative derivative of E1392/75/2A was constructed for use as a control. This was done by specific curing of the CS encoding plasmids from ETEC strain E1392/75-2A. A short fragment of DNA was amplified from the *cooB* gene using PCR with

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oligonucleotides CSA01 and CSA02 as primers and ligated into pGEM-T Easy plasmid vector (Trade Name, Promega) designed for the cloning of PCR products. The fragment was subcloned into pCVD442 by virtue of the *SalI* and *SphI* restriction enzyme sites. The pCVD442-*cooB* derivative was introduced into ETEC strain E1392/75/2A by conjugation from SM10 λ pir. Ampicillin resistant transconjugants are most likely to be the result of fusion of the pCVD442-*cooB* derivative with *cooB*-bearing plasmid. Such transconjugates were then grown on L-agar supplemented with 5% sucrose to select for loss of the *sacB* gene of pCVD442. Resulting colonies were tested for ampicillin sensitivity, and by PCR using CSA01 and CSA02 as primers. Three colonies of E1392/75/2A were included as positive controls among these PCRs. Two sucrose resistant colonies that gave no product with the PCR were streaked out onto fresh L-agar supplemented with 5% sucrose to obtain pure cultures. These were then grown in L-broth at 37°C for approximately 16 h and microbanked at -70°C. Loss of the CS1 encoding plasmid was confirmed by analysis of the plasmid profiles of the derivatives using agarose gel electrophoresis. Two derivatives were confirmed as CS1 negative, but were still CS3+.

6) Southern blotting of PTL003:
Structure of deletion mutations. Total DNA was extracted from cultures of the three deletion mutants grown from the microbanked stocks, digested with restriction endonuclease *EcoRV*, and the digested DNA subjected to pulsed field agarose gel electrophoresis. DNA was blotted from the gels onto Hybond N+ (Trade Name) nylon membranes and

hybridised with appropriate DNA probes according to standard procedures. Results (Figure 6) show that the hybridising chromosomal DNA fragments of the mutants are shorter than the wild-type, consistent with the mutations being deletions.

Confirmation of absence of Heat-Stable (ST) and Heat-Labile (LT) toxin genes in E.coli strain E1392/75-2A. For this the ST and LT-AB genes were used as DNA probes against total DNA from E1392/75-2A. Total DNA from the toxin positive ETEC strain E1393/75 was included as a positive control, while that from the laboratory *E.coli* strain JM109 was included as a negative. Hybridised membranes were left under Hyperfilm-ECL (Trade Name) for 1 h to obtain the maximum amount of signal. Probes were prepared using PCR with plasmid DNA extracted from E1392/75-2A as template and oligonucleotides EST01 and EST02 as primers for ST, or LT-R1 and LT-03 for LT-AB. There was no significant hybridisation with total DNA using either the LT-AB or the ST probe, despite obtaining a very intense signal from the positive control total DNA.

Confirmation of absence of pCVD442 sequences from the chromosome of deletion mutants. The plasmid pCVD442 was labelled and hybridised to total DNA from deletion mutants PTL001, PTL002 and PTL003 digested with *EcoRV*. Total DNA from ETEC strain E1392/75-2A was included as a control. A complex pattern of hybridising DNA fragments was obtained. But, there was no significant difference between the pattern obtained for the wild-type and that for the mutants, indicating that probably no residual pCVD442 nucleotide sequences were left in the genomes of the mutants. The complex pattern of

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hybridising fragments was most likely due to the pCVD442 probe hybridising with the plasmid DNA components of the E1392/75-2A strain and mutant derivatives.

5

Table 1 - PCR primers

Name	Target	Use	Sequence (5'-3')
TT1	<i>ompF</i>	Primer A for cloning	ATC TGT TTG TTG AGC TCA GCA ATC TAT TTG CAA CC
10 TT2	<i>ompF</i>	Primer B for cloning	TTT TTT GCC AGC ATG CCG GCA GCC ACG CGT AGT G
TT3	<i>ompF</i>	Primer C for cloning	CTC GAG GCT TAG CTC TAT TTA TTA CCC TCA TGG
TT4	<i>ompF</i>	Primer D for cloning	GAG CTA AGC CTC GAG TAA TAG CAC ACC TCT TTG
TT7	<i>ompC</i>	Primer A for cloning	TTG CTG GAA AGT CGA CGG ATG TTA ATT ATT TGT G
TT8	<i>ompC</i>	Primer B for cloning	GGC CAA AGC CGA GCT CAT TCA CCA GCG GCC CGA CG
15 TT9	<i>ompC</i>	Primer C for cloning	GCT AAG CCT CGA GTA ATC TCG ATT GAT ATC CG
TT10	<i>ompC</i>	Primer D for cloning	CTC GAG GCT TAG CGT TAT TAA CCC TCT GTT A

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TT19	aroC	Primer A for cloning	CCG CGC TCG CTC TAG AGT GAA CTG ATC AAC AAT A
TT20	aroC	Primer B for cloning	ATG CGC GCG AGA GCT CAA CCA GCG TCG CAC TTT G
TT21	aroC	Primer C for cloning	CTC GAG GCA TGC TGA ATA AAA CCG CGA TTG
TT22	aroC	Primer D for cloning	GCA TGC CCT CGA GGG CTCC GTT ATT GTT GTG
MGR169	CS1	Binds in CS1 sequence	TGA TTC CCT TTG TTG CGA AGG CGA A
MGR170	CS1	Binds in CS1 sequence	ATT AAG ATA CCC AAG TAA TAC TCA A
LT-R1	LT-AB	See text	GCT TTT AAA GGA TCC TAG TT
LT-03	LT-AB	See text	GGT TAT CTT TCC GGA TTG TC
EST01	ST	See text	CAT GTT CCG GAG GTA ATA TGA A
EST02	ST	See text	AGT TCC CTT TAT ATT ATT AAT A
CSA01	CS1	See text	TGG AGT TTA TAT GAA ACT AA
CSA02	CS1	See text	TGA CTT AGT CAG GAT AAT TG
CS3-01	CS3	See text	ATA CTT ATT AAT AGG TCT TT
CS3-02	CS3	See text	TTG TCG AAG TAA TTG TTA TA

15

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Table 2

5	Target gene	Sites used for cloning into pCVD442		Sites introduced for screening purposes	
		Site 1	Site 2	Site 3	Site 4
	aroC	XbaI	SacI	XhoI	SphI
	htrA	SalI	SphI	XhoI	XbaI
	ompC	SalI	SacI	BlpI	XhoI
	ompF	SacI	SphI	BlpI	XhoI
10	ompR	SalI	SacI	BlpI	SphI

EXAMPLE 2: SAFETY AND IMMUNOGENICITY OF ATTENUATED VACCINE STRAIN OF ENTEROTOXIGENIC E. COLI

15 **(Δ aroC/ Δ ompC/ Δ ompF) IN HUMAN VOLUNTEERS**

The study was designed to evaluate a candidate live attenuated vaccine strain of enterotoxigenic *E. coli*, namely the Δ aroC/ Δ ompC/ Δ ompF PTL003 described above.

20

Preparation of the vaccine seed lots

The bacterial strain was plated onto MacConkey agar for
 25 purity and for confirmation of identity, and 5 colonies used to inoculate a flask containing 200 ml of luria broth. After 8 hours incubation at +37°C, 30 ml of sterile glycerol was added to the broth culture and aliquots prepared (1 ml per vial). One hundred such vials were
 30 frozen at -70°C. These vials constituted the seed lot for the vaccine strain.

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Purity of the seed lot was ensured by selecting ten random vials, and testing them for bacterial purity and freedom from fungi. An additional three vials were tested to determine the number of bacteria in the vials using
5 standard plate count methods with serial dilutions of the culture broth.

Preparation of the vaccine

10 The vaccine was prepared fresh prior to each vaccination and all steps in the preparation of the inoculum carried out in a safety cabinet. The day prior to vaccination, 0.2 ml was spread onto the surface of luria agar plates using sterile cotton swabs to prepare the lawn of bacteria. The
15 same culture broth was streaked onto MacConkey and luria agar plates for purity. The agar plates were incubated at 37°C for 18 hours in a sealed container with tamper-resistant indicator tape to ensure that the plates were not tampered with during incubation. After incubation, the lawn
20 of bacteria was harvested with 5 ml of sterile phosphate buffered saline (PBS), and the optical density of the suspension measured. The appropriate volume of this suspension, corresponding to the desired dose, was then placed into unit dose bottles with 30 ml of bicarbonate
25 buffer and administered to the volunteers. An extra dose of vaccine was prepared and left in the laboratory, and immediately after the volunteers had been vaccinated the actual number of bacteria in each dose of vaccine was validated using standard colony count procedures with ten
30 fold dilutions of vaccine.

The procedure for diluting the bacteria was established during preliminary studies using lawn cultures prepared and incubated exactly as done for the vaccine preparations
35 administered to volunteers. Suspensions were made and the

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number of viable bacteria enumerated by colony counts of serial dilutions and related to the determined optical density. Based on these preliminary studies, a standard procedure was developed for preparing and validating the correct dilutions of bacteria in order to give the doses stated.

