TWO-COMPONENT SYSTEM THAT CONTROLS BACTERIAL MEMBRANE SYNTHESIS

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Notice: This patent is based on a continued prosecution application filed under 37 CFR 1.53(d) and is subject to the twenty-year patent term provisions of 35 U.S.C. 154(a)(2).

Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

Appl. No.: 09/439,226
Filed: Nov. 12, 1999

Prior Publication Data
US 2001/0016349 A1 Aug. 23, 2001

Int. Cl. C12Q 1/18; C12Q 1/68; C12Q 1/02; C12N 1/00; C12N 1/20

U.S. Cl. 435/32; 435/6; 435/7; 435/29; 435/32; 435/243; 435/871

Field of Search 424/249.1, 250.1; 435/252.1, 29, 32, 6, 7, 243, 871

References Cited
U.S. PATENT DOCUMENTS
6,180,111 B1 * 1/2001 Stein et al.

FOREIGN PATENT DOCUMENTS
WO 99/59625 11/1999

OTHER PUBLICATIONS
Pettit, R.K. et al, Molecular Microbiology, 6(6), 729–734.


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ABSTRACT

The present invention discloses a mutant Neisseria having extensive membrane blebbing, both an indicium and a cause of virulence in the gonococcus and meningococcus. Methods are disclosed for making and characterizing the mutant, bmrRS. Methods are disclosed for isolating bmrRS membranes for use as a vaccine. Methods are also disclosed for the use of the mutant for determining the virulence of clinical samples of N. gonorrhoeae and N. meningitidis. Methods are also disclosed for the screening of antibiotics targeted to virulent Neisseria.

5 Claims, 4 Drawing Sheets
BASR
NM: MRVLLVEDDA MIAEAVSASL KGQYAVDWW KNGARLPLPS IMT*.......
GC: MRVLLVEDDA MIA*AVSASL KGQYAVDWW KNGAQVAAAA AAQPYDLMLL
NC: MRVLLVEDDA MIAEAVSANL KGQYAVDWW KNGAQVAAAA AAQPYDLMLL

DLGGLRGRDL DV
NM: MFVPL(BasS)....
GC: DLGLPGRDL DVLEIRAGG CTVPVLIYTA RDDLYSRLNG LDGADDYIV
NC: DLGLPGRDL DVLEIRAGG CTVPVLIYTA RDDLYSRLNG LDGADDYIV

GC: KPFDMARFKA RMRAVLRRGS GQAACLNSG ALSLNFPATQ VEIIAERGQV
NC: KPFQDMARFKA RMRAVLRRGS GQAACLNSG ALSLNFPATQ VEIIAERGQV

GC: ALSNQFFSVL QALLARGPGI LSRSDSEDKV YGWGGEVESN AVDOFLHGLC
NC: ALSNKEFAVL QALLARGPGI LSRSDLEDKI YGWGGEVESN AVDOFLHALR

GC: KKLGKESIQN VRGVCWLMPR PDAV*
NC: KKLGKENIQN VRGVCWLVPG AV*

BASS
NM: MFVPLAM LAGMFSYET HETEAALQDD
GC: MPDFFPKLKL HLSQVRISLA LNMFFPVLM LAGMFSYET HETEAALQDD
NC: MRNLNLMKLS GLSQVLRICL LMMFPLML VAGTFSYYDT HFEAEELQDD

NM: LRLQALYLYL PSDKPFLPGE GDGDTRIFVQ MPQQEPDFVVS LPALHADDGLH
GC: LRLQALYLYL PSDKPFLPGE GDGDTRILVQ MPQQEPDFVVS LPALHADDGLH
NC: LRLQALYLYL PSDKPFLPGE GDGDTRILVQ MPQQEPDFVVS LPALHADDGLH

NM: TLQADDDDDY YRYIERTTEQ GRIAVQCGNE YREDLAADAA RQSVPLLAQ
GC: TLQADDDDDY YRYIERTTEQ GRIAVQCGNE YREDLAADAA RQSVPLLAQ
NC: TLQADDDDDY YRYIERTTEQ GRIAVQCGNE YREDLAADAA RQSVPLLAQ