Preparation of buffer

10 A buffer consisting of sodium bicarbonate in water was used. For each dose of vaccine 150 ml of deionised water containing 2 gram of sodium bicarbonate was prepared and filter sterilised. 30 ml of the buffer was placed into 50 ml sterile vials and the dose of vaccine bacteria was added
15 to these vials. The remaining 120 ml of buffer was placed into separate sterile bottles. At the time of vaccination, the volunteers were first administered 120 ml of buffer, then a minute later, 30 ml of buffer containing the vaccine.

20

Vaccination schedule

Groups of volunteers were studied in a dose escalation manner. The first group of volunteers received a dose of
25 approximately 5×10^7 bacteria, the second a dose of approximately 5×10^9 and the third group a dose of approximately 5×10^8 .

The volunteers were given Ciprofloxacin 500 mg BID for
30 three days beginning on day 4. They were discharged on day 6, having had a haematology and chemistry screen for safety. Serum was saved for antibody measurement.

On days 9 and 14 the volunteers returned for follow-up
35 outpatient visits at which time an interval history was

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done and a blood sample was obtained for serological assays. In total, blood (40 ml) was collected for serology three times, prior to vaccination and on day 9 and day 14 after vaccination.

5

Laboratory Assay Procedures

Up to two faecal specimens were cultured each day while the volunteers were in hospital. For qualitative cultures, a
10 faecal swab was placed into Cary Blair transport media and taken to the laboratory where it was inoculated directly onto MacConkey agar and onto MacConkey agar containing antibiotics selective for the vaccine strain. Up to five colonies were shown to be agglutinated using antisera
15 specific for the vaccine strain. For quantitative culture (first specimen each day only) faecal specimens were weighed and diluted in PBS, with serial 10-fold dilutions up to 10^{-4} , and then 100 μ l of each dilution was spread onto MacConkey agar with antibiotics. Suspected colonies were
20 confirmed by agglutination with anti-O serum.

Serum was collected and saved for subsequent assay for antibody against CFA II antigens by ELISA and bactericidal antibody against the vaccine strain.

25

Peripheral blood mononuclear cells were separated from whole blood collected into citrate and washed. These cells were cultured at a density of 10^7 cells per ml in RPMI tissue culture medium at 37°C for 48 hours. After 48 hours
30 the supernatant was transferred to a cryovial and frozen at -20°C until it could be assayed for IgG and IgA antibody to CFA II by ELISA.

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Table 3 - Summary of the procedures of the protocol

	Day (Vaccination day is day 0)	pre	-1	0	1	2	3	4	5	6	9	14
5	Recruitment / screening	x										
	HCG (urine)	x				x						
	Training/ consent	x										
10	Inpatient stay		x	x	x	x	x	x	x	x		
	Vaccination			x								
	Outpatient visit	x									x	x
	Stool cultures - quantitative		x	x	x	x	x	x	x	x	x	x
15	Stool cultures - qualitative		x	x	x	x	x	x	x	x	x	x
	Serology		x								x	x
	CBC/Chem panel	x								x		
20	Ciprofloxacin 500mg BID for 3d							x	x	x		

Results:

25 No symptoms were seen at all actual doses of 6.8×10^7 and 3.7×10^8 cfu. At the higher dose of 4.7×10^9 1/6 volunteers experienced diarrhoea and 2/6 had mild abdominal cramps. Bacterial shedding was seen in all volunteers at the 5×10^9 cfu dose level from day 1 post vaccination until,

30 as per protocol, ciprofloxacin was started on day 4 after vaccination. This indicates good intestinal colonisation, which is indicative of the potential to induce a good immune response. At the two lower doses, vaccine strain was recovered from all volunteers on at least one time

35 point following vaccination but the duration of the excretion was reduced compared to that seen at the highest dose.

At the time of filing the application, the analysis of the

40 immune responses generated by the vaccine was incomplete.

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However, the IgA anti-CFA II responses in the culture supernatants of PBMNC purified from the blood of recipients of the highest dose of vaccine at day 0 (before vaccination) and days 7 and 10 post vaccination have been
5 analysed (see Figure 7). Supernatants were analysed by ELISA on assay plates coated with purified CFA II antigen. The OD values observed from the day 7 and day 10 samples were significantly higher than those from the pre-vaccination samples, demonstrating the induction of a
10 specific IgA response at these time points. As expected, the responses show a peak at day 7 and are reduced at day 10, consistent with the homing of primed IgA secreting B-cells from the blood to the mucosal effector sites of the Gut Associated Lymphoid Tissue.

15

Conclusions:

The attenuated live strain of ETEC (Δ aroC/ Δ ompC/ Δ ompF) has been shown to be well tolerated in healthy adult volunteers and to colonise the intestine in a manner
20 consistent with its utility as an oral vaccine to protect against travellers diarrhoea. It has also been demonstrated to elicit a specific mucosal immune response.

25

30

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT:

(A) NAME: PEPTIDE THERAPEUTICS LIMITED

(B) STREET: 100 Fulbourn Road

(C) CITY: Cambridge

10

(D) STATE: not applicable

(E) COUNTRY: United Kingdom

(F) POSTAL CODE (ZIP): CB1 9PT

(ii) TITLE OF INVENTION: ATTENUATED BACTERIA USEFUL IN VACCINES

15

(iii) NUMBER OF SEQUENCES: 6

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

20

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

25

APPLICATION NUMBER:

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 1690 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: aroC of E.coli

(ix) FEATURE:

(A) NAME/KEY: CDS

5

(B) LOCATION:492..1562

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

	GTCGACGCGG TGGATATCTC TCCAGACGCG CTGGCGGTTG CTGAACAGAA CATCGAAGAA	60
10	CACGGTCTGA TCCACAACGT CATTCCGATT CGTTCCGATC TGTTCGCGA CTTGCCGAAA	120
	GTGCAGTACG ACCTGATTGT CACTAACCCG CCGTATGTCG ATGCGAAGAT ATGTCCGACC	180
	TGCCAAACAA TACCGCCACG AGCCGGAAC TGGCCTGGCA TCTGGCACTG ACGGCCTGAA	240
	ACTGACGCGT CGCATTCTCG GTAACGCGGC AGATTACCTT GCTGATGATG GCGTGTGAT	300
	TTGTGAAGTC GGCAACAGCA TGGTACATCT TATGGAACAA TATCCGGATG TTCCGTTAC	360
15	CTGGCTGGAG TTTGATAACG GCGGCGATGG TGTGTTTATG CTCACCAAAG AGCAGCTTAT	420
	TGCCGCACGA GAACATTTCTG CGATTTATAA AGATTAAGTA AACACGCAAA CACAACAATA	480
	ACGGAGCCGT G ATG GCT GGA AAC ACA ATT GGA CAA CTC TTT CGC GTA ACC	530
	Met Ala Gly Asn Thr Ile Gly Gln Leu Phe Arg Val Thr	
	1 5 10	
20	ACC TTC GGC GAA TCG CAC GGG CTG GCG CTC GGC TGC ATC GTC GAT GGT	578
	Thr Phe Gly Glu Ser His Gly Leu Ala Leu Gly Cys Ile Val Asp Gly	
	15 20 25	
25	GTT CCG CCA GGC ATT CCG CTG ACG GAA GCG GAC CTG CAA CAT GAC CTC	626
	Val Pro Pro Gly Ile Pro Leu Thr Glu Ala Asp Leu Gln His Asp Leu	
	30 35 40 45	
	GAC CGT CGT CGC CCT GGG ACA TCG CGC TAT ACC ACC CAG CGC CGC GAG	674
30	Asp Arg Arg Arg Pro Gly Thr Ser Arg Tyr Thr Thr Gln Arg Arg Glu	
	50 55 60	
	CCG GAT CAG GTC AAA ATT CTC TCC GGT GTT TTT GAA GGC GTT ACT ACC	722
	Pro Asp Gln Val Lys Ile Leu Ser Gly Val Phe Glu Gly Val Thr Thr	
35	65 70 75	
	GGC ACC AGC ATT GGC TTG TTG ATC GAA AAC ACT GAC CAG CGC TCT CAG	770

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	Gly Thr Ser Ile Gly Leu Leu Ile Glu Asn Thr Asp Gln Arg Ser Gln	
	80 85 90	
	GAT TAC AGT GCG ATT AAG GAC GTT TTC CGT CCA GGC CAT GCC GAT TAC	818
5	Asp Tyr Ser Ala Ile Lys Asp Val Phe Arg Pro Gly His Ala Asp Tyr	
	95 100 105	
	ACC TAC GAA CAA AAA TAC GGT CTG CGC GAT TAT CGC GGC GGT GGA CGT	866
	Thr Tyr Glu Gln Lys Tyr Gly Leu Arg Asp Tyr Arg Gly Gly Gly Arg	
10	110 115 120 125	
	TCT TCC GCC CGC GAA ACC GCC ATG CGC GTG GCG GCA GGA GCT ATT GCC	914
	Ser Ser Ala Arg Glu Thr Ala Met Arg Val Ala Ala Gly Ala Ile Ala	
	130 135 140	
15	AAA AAA TAT CTC GCC GAG AAA TTT GGT ATT GAA ATC CGT GGC TGC CTG	962
	Lys Lys Tyr Leu Ala Glu Lys Phe Gly Ile Glu Ile Arg Gly Cys Leu	
	145 150 155	
20	ACC CAG ATG GGC GAC ATT CCG CTG GAT ATC AAA GAC TGG TCG CAG GTC	1010
	Thr Gln Met Gly Asp Ile Pro Leu Asp Ile Lys Asp Trp Ser Gln Val	
	160 165 170	
	GAG CAA AAT CCG TTT TTT TGC CCG GAC CCC GAC AAA ATC GAC GCG TTA	1058
25	Glu Gln Asn Pro Phe Phe Cys Pro Asp Pro Asp Lys Ile Asp Ala Leu	
	175 180 185	
	GAC GAG TTG ATG CGT GCG CTG AAA AAA GAG GGC GAC TCC ATC GGC GCT	1106
	Asp Glu Leu Met Arg Ala Leu Lys Lys Glu Gly Asp Ser Ile Gly Ala	
30	190 195 200 205	
	AAA GTC ACC GTT GTT GCC AGT GGC GTT CCT GCC GGA CTT GGC GAG CCG	1154
	Lys Val Thr Val Val Ala Ser Gly Val Pro Ala Gly Leu Gly Glu Pro	
	210 215 220	
35	GTC TTT GAC CGC CTG GAT GCT GAC ATC GCC CAT GCG CTG ATG AGC ATC	1202
	Val Phe Asp Arg Leu Asp Ala Asp Ile Ala His Ala Leu Met Ser Ile	

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	225	230	235	
	AAC GCG GTG AAA GGC GTG GAA ATT GGC GAC GGC TTT GAC GTG GTG GCG			1250
	Asn Ala Val Lys Gly Val Glu Ile Gly Asp Gly Phe Asp Val Val Ala			
5	240	245	250	
	CTG CGC GGC AGC CAG AAC CGC GAT GAA ATC ACC AAA GAC GGT TTC CAG			1298
	Leu Arg Gly Ser Gln Asn Arg Asp Glu Ile Thr Lys Asp Gly Phe Gln			
	255	260	265	
10				
	AGC AAC CAT GCG GGC GGC ATT CTC GGC GGT ATC AGC AGC GGG CAG CAA			1346
	Ser Asn His Ala Gly Gly Ile Leu Gly Gly Ile Ser Ser Gly Gln Gln			
	270	275	280	285
15	ATC ATT GCC CAT ATG GCG CTG AAA CCG ACC TCC AGC ATT ACC GTG CCG			1394
	Ile Ile Ala His Met Ala Leu Lys Pro Thr Ser Ser Ile Thr Val Pro			
	290	295	300	
	GGT CGT ACC ATT AAC CGC TTT GGC GAA GAA GTT GAG ATG ATC ACC AAA			1442
20	Gly Arg Thr Ile Asn Arg Phe Gly Glu Glu Val Glu Met Ile Thr Lys			
	305	310	315	
	GGC CGT CAC GAT CCC TGT GTC GGC ATC CGC GCA GTG CCG ATC GCA GAA			1490
	Gly Arg His Asp Pro Cys Val Gly Ile Arg Ala Val Pro Ile Ala Glu			
25	320	325	330	
	GCG AAT GCT GGC GAT CGT TTT AAT GGA TCA CCT GTT ACG GCA ACG GGC			1538
	Ala Asn Ala Gly Asp Arg Phe Asn Gly Ser Pro Val Thr Ala Thr Gly			
	335	340	345	
30				
	GCA AAA TGC CGA TGT GAA GAC TGA TATTCCACGC TGGTAAAAAA TGAATAAAAC			1592
	Ala Lys Cys Arg Cys Glu Asp *			
	350	355		
35	CGCGATTGCG CTGCTGGCTC TGCTTGCCAG TAGCGCCAGC CTGGCAGCGA CGCCGTGGCA			1652
	AAAAATAACC CAACCTGTGC CGGGTAGCGC CAAATCGA			1690

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 356 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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

Met Ala Gly Asn Thr Ile Gly Gln Leu Phe Arg Val Thr Thr Phe Gly
 1 5 10 15

15 Glu Ser His Gly Leu Ala Leu Gly Cys Ile Val Asp Gly Val Pro Pro
 20 25 30

Gly Ile Pro Leu Thr Glu Ala Asp Leu Gln His Asp Leu Asp Arg Arg
 35 40 45

20 Arg Pro Gly Thr Ser Arg Tyr Thr Thr Gln Arg Arg Glu Pro Asp Gln
 50 55 60

Val Lys Ile Leu Ser Gly Val Phe Glu Gly Val Thr Thr Gly Thr Ser
 25 65 70 75 80

Ile Gly Leu Leu Ile Glu Asn Thr Asp Gln Arg Ser Gln Asp Tyr Ser
 85 90 95

30 Ala Ile Lys Asp Val Phe Arg Pro Gly His Ala Asp Tyr Thr Tyr Glu
 100 105 110

Gln Lys Tyr Gly Leu Arg Asp Tyr Arg Gly Gly Gly Arg Ser Ser Ala
 115 120 125

35 Arg Glu Thr Ala Met Arg Val Ala Ala Gly Ala Ile Ala Lys Lys Tyr
 130 135 140

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Leu Ala Glu Lys Phe Gly Ile Glu Ile Arg Gly Cys Leu Thr Gln Met
 145 150 155 160

Gly Asp Ile Pro Leu Asp Ile Lys Asp Trp Ser Gln Val Glu Gln Asn
 5 165 170 175

Pro Phe Phe Cys Pro Asp Pro Asp Lys Ile Asp Ala Leu Asp Glu Leu
 180 185 190

10 Met Arg Ala Leu Lys Lys Glu Gly Asp Ser Ile Gly Ala Lys Val Thr
 195 200 205

Val Val Ala Ser Gly Val Pro Ala Gly Leu Gly Glu Pro Val Phe Asp
 210 215 220

15 Arg Leu Asp Ala Asp Ile Ala His Ala Leu Met Ser Ile Asn Ala Val
 225 230 235 240

Lys Gly Val Glu Ile Gly Asp Gly Phe Asp Val Val Ala Leu Arg Gly
 20 245 250 255

Ser Gln Asn Arg Asp Glu Ile Thr Lys Asp Gly Phe Gln Ser Asn His
 260 265 270

25 Ala Gly Gly Ile Leu Gly Gly Ile Ser Ser Gly Gln Gln Ile Ile Ala
 275 280 285

His Met Ala Leu Lys Pro Thr Ser Ser Ile Thr Val Pro Gly Arg Thr
 290 295 300

30 Ile Asn Arg Phe Gly Glu Glu Val Glu Met Ile Thr Lys Gly Arg His
 305 310 315 320

35 Asp Pro Cys Val Gly Ile Arg Ala Val Pro Ile Ala Glu Ala Asn Ala
 325 330 335

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Gly Asp Arg Phe Asn Gly Ser Pro Val Thr Ala Thr Gly Ala Lys Cys
340 345 350

Arg Cys Glu Asp *
5 355

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1713 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- 15 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: ompC of E.coli

- 20 (ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 491..1594

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

GTTAACAAGC GTTATAGTTT TTCTGTGGTA GCACAGAATA ATGAAAAGTG TGTAAGAAG 60
GGTAAAAAAA ACCGAATGCG AGGCATCCGG TTGAAATAGG GGTAAACAGA CATTGAGAAA 120
30 TGAATGACGG TAATAAATAA AGTTAATGAT GATAGCGGGA GTTATTCTAG TTGCGAGTGA 180
AGGTTTTGTT TTGACATTCA GTGCTGTCAA ATACTTAAGA ATAAGTTATT GATTTTAACC 240
35 TTGAATTATT ATTGCTTGAT GTTAGGTGCT TATTCGCCA TTCCGCAATA ATCTTAAAAA 300
GTTCCCTTGC ATTTACATTT TGAAACATCT ATAGCGATAA ATGAAACATC TTAAAAGTTT 360

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	TAGTATCATA TTCGTGTTGG ATTATTCTGC ATTTTGGGG AGAATGGACT TGCCGACTGA	420
	TTAATGAGGG TTAATCAGTA TGCAGTGGCA TAAAAAGCA AATAAAGGCA TATAACAGAG	480
5	GGTTAATAAC ATG AAA GTT AAA GTA CTG TCC CTC CTG GTC CCA GCT CTG	529
	Met Lys Val Lys Val Leu Ser Leu Leu Val Pro Ala Leu	
	360 365 370	
10	CTG GTA GCA GGC GCA GCA AAC GCT GCT GAA GTT TAC AAC AAA GAC GGC	577
	Leu Val Ala Gly Ala Ala Asn Ala Ala Glu Val Tyr Asn Lys Asp Gly	
	375 380 385	
	AAC AAA TTA GAT CTG TAC GGT AAA GTA GAC GGC CTG CAC TAT TTC TCT	625
15	Asn Lys Leu Asp Leu Tyr Gly Lys Val Asp Gly Leu His Tyr Phe Ser	
	390 395 400	
	GAC AAC AAA GAT GTA GAT GGC GAC CAG ACC TAC ATG CGT CTT GGC TTC	673
	Asp Asn Lys Asp Val Asp Gly Asp Gln Thr Tyr Met Arg Leu Gly Phe	
20	405 410 415	
	AAA GGT GAA ACT CAG GTT ACT GAC CAG CTG ACC GGT TAC GGC CAG TGG	721
	Lys Gly Glu Thr Gln Val Thr Asp Gln Leu Thr Gly Tyr Gly Gln Trp	
	420 425 430	
25	GAA TAT CAG ATC CAG GGC AAC AGC GCT GAA AAC GAA AAC AAC TCC TGG	769
	Glu Tyr Gln Ile Gln Gly Asn Ser Ala Glu Asn Glu Asn Asn Ser Trp	
	435 440 445 450	
30	ACC CGT GTG GCA TTC GCA GGT CTG AAA TTC CAG GAT GTG GGT TCT TTC	817
	Thr Arg Val Ala Phe Ala Gly Leu Lys Phe Gln Asp Val Gly Ser Phe	
	455 460 465	
	GAC TAC GGT CGT AAC TAC GGC GTT GTT TAT GAC GTA ACT TCC TGG ACC	865
35	Asp Tyr Gly Arg Asn Tyr Gly Val Val Tyr Asp Val Thr Ser Trp Thr	
	470 475 480	