NM: LPLMILLTWV ITHAMRPVR KLSQSLQQR VHDLSALSDV WIPSEIRGQV
GC: LPLMILLTWV ITHAMRPVR KLSQSLQQR VHDLSALSDV WIPSEIRGQV
NC: LPLMILLTWV ITHAMRPVR KLSQSLQQR VHDLSALSDV WIPSEIRGQV

NM: TAINLKLKLKRA DEDIRHRQRF VADAHERLRT PMAVISLQAE RILMMLSLPPD
GC: TAINLKLKLKRA DEDIRHRQRF VADAHERLRT PMAVISLQAE RILMMLSLPPD
NC: TAINLKLKLKRA DEDIRHRQRF VADAHERLRT PMAVISLQAE RILMMLSLPPD

NM: AARQSAVLQQ SIRRNKXELE QLLALAREQS DETPLXATTF GLQSRFRQVL
GC: AARQSAVLQQ SIRRNKXELE QLLALAREQS DETPLXATTF GLQSRFRQVL
NC: AARQSAVLQQ SIRRNKXELE QLLALAREQS DETPLXATTF GLQSRFRQVL

NM: QELMPAELEK QRQIGAVVGG DVESADATE ITYLLKTXTD NAVRRYTPPEG
GC: QELMPAELEK QRQIGAVVGG DVESADATE ITYLLKTXTD NAVRRYTPPEG
NC: QELMPAELEK QRQIGAVVGG DVESADATE ITYLLKTXTD NAVRRYTPPEG

NM: RIDLGFDEG KLYAVWVEDN GNGIPSEERA RVLDPFYYRIL GSTQQQTGLG
GC: RIDLGFDEG KLYAVWVEDN GNGIPSEERA RVLDPFYYRIL GSTQQQTGLG
NC: RIDLGFDEG KLYAVWVEDN GNGIPSEERA RVLDPFYYRIL GSTQQQTGLG

NM: LSIADTLAKK YGGHLELTDS RRGHGGLLIR ALLEDKETLK*
GC: LSIADTLAKK YGGHLELTDS RRGHGGLLIR ALLEDKETLK*

Fig. 2
TWO-COMPONENT SYSTEM THAT CONTROLS BACTERIAL MEMBRANE SYNTHESIS

The U.S. government sponsored the research leading to this invention under grants AI18384 and AI43924 from the National Institutes of Health. The Government retains certain rights in this invention.

BACKGROUND OF THE INVENTION

Neisseria gonorrhoeae ("gonococcus") and N. meningitidis ("meningococcus") are Gram-negative diplococci that are strictly human pathogens. N. gonorrhoeae causes primarily urethritis in males and pelvic inflammatory disease in females. N. meningitidis is the causative agent of middle ear infections and meningitis.

As is commonly found in other bacterial pathogens, strains of Neisseria sp. vary greatly in pathogenicity. Treatment and outcome of neisserial infections are dictated by pathogenicity. For example, N. meningitidis is frequently found in the throats of normal humans, where it can reside as a commensal without causing symptoms. However, virulent strains of N. meningitidis may cause a fulminating meningitis, resulting in brain damage or death before treatment can control the disease. Diagnostic methods to date have not been useful in distinguishing the mild, commensal Neisseria meningitidis from the virulent strains.

The standard method of diagnosing a bacterial disease is culturing, followed by identification by immunoreactivity, morphology, and biochemical reactions. In the case of neisserial pathogens, because of its fastidious growth requirements, the organism has often lost viability and will no longer grow in culture once isolated from the patient. U.S. Pat. No. 4,446,230 discloses a test method and bacterial strain for the laboratory diagnosis of gonorrhea. This strain can be maintained in a laboratory and will become transformed by exogenous neisserial DNA, even from a non-viable clinical sample. The transformation corrects an induced specific growth requirement, thereby permitting the strain to grow. However, this test does not distinguish virulent from non-virulent strains.

In vivo models of N. gonorrhoeae infection using male human volunteers have been done to elucidate the factors that contribute to bacterial virulence. However, such studies are costly and limited in scope. Recent tissue culture models of gonococcal infection have begun to define the interactions between the bacterium and the host. In brief, it is evident that the bacteria attach and invade human urethral epithelial cells, a niche that probably represents the primary site of infection during the course of urethritis. Gonococci reside and replicate within vacuoles within these cells. Infected cells can rupture or be shed into the urethral lumen, releasing gonococci to invade neighboring epithelial cells or to be excreted in the urine. Several gonococcal components, including Pil, Opa proteins and lipooligosaccharide (LOS) have been implicated in the ability of gonococcus to attach to and invade host cells, and implicated in the pathogenesis of gonococcal infection.