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	GAC GTA CTG CCA GAA TTC GGT GGT GAC ACC TAC GGT TCT GAC AAC TTC	913
	Asp Val Leu Pro Glu Phe Gly Gly Asp Thr Tyr Gly Ser Asp Asn Phe	
	485 490 495	
5	ATG CAG CAG CGT GGT AAC GGC TTC GCG ACC TAC CGT AAC ACT GAC TTC	961
	Met Gln Gln Arg Gly Asn Gly Phe Ala Thr Tyr Arg Asn Thr Asp Phe	
	500 505 510	
	TTC GGT CTG GTT GAC GGC CTG AAC TTT GCT GTT CAG TAC CAG GGT AAA	1009
10	Phe Gly Leu Val Asp Gly Leu Asn Phe Ala Val Gln Tyr Gln Gly Lys	
	515 520 525 530	
	AAC GGC AAC CCA TCT GGT GAA GGC TTT ACT AGT GGC GTA ACT AAC AAC	1057
	Asn Gly Asn Pro Ser Gly Glu Gly Phe Thr Ser Gly Val Thr Asn Asn	
15	535 540 545	
	GGT CGT GAC GCA CTG CGT CAA AAC GGC GAC GGC GTC GGC GGT TCT ATC	1105
	Gly Arg Asp Ala Leu Arg Gln Asn Gly Asp Gly Val Gly Gly Ser Ile	
	550 555 560	
20	ACT TAT GAT TAC GAA GGT TTC GGT ATC GGT GGT GCG ATC TCC AGC TCC	1153
	Thr Tyr Asp Tyr Glu Gly Phe Gly Ile Gly Gly Ala Ile Ser Ser Ser	
	565 570 575	
25	AAA CGT ACT GAT GCT CAG AAC ACC GCT GCT TAC ATC GGT AAC GGC GAC	1201
	Lys Arg Thr Asp Ala Gln Asn Thr Ala Ala Tyr Ile Gly Asn Gly Asp	
	580 585 590	
	CGT GCT GAA ACC TAC ACT GGT GGT CTG AAA TAC GAC GCT AAC AAC ATC	1249
30	Arg Ala Glu Thr Tyr Thr Gly Gly Leu Lys Tyr Asp Ala Asn Asn Ile	
	595 600 605 610	
	TAC CTG GCT GCT CAG TAC ACC CAG ACC TAC AAC GCA ACT CGC GTA GGT	1297
	Tyr Leu Ala Ala Gln Tyr Thr Gln Thr Tyr Asn Ala Thr Arg Val Gly	
35	615 620 625	
	TCC CTG GGT TGG GCG AAC AAA GCA CAG AAC TTC GAA GCT GTT GCT CAG	1345

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	Ser Leu Gly Trp Ala Asn Lys Ala Gln Asn Phe Glu Ala Val Ala Gln	
	630 635 640	
	TAC CAG TTC GAC TTC GGT CTG CGT CCG TCC CTG GCT TAC CTG CAG TCT	1393
5	Tyr Gln Phe Asp Phe Gly Leu Arg Pro Ser Leu Ala Tyr Leu Gln Ser	
	645 650 655	
	AAA GGT AAA AAC CTG GGT CGT GGC TAC GAC GAC GAA GAT ATC CTG AAA	1441
	Lys Gly Lys Asn Leu Gly Arg Gly Tyr Asp Asp Glu Asp Ile Leu Lys	
10	660 665 670	
	TAT GTT GAT GTT GGT GCT ACC TAC TAC TTC AAC AAA AAC ATG TCC ACC	1489
	Tyr Val Asp Val Gly Ala Thr Tyr Tyr Phe Asn Lys Asn Met Ser Thr	
	675 680 685 690	
15		
	TAC GTT GAC TAC AAA ATC AAC CTG CTG GAC GAC AAC CAG TTC ACT CGT	1537
	Tyr Val Asp Tyr Lys Ile Asn Leu Leu Asp Asp Asn Gln Phe Thr Arg	
	695 700 705	
20	GAC GCT GGC ATC AAC ACT GAT AAC ATC GTA GCT CTG GGT CTG GTT TAC	1585
	Asp Ala Gly Ile Asn Thr Asp Asn Ile Val Ala Leu Gly Leu Val Tyr	
	710 715 720	
	CAG TTC TAA TCTCGATTGA TATCGAACAA GGGCCTGCGG GCCCTTTTTT	1634
25	Gln Phe *	
	725	
	CATTGTTTTT AGCGTACAAA CTCAGTTTTT TGGTGACTC TTGCGACCGT TCGCATGAGG	1694
30	ATAATCACGT ACGGAAATA	1713

(2) INFORMATION FOR SEQ ID NO: 4:

- 35 (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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

5 Met Lys Val Lys Val Leu Ser Leu Leu Val Pro Ala Leu Leu Val Ala
 1 5 10 15
 Gly Ala Ala Asn Ala Ala Glu Val Tyr Asn Lys Asp Gly Asn Lys Leu
 10 20 25 30
 Asp Leu Tyr Gly Lys Val Asp Gly Leu His Tyr Phe Ser Asp Asn Lys
 35 40 45
 15 Asp Val Asp Gly Asp Gln Thr Tyr Met Arg Leu Gly Phe Lys Gly Glu
 50 55 60
 Thr Gln Val Thr Asp Gln Leu Thr Gly Tyr Gly Gln Trp Glu Tyr Gln
 65 70 75 80
 20 Ile Gln Gly Asn Ser Ala Glu Asn Glu Asn Asn Ser Trp Thr Arg Val
 85 90 95
 Ala Phe Ala Gly Leu Lys Phe Gln Asp Val Gly Ser Phe Asp Tyr Gly
 25 100 105 110
 Arg Asn Tyr Gly Val Val Tyr Asp Val Thr Ser Trp Thr Asp Val Leu
 115 120 125
 30 Pro Glu Phe Gly Gly Asp Thr Tyr Gly Ser Asp Asn Phe Met Gln Gln
 130 135 140
 Arg Gly Asn Gly Phe Ala Thr Tyr Arg Asn Thr Asp Phe Phe Gly Leu
 145 150 155 160
 35 Val Asp Gly Leu Asn Phe Ala Val Gln Tyr Gln Gly Lys Asn Gly Asn
 165 170 175

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	Pro Ser Gly Glu Gly Phe Thr Ser Gly Val Thr Asn Asn Gly Arg Asp
	180 185 190
5	Ala Leu Arg Gln Asn Gly Asp Gly Val Gly Gly Ser Ile Thr Tyr Asp
	195 200 205
	Tyr Glu Gly Phe Gly Ile Gly Gly Ala Ile Ser Ser Ser Lys Arg Thr
	210 215 220
10	Asp Ala Gln Asn Thr Ala Ala Tyr Ile Gly Asn Gly Asp Arg Ala Glu
	225 230 235 240
	Thr Tyr Thr Gly Gly Leu Lys Tyr Asp Ala Asn Asn Ile Tyr Leu Ala
	245 250 255
15	Ala Gln Tyr Thr Gln Thr Tyr Asn Ala Thr Arg Val Gly Ser Leu Gly
	260 265 270
	Trp Ala Asn Lys Ala Gln Asn Phe Glu Ala Val Ala Gln Tyr Gln Phe
20	275 280 285
	Asp Phe Gly Leu Arg Pro Ser Leu Ala Tyr Leu Gln Ser Lys Gly Lys
	290 295 300
25	Asn Leu Gly Arg Gly Tyr Asp Asp Glu Asp Ile Leu Lys Tyr Val Asp
	305 310 315 320
	Val Gly Ala Thr Tyr Tyr Phe Asn Lys Asn Met Ser Thr Tyr Val Asp
	325 330 335
30	Tyr Lys Ile Asn Leu Leu Asp Asp Asn Gln Phe Thr Arg Asp Ala Gly
	340 345 350
	Ile Asn Thr Asp Asn Ile Val Ala Leu Gly Leu Val Tyr Gln Phe *
35	355 360 365

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(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1808 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: ompF of E.coli

(ix) FEATURE:

- 15 (A) NAME/KEY: CDS
(B) LOCATION: 457..1545

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

20

AAACTAATC CGCATTCTTA TTGCGGATTA GTTTTTCTT AGCTAATAGC ACAATTTTCA 60

TACTATTTTT TGGCATTCTG GATGTCTGAA AGAAGATTTT GTGCCAGGTC GATAAAGTTT 120

25 CCATCAGAAA CAAAATTTCC GTTTAGTTAA TTAAATATA AGGAAATCAT ATAAATAGAT 180

TAAAATTGCT GTAAATATCA TCACGTCTCT ATGGAAATAT GACGGTGTTC ACAAAGTTCC 240

TTAAATTTTA CTTTGGTTA CATATTTTTT CTTTGTGAAA CCAAATCTTT ATCTTTGTAG 300

30

CACTTTCACG GTAGCGAAAC GTTAGTTTGA ATGGAAAGAT GCCTGCAGAC ACATAAAGAC 360

ACCAAATCT CATCAATAGT TCCGTAAATT TTTATTGACA GAACTTATTG ACGGCAGTGG 420

35 CAGGTGTCAT AAAAAAACC ATGAGGGTAA TAAATA ATG ATG AAG CGC AAT ATT 474

Met Met Lys Arg Asn Ile

1

5

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	CTG GCA GTG ATC GTC CCT GCT CTG TTA GTA GCA GGT ACT GCA AAC GCT	522
	Leu Ala Val Ile Val Pro Ala Leu Leu Val Ala Gly Thr Ala Asn Ala	
	10 15 20	
5	GCA GAA ATC TAT AAC AAA GAT GGC AAC AAA GTA GAT CTG TAC GGT AAA	570
	Ala Glu Ile Tyr Asn Lys Asp Gly Asn Lys Val Asp Leu Tyr Gly Lys	
	25 30 35	
	GCT GTT GGT CTG CAT TAT TTT TCC AAG GGT AAC GGT GAA AAC AGT TAC	618
10	Ala Val Gly Leu His Tyr Phe Ser Lys Gly Asn Gly Glu Asn Ser Tyr	
	40 45 50	
	GGT GGC AAT GGC GAC ATG ACC TAT GCC CGT CTT GGT TTT AAA GGG GAA	666
	Gly Gly Asn Gly Asp Met Thr Tyr Ala Arg Leu Gly Phe Lys Gly Glu	
15	55 60 65 70	
	ACT CAA ATC AAT TCC GAT CTG ACC GGT TAT GGT CAG TGG GAA TAT AAC	714
	Thr Gln Ile Asn Ser Asp Leu Thr Gly Tyr Gly Gln Trp Glu Tyr Asn	
	75 80 85	
20	TTC CAG GGT AAC AAC TCT GAA GGC GCT GAC GCT CAA ACT GGT AAC AAA	762
	Phe Gln Gly Asn Asn Ser Glu Gly Ala Asp Ala Gln Thr Gly Asn Lys	
	90 95 100	
25	ACG CGT CTG GCA TTC GCG GGT CTT AAA TAC GCT GAC GTT GGT TCT TTC	810
	Thr Arg Leu Ala Phe Ala Gly Leu Lys Tyr Ala Asp Val Gly Ser Phe	
	105 110 115	
	GAT TAC GGC CGT AAC TAC GGT GTG GTT TAT GAT GCA CTG GGT TAC ACC	858
30	Asp Tyr Gly Arg Asn Tyr Gly Val Val Tyr Asp Ala Leu Gly Tyr Thr	
	120 125 130	
	GAT ATG CTG CCA GAA TTT GGT GGT GAT ACT GCA TAC AGC GAT GAC TTC	906
	Asp Met Leu Pro Glu Phe Gly Gly Asp Thr Ala Tyr Ser Asp Asp Phe	
35	135 140 145 150	
	TTC GTT GGT CGT GTT GGC GGC GTT GCT ACC TAT CGT AAC TCC AAC TTC	954

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	Phe Val Gly Arg Val Gly Gly Val Ala Thr Tyr Arg Asn Ser Asn Phe	
	155 160 165	
	TTT GGT CTG GTT GAT GGC CTG AAC TTC GCT GTT CAG TAC CTG GGT AAA	1002
5	Phe Gly Leu Val Asp Gly Leu Asn Phe Ala Val Gln Tyr Leu Gly Lys	
	170 175 180	
	AAC GAG CGT GAC ACT GCA CGC CGT TCT AAC GGC GAC GGT GTT GGC GGT	1050
10	Asn Glu Arg Asp Thr Ala Arg Arg Ser Asn Gly Asp Gly Val Gly Gly	
	185 190 195	
	TCT ATC AGC TAC GAA TAC GAA GGC TTT GGT ATC GTT GGT GCT TAT GGT	1098
	Ser Ile Ser Tyr Glu Tyr Glu Gly Phe Gly Ile Val Gly Ala Tyr Gly	
	200 205 210	
15	GCA GCT GAC CGT ACC AAC CTG CAA GAA GCT CAA CCT CTT GGC AAC GGT	1146
	Ala Ala Asp Arg Thr Asn Leu Gln Glu Ala Gln Pro Leu Gly Asn Gly	
	215 220 225 230	
20	AAA AAA GCT GAA CAG TGG GCT ACT GGT CTG AAG TAC GAC GCG AAC AAC	1194
	Lys Lys Ala Glu Gln Trp Ala Thr Gly Leu Lys Tyr Asp Ala Asn Asn	
	235 240 245	
	ATC TAC CTG GCA GCG AAC TAC GGT GAA ACC CGT AAC GCT ACG CCG ATC	1242
25	Ile Tyr Leu Ala Ala Asn Tyr Gly Glu Thr Arg Asn Ala Thr Pro Ile	
	250 255 260	
	ACT AAT AAA TTT ACA AAC ACC AGC GGC TTC GCC AAC AAA ACG CAA GAC	1290
	Thr Asn Lys Phe Thr Asn Thr Ser Gly Phe Ala Asn Lys Thr Gln Asp	
30	265 270 275	
	GTT CTG TTA GTT GCG CAA TAC CAG TTC GAT TTC GGT CTG CGT CCG TCC	1338
	Val Leu Leu Val Ala Gln Tyr Gln Phe Asp Phe Gly Leu Arg Pro Ser	
	280 285 290	
35	ATC GCT TAC ACC AAA TCT AAA GCG AAA GAC GTA GAA GGT ATC GGT GAT	1386
	Ile Ala Tyr Thr Lys Ser Lys Ala Lys Asp Val Glu Gly Ile Gly Asp	

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	295	300	305	310	
	GTT GAT CTG GTG AAC TAC TTT GAA GTG GGC GCA ACC TAC TAC TTC AAC				1434
	Val Asp Leu Val Asn Tyr Phe Glu Val Gly Ala Thr Tyr Tyr Phe Asn				
5		315	320	325	
	AAA AAC ATG TCC ACC TAT GTT GAC TAC ATC ATC AAC CAG ATC GAT TCT				1482
	Lys Asn Met Ser Thr Tyr Val Asp Tyr Ile Ile Asn Gln Ile Asp Ser				
		330	335	340	
10	GAC AAC AAA CTG GGC GTA GGT TCA GAC GAC ACC GTT GCT GTG GGT ATC				1530
	Asp Asn Lys Leu Gly Val Gly Ser Asp Asp Thr Val Ala Val Gly Ile				
		345	350	355	
15	GTT TAC CAG TTC TAA TAGCACACCT CTTTGTAA TGCCGAAAA ACAGGACTTT				1585
	Val Tyr Gln Phe *				
		360			
	GGTCCTGTTT TTTTATACC TTCCAGAGCA ATCTCACGTC TTGCAAAAAC AGCCTGCGTT				1645
20	TTCATCAGTA ATAGTTGGAA TTTTGTAAT CTCCGTTAC CCTGATAGCG GACTTCCCTT				1705
	CTGTAACCAT AATGGAACCT CGTCATGTTT GAGAACATTA CCGCCGCTCC TGCCGACCCG				1765
25	ATTCTGGGCC TGGCCGATCT GTTTCGTGCC GATGAACGTC CCG				1808

(2) INFORMATION FOR SEQ ID NO: 6:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 362 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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Met Met Lys Arg Asn Ile Leu Ala Val Ile Val Pro Ala Leu Leu Val
 1 5 10 15
 Ala Gly Thr Ala Asn Ala Ala Glu Ile Tyr Asn Lys Asp Gly Asn Lys
 5 20 25 30
 Val Asp Leu Tyr Gly Lys Ala Val Gly Leu His Tyr Phe Ser Lys Gly
 35 40 45
 10 Asn Gly Glu Asn Ser Tyr Gly Gly Asn Gly Asp Met Thr Tyr Ala Arg
 50 55 60
 Leu Gly Phe Lys Gly Glu Thr Gln Ile Asn Ser Asp Leu Thr Gly Tyr
 65 70 75 80
 15 Gly Gln Trp Glu Tyr Asn Phe Gln Gly Asn Asn Ser Glu Gly Ala Asp
 85 90 95
 Ala Gln Thr Gly Asn Lys Thr Arg Leu Ala Phe Ala Gly Leu Lys Tyr
 20 100 105 110
 Ala Asp Val Gly Ser Phe Asp Tyr Gly Arg Asn Tyr Gly Val Val Tyr
 115 120 125
 25 Asp Ala Leu Gly Tyr Thr Asp Met Leu Pro Glu Phe Gly Gly Asp Thr
 130 135 140
 Ala Tyr Ser Asp Asp Phe Phe Val Gly Arg Val Gly Gly Val Ala Thr
 145 150 155 160
 30 Tyr Arg Asn Ser Asn Phe Phe Gly Leu Val Asp Gly Leu Asn Phe Ala
 165 170 175
 Val Gln Tyr Leu Gly Lys Asn Glu Arg Asp Thr Ala Arg Arg Ser Asn
 35 180 185 190
 Gly Asp Gly Val Gly Gly Ser Ile Ser Tyr Glu Tyr Glu Gly Phe Gly