Our current knowledge clearly suggests that the gonococcus exists within different environments during the course of infection, such as extra- and intra-cellular and vascular locations. It is also likely that the site of infection of N. gonorrhoeae, the genital tract, differs significantly between males and females. How N. gonorrhoeae adapts to these different conditions is not well understood. It has been observed that a gonococcus thought to be pathogenic quickly converts to a less virulent type under the conditions of culture that are used to identify the bacterium and to test for antibiotic sensitivity.

Current treatment of neisserial infections is with broad spectrum antibiotics. However, treatment with broad spectrum antibiotics leads to the disturbance of the natural microflora, leaving the patient susceptible to infections with such opportunistic pathogens as Candida albicans and Gardnerella. An antibiotic targeted specifically at pathogenic, rather than commensal Neisseria, would avoid this complication. It is currently difficult to test virulent clinical isolates of Neisseria to determine each strain's sensitivity to targeted-specificity antibiotics because of the difficulty of maintaining virulence during growth of the strains in culture. Therefore, such an antimicrobial sensitivity test as is disclosed in U.S. Pat. No. 5,789,173 may not be useful in determining neisserial sensitivity to antibiotics.

If the factors that convert a commensal, mildly or non-pathogen Neisseria meningitidis or N. gonorrhoeae into a pathogenic, invasive bacterium were known, it would be possible to use the identification of such factors as an aid for the diagnosis and therapy of neisserial disease. There is a need to determine these so that they can be used as a target in screening bacteriostatic or bacteriocidal drugs that are selectively effective against virulent Neisseria.

BRIEF SUMMARY OF THE INVENTION

The present invention provides a mutant Neisseria bacterium having excessive outer membrane. The bacterium may be Neisseria gonorrhoeae or Neisseria meningitidis.

The present invention also provides a method of identifying a pathogenic bacterium comprising culturing under identical conditions 1) a mutant Neisseria bacterium having excessive outer membrane, 2) a wild type Neisseria and 3) a clinical sample taken from a patient suspected of having a neisserial infection; examining the extent of blebbing in each cultured bacterium; and comparing the extent of blebbing of the clinical sample to that to the bacterium having excessive outer membrane and to that of the wild type Neisseria so as to determine the pathogenicity of the clinical sample.

The present invention further provides a method of identifying an inhibitor compound of virulent Neisseria providing a culture containing a bacterium having a mutation which results in blebbing of the outer membrane and the test inhibitor compound, and providing a culture containing a wild type bacterium having no blebbing and the test inhibitor; and comparing the growth of the mutant bacterium to that of the wild type in order to identify an inhibitor compound that inhibits the growth of the mutant to a greater degree than the inhibitor compound inhibits the growth of the wild type.

The present invention further provides individual, isolated proteins coded for or otherwise under the control of the two-component system, the presence of which quickly and easily determined and is indicative of virulence.

DESCRIPTION OF THE DRAWINGS

FIG. 1 shows a diagram of the bnr locus of N. gonorrhoeae (NG), N. meningitidis (NM) and N. cinerea (NC).

FIG. 2 shows the alignment of the amino acid sequences of the BnrR open reading frames (ORF) from N. gonorrhoeae (GC) (SEQ ID NO:2, SEQ ID NO:3) , N. meningitidis (NM) (SEQ ID NO:1) and N. cinerea (NC) (SEQ ID NO:4); and the alignment of the amino acid sequences of the
BmrS ORFs from GC (SEQ ID NO:6), NM (SEQ ID NO:5), and NC (SEQ ID NO:7).

FIGS. 3A–F show scanning electron micrographs of wild type and mutant N. gonorrhoeae.

FIGS. 4A–D shows scanning electron micrographs of wild type and mutant N. meningitidis.

DETAILED DESCRIPTION OF THE INVENTION

Neisseria gonorrhoeae and N. meningitidis are strictly human pathogens. Current knowledge of the pathogenesis of these organisms suggests that these bacteria encounter different environments within the host during infection. However, little is known of how Neisseria sense and respond to these different environments or what systems contribute to virulence. Many bacteria respond to changes in their environment through changes in the expression level of particular genes. Two-component regulatory systems are now recognized as significant mediators of signaling in bacteria, relaying environmental signals that produce changes in gene expression patterns. During signal transduction by a typical two-component regulator, a membrane sensor protein detects a specific environmental stimulus presumably either through a direct interaction with a ligand or through conformational changes induced by changes in environmental conditions. Such a regulatory system might be useful as a diagnostic marker of virulence in Neisseria.

However, information regarding signaling within the gonococcus is limited. Previously a two-component regulator-like system was reported in pilus gene expression, although the environmental cue to which the system responds is unknown. Since membrane blebbing has been found to be associated with virulence, it was thought that a quantitative assay of the amount of membrane would be indicative of increased virulence. In order to further investigate a possible two-component regulator-mediated signaling pathway in N. gonorrhoeae, the polymerase chain reaction (PCR) with degenerate oligonucleotide primers was used to amplify a region from the DNA-binding component of a novel N. gonorrhoeae two-component regulator.

This regulatory system is known to be present in other Neisseria species and to have a role in outer-membrane blebbing. The term “blebbing” is used to mean the bubble- or blister-like extrusion of membrane from the surface of the bacterial cell. The term “high-blebbing” is used to describe bacteria showing such extensive outer membrane formation. “Blebs” are easily separated from the outer membrane by mild physical manipulation, such as differential centrifugation.

Outer membrane bleb formation by Neisseria meningitidis and N. gonorrhoeae has long been recognized as an important factor in Neisseria infection, particularly that due to N. meningitidis. Numerous membrane blebs were found at the tissue surface during ultrastructural analysis of cervical gonorrhoea (Evans et al. J. Infect. Dis. (1977) 136:248–255) and a meningococcus recovered from the plasma of an infected patient contained multiple, long membranous protrusions typical of blebbing (Brandtzaeas et al. J. Infect. Dis. (1989) 155:195–204). Lipooligosaccharide (LOS), which is a component of the blebs shed by the gonococcus and meningococcus, has major physiological effects during septis and meningitis caused by N. meningitidis and the plasma LOS levels are closely correlated to prognosis. Furthermore, compartmentalization of LOS production correlates with the clinical presentation in meningococcal infection. LOS levels in patients defined as having septicaemia showed high levels in plasma (median 3500 ng/ml) and low levels in cerebrospinal fluid, while with patients with meningitis, LOS was detectable in the plasma of three out of 19 patients and in the CSF in 18 of 19 patients, with median levels of 2500 ng/ml.

From these observations, it is possible that blebbing is both the indiction and the cause of pathogenicity in Neisseria. Agents that control or inhibit blebbing may be useful in therapy against Neisseria infections. However, the standard laboratory cultures of Neisseria typically show little or no blebbing after repeated laboratory passage and are therefore not useful in screening for agents that control or inhibit blebbing. Identification of the degree of blebbing of newly isolated strains from clinical samples may be an early indication of the virulence of the pathogen and whether immediate, aggressive therapy is necessary.

Factors affecting the blebbing process are poorly understood. Strains of meningococcal serogroup A, B and C release membrane blebs in the log phase of growth but not in the lag phase, suggesting some form of regulation. The identification of a putative regulatory system, the mutation of which produces clear differences in the blebbing process is potentially of great interest to improvement of therapeutic strategies for treatment of Neisseria infections in which blebbing is a serious complication.

During the course of investigation, mutation of the genes controlling blebbing was successful, and after insertion into a strain, the resultant high-blebbing bacterium is a “super blebler” that shows extensive membrane blebbing in all culture conditions. Unlike virulent, high-blebbing clinical isolates of Neisseria, these super blebler mutants, termed bmrRS, are stable and do not revert to non-blebbing strains on repeated culture. For this reason, they are particularly useful as controls to estimate the virulence of clinical samples, for the production of neisserial membranes for use as a vaccine and for screening of antibiotics targeted at virulent Neisseria.