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	195	200	205
	Ile Val Gly Ala Tyr Gly Ala Ala Asp Arg Thr Asn Leu Gln Glu Ala		
	210	215	220
5	Gln Pro Leu Gly Asn Gly Lys Lys Ala Glu Gln Trp Ala Thr Gly Leu		
	225	230	235 240
	Lys Tyr Asp Ala Asn Asn Ile Tyr Leu Ala Ala Asn Tyr Gly Glu Thr		
10	245	250	255
	Arg Asn Ala Thr Pro Ile Thr Asn Lys Phe Thr Asn Thr Ser Gly Phe		
	260	265	270
15	Ala Asn Lys Thr Gln Asp Val Leu Leu Val Ala Gln Tyr Gln Phe Asp		
	275	280	285
	Phe Gly Leu Arg Pro Ser Ile Ala Tyr Thr Lys Ser Lys Ala Lys Asp		
	290	295	300
20	Val Glu Gly Ile Gly Asp Val Asp Leu Val Asn Tyr Phe Glu Val Gly		
	305	310	315 320
	Ala Thr Tyr Tyr Phe Asn Lys Asn Met Ser Thr Tyr Val Asp Tyr Ile		
25	325	330	335
	Ile Asn Gln Ile Asp Ser Asp Asn Lys Leu Gly Val Gly Ser Asp Asp		
	340	345	350
30	Thr Val Ala Val Gly Ile Val Tyr Gln Phe *		
	355	360	

CLAIMS

1. A bacterium attenuated by a non-reverting mutation in each of the *aroC* gene, the *ompF* gene and the *ompC* gene.
2. A bacterium according to claim 1 which infects by the oral route.
3. A bacterium according to claim 1 which is from the genera *Escherichia*, *Salmonella*, *Vibrio*, *Haemophilus*, *Neisseria*, *Yersinia*, *Bordetella* or *Brucella*.
4. A bacterium according to claim 3 which is a strain of *Escherichia coli*, *Salmonella typhimurium*, *Salmonella typhi*, *Salmonella enteritidis*, *Salmonella choleraesuis*, *Salmonella dublin*, *Haemophilus influenzae*, *Neisseria gonorrhoeae*, *Yersinia enterocolitica*, *Bordetella pertussis* or *Brucella abortus*.
5. A bacterium according to claim 4 which is a strain of enterotoxigenic *E.coli* (ETEC).
6. A bacterium according to any one of the preceding claims which is further attenuated by a mutation in a fourth gene.

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7. A bacterium according to claim 6 wherein the fourth gene is *aroA*, *aroD*, *aroE*, *pur*, *htrA*, *galE*, *cya*, *crp*, *phoP* or *surA*.
- 5 8. A bacterium according to any one of the preceding claims, wherein the mutation in each gene is a defined mutation.
9. A bacterium according to any one of the preceding
10 claims, wherein the mutation in each gene is deletion of the entire coding sequence.
10. A bacterium according to any one of the preceding
15 claims which has been genetically engineered to express a heterologous antigen.
11. A bacterium according to claim 10, wherein expression of the antigen is driven by the *nirB* promoter or the *htrA* promoter.
- 20 12. A vaccine comprising a bacterium as defined in any one of the preceding claims and a pharmaceutically acceptable carrier or diluent.
- 25 13. A bacterium as defined in any one of claims 1 to 11 for use in a method of vaccinating a human or animal.
- 30 14. An enterotoxigenic *E.coli* cell attenuated by a non-reverting mutation in each of the *aroC* gene, the

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ompF gene and the *ompC* gene, for use in a method of vaccinating a human or animal against diarrhoea.

15. Use of a bacterium as defined in any one of claims
5 1 to 11 for the manufacture of a medicament for
vaccinating a human or animal.
16. A method of raising an immune response in a
mammalian host, which comprises administering to
10 the host a bacterium attenuated by a non-reverting
mutation in each of the *aroC* gene, the *ompF* gene
and the *ompC* gene.

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Fig.1.