Outer membrane proteins and LOS are known to be useful as vaccines. (See, e.g., U.S. Pat. No. 5,902,586 issued May 11, 1999 to Jennings et al.) Because the super bleblers produce two to four times as much outer membrane as the wild type strains, they are a particularly useful source of neisseria vaccine material. Thus, a novel two-component regulatory system has been identified in N. gonorrhoeae, N. meningitidis and N. cinerea. DNA sequence analysis suggested that the system may be non-functional in laboratory strains of Neisseria. However, experimental mutation of the system in each of the three species resulted in increased membrane production in the mutant compared to the wild type. This correlated with an increase in outer membrane blebbing. These data suggest that outer membrane blebbing, which is regarded as an important contributor to the pathogenesis of neisserial diseases, is regulated as part of a coordinated response to environmental cues.

The references identified in the specification are incorporated herein by reference to the extent that they supplement, explain, provide a background for or teach methodology, techniques, and/or compositions employed herein.

The following examples are included to demonstrate the preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples that follow represent techniques discovered by the inventors to function well in the practice of the invention and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments
that are disclosed and still obtain a like or similar result without departing from the concept and scope of the invention. More specifically, it will be apparent that certain agents, such as DNA constructs, that are both chemically and biologically equivalent may be substituted for the agents described herein while the same or equivalent results would be achieved. It will also be apparent that the techniques are not limited by the order in which the steps are carried out. All such substitutions and modifications apparent to those skilled in the art are deemed to be within the spirit and scope of the invention as defined by the appended claims.

The present invention provides a target for control of the neisserial membrane synthesis. The present invention also provides a quantitative assay of neisserial membrane. The present invention also provides a neisserial bacterium with increased amounts of membrane, more specifically, blebs of outer membrane, which bacterium is useful as a production cell for isolation of vaccine related membrane proteins and glycolipids. The present invention also provides a standard with which to compare clinical isolates of Neisseria spp. in order to estimate the pathogenicity of such isolates. The present invention also provides a screening assay for drugs that are specifically effective against virulent strains of Neisseria.

The invention is illustrated by the following examples.

**EXAMPLE 1**

Construction of the Super Blesser

A. Bacterial strains and plasmids

Wild type Neisseria strains used were *N. gonorrhoeae* 1291, *N. meningitidis* NMB and *N. cinerea* 601. Neisseria were grown on solid GC Base medium (Difco Laboratories, Detroit) supplemented with amino acids and vitamins. For growth of kittenancytis resistant Neisseria, BHI agar was used (Difco) supplemented with 2.5% FCS. Liquid Neisseria cultures were grown in proteose peptone broth (proteose peptone No. 3, Difco) 15 grams per liter; soluble starch (Difco) 1 gram per liter, dibasic potassium phosphate 4 grams per liter, monobasic potassium phosphate 1 gram per liter, sodium chloride 15 grams per liter or in Mose’s defined medium.

*Escherichia coli* strain XL-1-Blue (Stratagene, LaJolla, Calif.) was used to maintain plasmids and was grown in liquid culture using LB broth or on solid medium using LB agar. Antibiotics were used at the following concentrations: ampicillin 100 µg/ml; kanamycin 50 µg/ml (*E. coli*) or 25 µg/ml (*E. coli* K); erythromycin 150 µg/ml (*E. coli*) or 1 µg/ml (*Neisseria*).

pBluescript (Stratagene), pUC18 (Pharmacia, Piscataway, N.J.) and pCRIII (Invitrogen, Carlsbad, Calif.) were used as cloning vectors. PUC4K (Pharmacia) was used as a source of kanamycin cassette. Erythromycin resistance cassette was derived from pKermC plasmids (Zhou, D. G. and M. A. Apicella (1996) Gene 171:133–134.).

Plasmid DNA was prepared using Qiagen plasmid DNA preparation (Qiagen Inc., Chatsworth, Calif.). Chromosomal DNA was prepared from plate grown bacteria which were scraped from the plate into 100 µl of phosphate buffered saline (PBS). Cells were then pelleted by spinning for one minute at top speed in a microfuge before resuspension in 250 µl of TNE (10 mM Tris—HCl pH 8, 100 mM NaCl, 1 mM EDTA) 25 l of 10% SDS were added followed by 25 µl of Proteinase K (25 mg/ml). The reaction was incubated overnight at 55°C and then extracted twice with phenol and then twice with phenol/chloroform. DNA was precipitated by addition of 10 µl 3M sodium acetate pH 5.4 and 1 ml 100% ethanol, lifted from the tube on the end of a pipette tip and washed by repeated transfer to tubes containing 500 µl 70% ethanol. Washed DNA samples were air dried before resuspension in 100 µl TE RNase.

DNA sequencing was performed at the University of Iowa DNA sequencing facility using dye terminator sequencing chemistry with AmpliTaq DNA polymerase, FS enzyme (PE Applied Biosystems, Foster City, Calif.). The reactions were run on and analyzed using an Applied Biosystems Model 373A stretch fluorescent automated sequencer.

PCR was performed using Boehringer Mannheim (Philadelphia) reagents according to the protocols provided. PCRDOP was performed using degenerate oligonucleotides as described by Wren et al (FEMS Microbial Letters (1992) 99:267–291). PCR products were directly cloned using the TA cloning system (Invitrogen) according to the manufacturer’s instructions.

B. Results of PCR amplification and cloning in *N. gonorrhoeae*

PCR using the degenerate oligonucleotides described by Wren produced a product of the expected size (322 bp) from a *N. gonorrhoeae* genomic DNA template. The product was cloned and numerous clones were analyzed through DNA sequencing. This revealed that the PCR product contained many different DNA fragments that were clearly not from two-component regulator genes, which is in contrast to the report in which the same primer sequences amplified a region of two-component systems from numerous other bacteria without this apparent non-specific effect.

A single clone of 322 bp was obtained which through analysis of its deduced amino acid sequence clearly contained the 5’ region of the DNA-binding component of a two-component regulatory system. This clone was not identical to the pLAB system of *N. gonorrhoeae*.

Using the 322 bp PCR product as a probe, several genomic libraries were screened, but no positive signals were observed, although a Southern blot of *N. gonorrhoeae* genomic DNA identified many different fragments to which the probe stringently hybridized. Attempts to clone these fragments, all of which were 4 kbp or greater in size, failed. These fragments, which might have contained the entire two-component system sought, could not be cloned, suggesting that the system was toxic to *E. coli* when carried at high copy number. However, two Sau3AI fragments which were identified by the Southern analysis were successfully cloned and found to contain open reading frames (ORFs) that encoded for the majority of a two-component regulator, based on their deduced amino acid sequence. Successive cloning of other small genomic fragments, containing small parts of the two-component regulator, followed by reconstruction, produced a sequence contig of 3.97 kbp that contained the two ORFs of the putative ORF encoding the regulator and partial ORFs upstream and downstream of the system. We have named this two-component system bmr (for bacterial membrane regulator, see below). The upstream ORF was homologous to a hypothetical membrane protein of *Bacillus subtilis* (Genbank submission number P42308) and the downstream ORF was homologous to the cytoplasmic axial filament protein CofA, of *E. coli* (FIG. 1). *N. gonorrhoeae* bmr has been deposited with the American Type Culture Collection (P.O. Box 1549, Manassas, Va., 20108) under accession number PTA-801.

Comparison of the deduced amino acid sequence of the putative two-component regulator to the amino acid sequences of the Genbank database revealed homology to numerous other two-component regulators. The highest degree of homology was to the BshRS system of *E. coli* and *Salmonella typhimurium* and the putative Bas homologue in *Haemophilus influenzae*. The Bas system of *E. coli* and *S. typhimurium* is involved in regulation of lipopolysaccharide (LPS) substitution by phosphate and aminorabinoisose, that in the case of *S. typhimurium* is implicated in LPS changes during the course of infection. This is the putative regulation frequently found in bacteria. Biochemical capabilities of the bacteria are modified and extended by the duplication and
subsequent mutation of genes, resulting in gene products with considerable degrees of homology, but having different functions and characteristics, as is seen in the bmr and bmr gene products.

An interesting feature of *N. gonorrhoeae* bmr was the presence of a stop-codon at the fourteenth codon position of the DNA-binding component that was predicted to terminate translation of this ORF at that point (FIG. 2.)