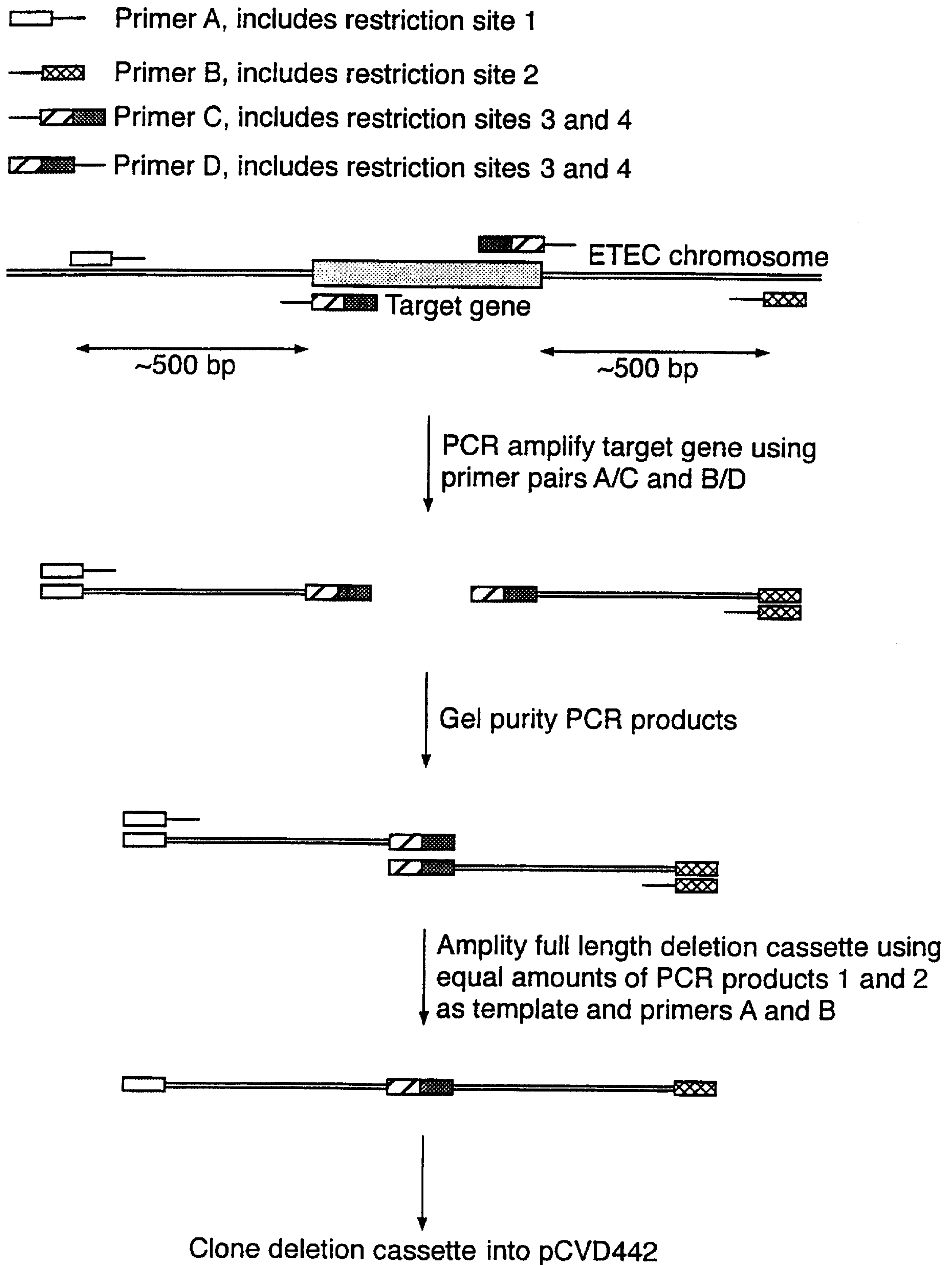


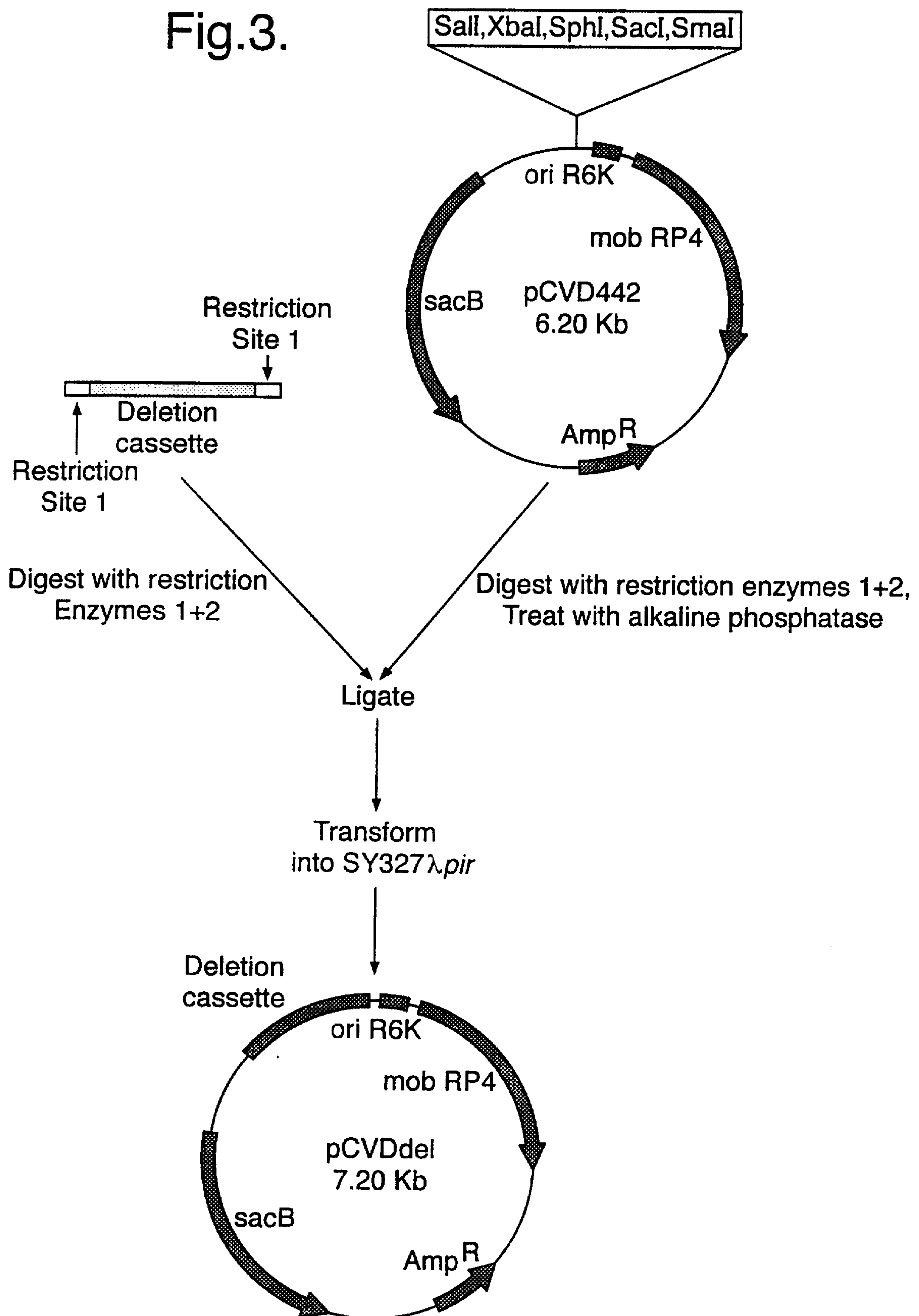
Fig.2.

aroC	
w.t.	AAACACAACAATAACGGAGCGTGATG---TAAAAATGAATAAAACCGCGATTG CG
deletion	<u>AAACACAACAATAACGGAGCCCTCGAGGCATGCTGAATAAAATGAATAAAACCGCGATTG CG</u>
htrA	
w.t.	TGTTAATCGAGAXTGAAATACATGAA---AGTAACTCTCCCTCAACCCCTTCCT GAA
deletion	<u>TGTTAATCGAGAXTGAAATACCTCGAGCTAGACTCCCTCAACCCCTTCCT GAA</u>
ompC	
w.t.	ATATAACAGAGGGTTAATAACATGAAA---CAGTTCTAA TCTCGATTGATATCGAAC
deletion	<u>ATATAACAGAGGGTTAATAACGCTAAGCCTCGAGTAA TCTCGATTGATATCGAAC</u>
ompF	
w.t.	AAACCATGAGGGTAATAAAATAATGATGAAGCGC---CCAGTTCTAA TAGCACACCTCTTTGTTA
deletion	<u>AAACCATGAGGGTAATAAAATAgagCTAAGCCTCGAGCAGTTCTAA TAGCACACCTCTTTGTTA</u>
ompR	
w.t.	CGAACCTTTGGGAGTACAAACAATGCAA---AAGCATGA GGCGATTGCGCTTCTCGCCA
deletion	<u>CGAACCTTTGGGAGTACAAACAGCTAAGCGCATGCGA GGCGATTGCGCTTCTCGCCA</u>

Stop and start codons
restriction enzyme sites introduced
primer binding sites
Lower case – extra n.t added to primers to avoid primer dimer formation
--- wild type gene
N.B. aroC deletion removes 16 n.t. 3' to the stop codon

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Fig.3.



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Fig.4.

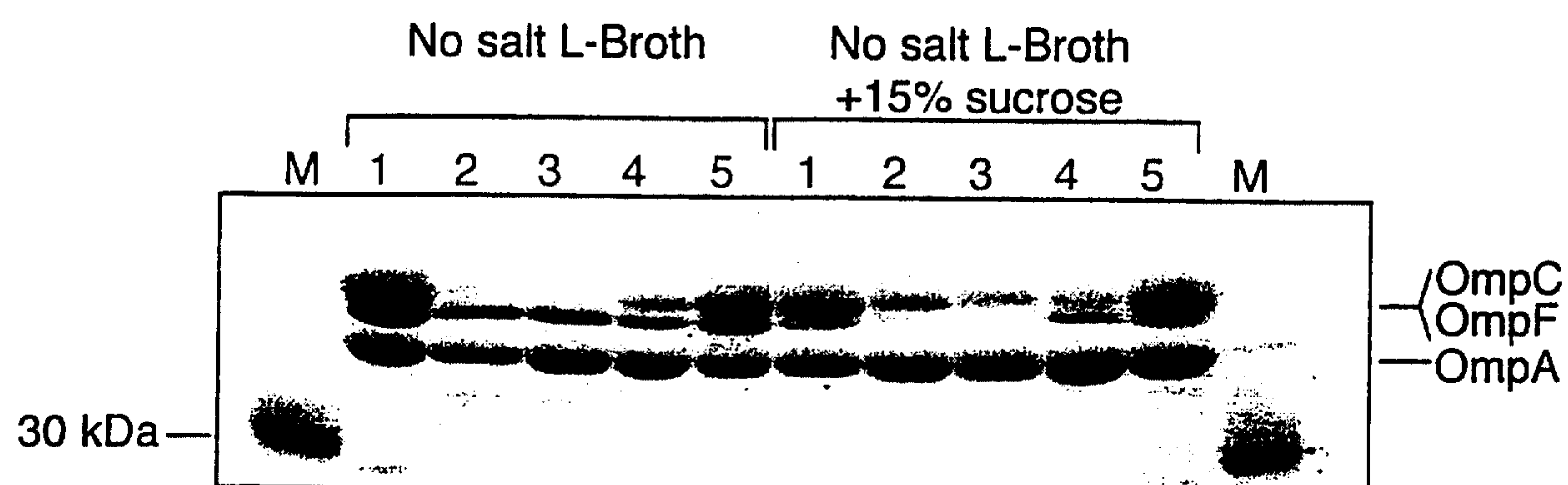
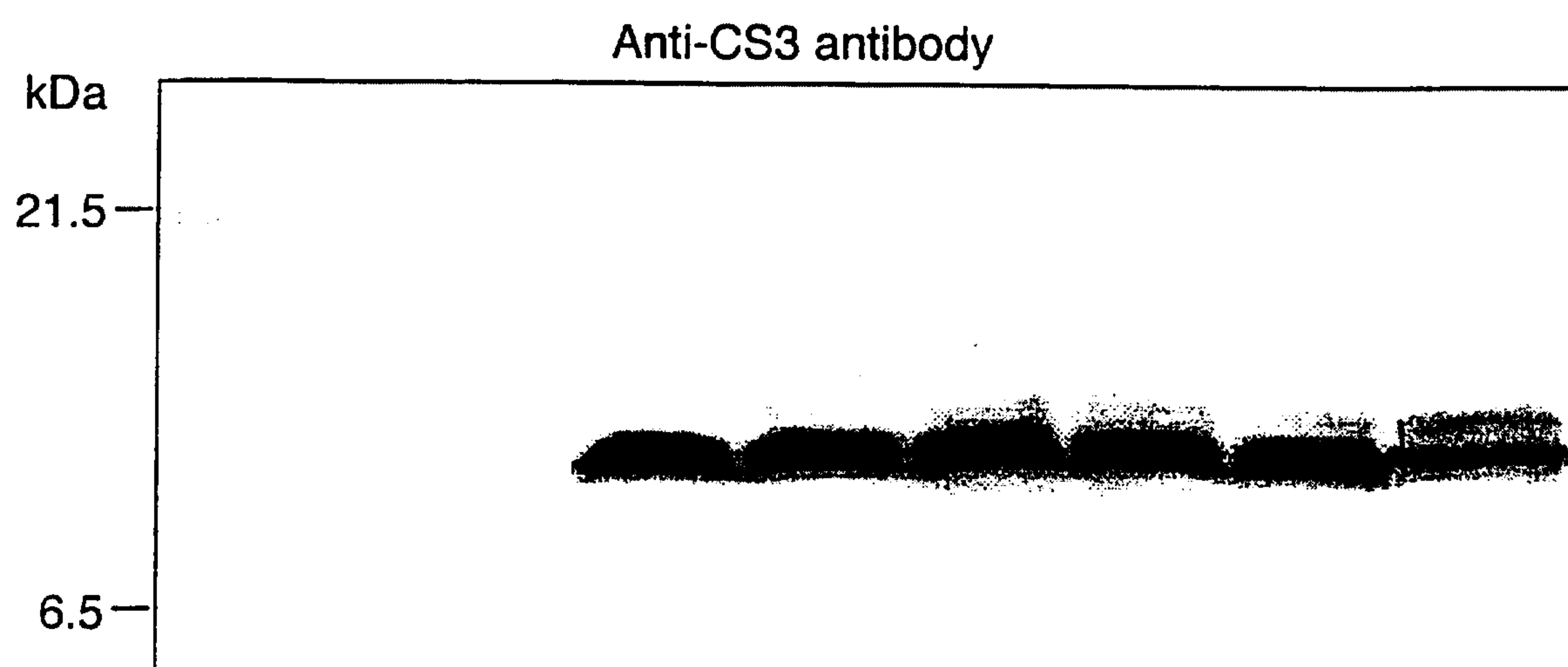
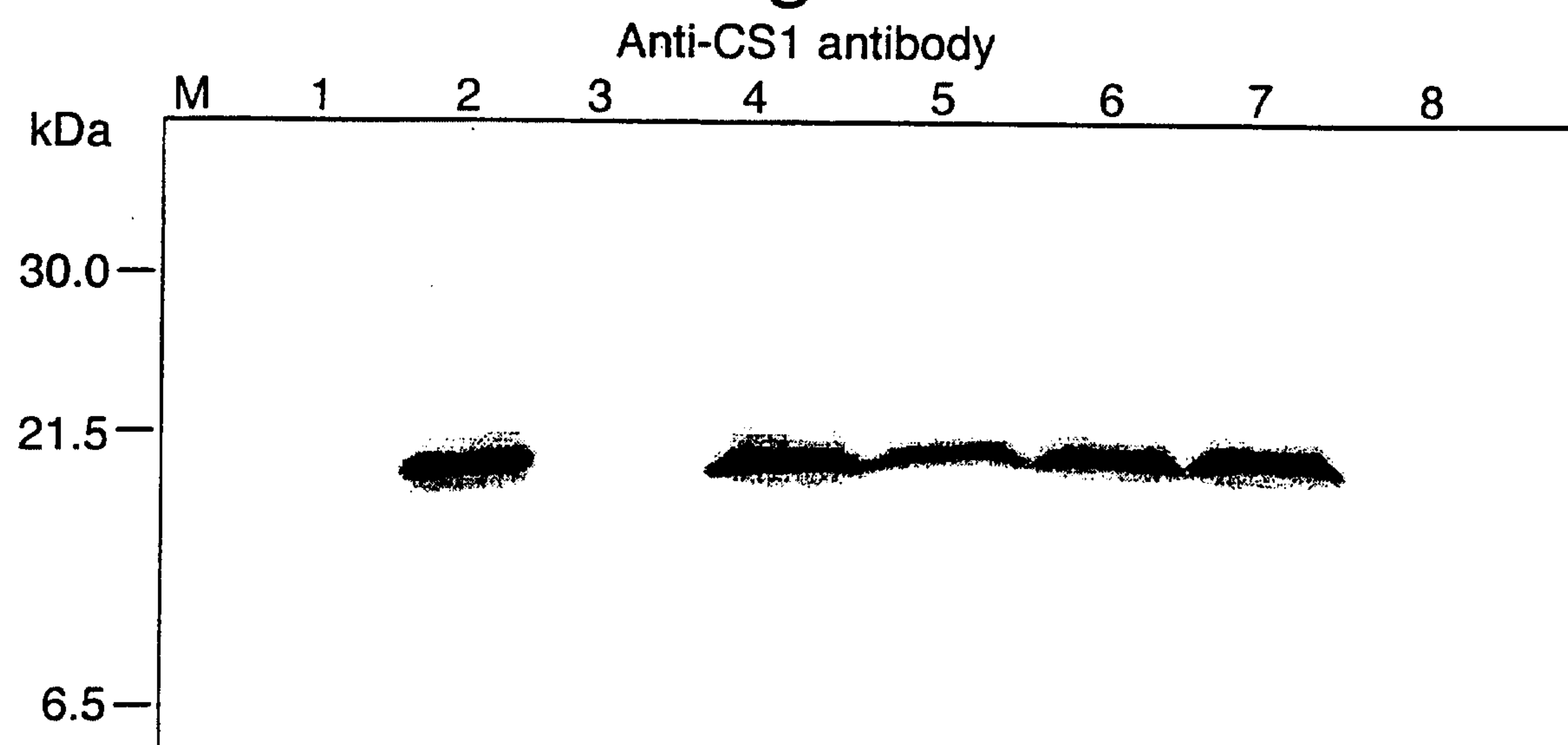
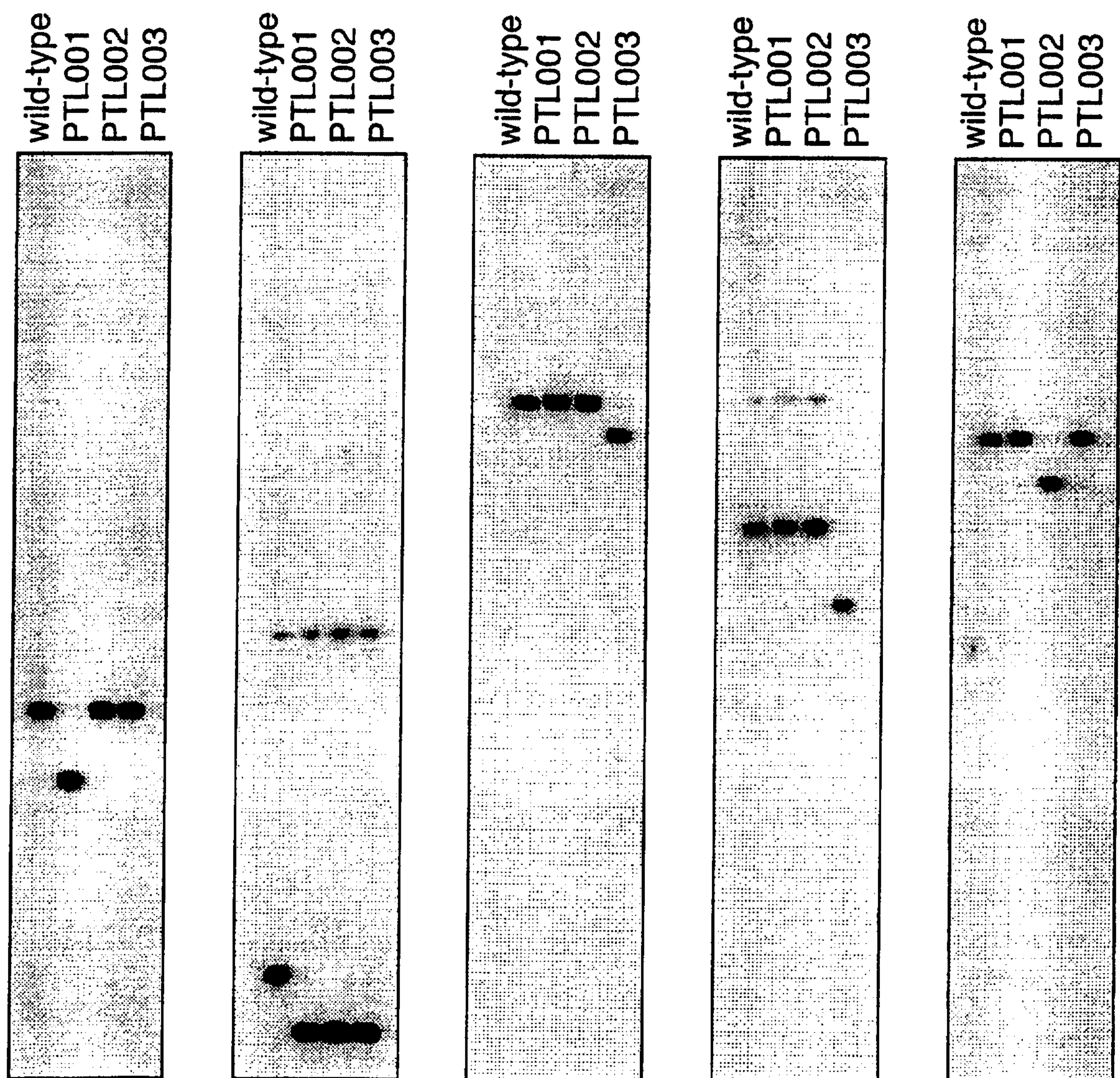


Fig.5.



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Fig.6.



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