Cloning of bmr from other Neisseria

*N. meningitidis* is closely related to *N. gonorrhoeae* and *N. cinerea* is a non-pathogenic member of the Neisseria genus. Southern blots of genomic DNA from these two bacteria, using the *N. gonorrhoeae* 322 bp PCR product as a probe, identified stringently hybridizing restriction fragments in each of these organisms. Using a strategy similar to that described above, the bmr locus was cloned from *N. meningitidis* and *N. cinerea*. The predicted amino acid sequences of the three loci are highly homologous, strongly suggesting that the equivalent locus from the three species had been cloned (FIG. 2). However, in *N. meningitidis*, a G to T substitution altered the premature TAA stop-codon of *N. gonorrhoeae* to a GAA glutamate codon. In *N. cinerea*, the codon was also for glutamate, but read GAG. However, the *N. meningitidis* locus contains a 591 bp deletion compared to both *N. gonorrhoeae* and *N. cinerea* that results in deletion of the 3' 486 bp of the putative DNA-binding component-encoding ORF, the integric region, and the 5' 69 bp of the putative sensor-encoding ORF (FIG. 1.) In addition, other nucleotide differences in the *N. meningitidis* locus immediately preceding the deletion cause frame shifts of the BmrR ORF (FIG. 2.) Thus, *N. meningitidis* is not predicted to encode a BmrR protein. Although the 5' 23 codons of the sensor-encoding ORF are deleted, an alternative coding region may allow translation of a near-full length sensor protein in *N. meningitidis*. The bmr locus was amplified by PCR from numerous *N. meningitidis* strains, including several from serotypes A, C and W 135. The primers used (5' CCGTCCGGTGTGTTCAATC 3' (SEQ ID NO:8) and 5' CCCTTCCGTGATCTCCTCAC 3' (SEQ ID NO:9)) amplify the region starting 166 bp upstream of the initiating codon of the deleted BmrR ORF and ending 200 bp upstream of the termination codon of the putative BmrR ORF. All of these PCR reactions produced a band of the same size as that from strain NMB (i.e., approximately 600 bp smaller than the fragment amplified from *N. gonorrhoeae*) (data not shown) suggesting that the deletion in bmr is common to many, if not all, *N. meningitidis* strains. *N. meningitidis* BmrR has been named the Neisseria Type Culture Collection (P.O. Box 1549, Manassas, Va., 20108) under accession number PTA-800.

*N. gonorrhoeae* bmr's insertion mutant was constructed by insertion of an erthrocytin resistance cassette at the site indicated in FIG. 1. An insertion mutant of *N. meningitidis* was constructed by insertion of a kanamycin resistance cassette within the sensor coding region (FIG. 1). The locus was mutated in *N. cinerea* by deletion of an internal BsrGI fragment and insertion of a kanamycin resistance cassette in its place. This mutation deletes the 3' 418 bp of bmrR and the 5' 565 bp of bmrR (FIG. 1).

FIG. 2 shows the alignment of the amino acid sequences of the BmrR and BmRS ORFs from the three Neisseria spp. The GC BmrR ORF contains a stop codon (*) at the fourteenth codon. The NM BmrR sequence contains a small deletion compared to the GC and NC sequences after the 34th codon, resulting in a frameshift (denoted by the amino acid sequence written on the line above). The amino acid sequences in frame with the N-terminal NM BmrR ORF is closed by the presence of a stop codon (*). Following the frameshift, the insertion results in the amino acids FVPLA in the NM sequence that are absent from both GC and NC. Following this is a large deletion that removes the remainder of the BmrR ORF and the N-terminal 23 codons of the BmRS ORF. Outside of this region, the three sequences are highly homologous.

**EXAMPLE 2**

Characteristics of the Super Blembers

A. Chemical analysis of the outer membrane of the super blembers

The effect of the bmr mutation on several parameters was investigated by comparison of the *N. gonorrhoeae* wild-type and the mutant. Overnight cultures (10 ml) were killed by the addition of 0.5% phenol for two hours and outer membrane enriched samples were isolated as described by Zollinger et al., International Symposium, Hanasaari, Espoo, Finland (1991). Samples were analyzed by SDS-PAGE on a 6–15% gradient gel. LOS was isolated by phenol/chloroform/petroleum ether extraction as described by Galanos et al. Eur. J. Biochem. (1969) 94:25–249 and analyzed as described by Rent et al. J. Biol. Chem. (1990) 270:27151–9.

The growth rate and outer membrane protein profile of the mutant were unaltered from the wild type.

Because of the homology of the Neisseria locus to the previously characterized bas locus of *E. coli* and *S. typhimurium* and the involvement of this system in LPS modulation in those bacteria, LOS was isolated from wild type and mutant and analyzed by mass spectrometry. No difference was found, showing that despite the homology, the system functioned differently in Neisseria and those other bacteria.

B. Morphology of the super blembers

For scanning electron microscopy (SEM), samples of proteose peptone broth cultures were taken directly without centrifugation or washing. Processing included treatment with 1% osmium tetroxide prior to dehydration through a graded ethanol series, with a final clearance in hexamethyldisilane (HMDS from Polysciences, Inc. Warrington, Pa.). After coating with gold-palladium, the specimens were viewed on an S-4000 Hitachi scanning electron microscope at 5 kV accelerating voltage.

For transmission electron microscopy, the samples were dehydrated in a graded ethanol series prior to embedment in LR White resin (Ted Pella, Inc., Redding, Calif.) and sectioned to approximately 85 nm thickness using an ultramicrotome. Samples were counter-stained with 5% uranyl acetate for viewing with an H-7000 Hitachi transmission electron microscope at 75 kV accelerating voltage.

SEM analysis revealed that the wild type and mutant bacteria differed with the mutant lacking new features observed to be distinct lipopolysaccharides with a smooth appearance (FIGS. 3A and 3B) However, the mutant produced large numbers of blebs. (FIGS. 3C and 3D) Shedding of outer-membrane particles (blebbing) is a characteristic of Neisseria. In these analyses the mutant bacteria were blebbing to a much higher degree than the wild type. In addition, many mutant dyscoollci were joined to others by membraneous connections (FIGS. 3C and 3E). When viewed by TEM, the connections did not contain electron dense material of the cytoplasm, suggesting that they consist of hollow membrane tubules joining pairs of lipopolysaccharides. (FIG. 3F). These connections were not observed with the wild type.

The morphological changes seen in the *N. meningitidis* bmr mutant are shown in FIG. 4A. FIGS. 4A and 4B show the parent strain of *N. meningitidis* NMB. FIG. 4C and FIG. 4D show the *N. meningitidis* NMBbmr mutant. As observed with the mutant *N. gonorrhoeae*, these mutants were also joined by membraneous connections. The bmr mutant of *N. cinerea* showed similar changes in morphology.

C. Phospholipid Analysis

The electron micrographs suggested that the mutants had alterations in their membranes that resulted in an increase in
membrane material. To test this hypothesis, wild type and mutant *N. gonorrhoeae* were grown in the presence of 14C-labeled acetate to label phospholipid and allow quantitation of membrane produced by the bacteria.

Bacteria were grown in 5 ml of Morse’s defined medium supplemented with 4 μCi/ml 14C-labeled acetate. *N. meningitidis* was grown for 5 hours and *N. gonorrhoeae* was grown for 20 hours at 37°C in a shaking incubator to achieve the appropriate bacterial growth. For *N. gonorrhoeae*, the blebs were separated from the bacteria by introducing the cultures with 2.5 ml of 10% sucrose in balanced salt buffer in centrifuge tubes and centrifuging in a SW-40 Ti rotor (Beckman, Palo Alto, Calif.) at 10,000 rpm at 4°C, for 30 minutes. The supernatant above the sucrose cushion was transferred to fresh centrifuge tubes. The sucrose cushion was removed for scintillation counting. The supernatant was centrifuged in a SW-40 Ti rotor at 25,000 rpm (100,000g) for 75 minutes at 4°C to pellet blebs. The supernatant from this spin was removed for scintillation counting. The centrifuge tube was partially dried using cotton swabs.

Labeled phospholipids were isolated by extraction with 100 μl of chloroform and 200 μl of methanol added to the sample and vortexed for 2 minutes. A further 100 μl of chloroform was added followed by 30 seconds of vortexing. 100 μl of deionized water was added followed by 30 seconds of vortexing. The mixture was centrifuged at 13,000 rpm in a microfuge for ten minutes at room temperature. The upper layer was removed for scintillation counting. The lower layer was removed from below the interface pellet and centrifuged before scintillation counting.

Blebs were separated from whole cells and the phospholipids in both samples extracted. The counts present in both bleb and cell-associated phospholipids are presented in Table I.

<table>
<thead>
<tr>
<th>TABLE I</th>
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<tr>
<td>14C-acetate Incorporation, Counts per Minute</td>
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<tr>
<td><em>N. gonorrhoeae</em> strain 1291, wild type and bmr mutant.</td>
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<tr>
<td>CPM in bleb-associated phospholipids</td>
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<tr>
<td>Mutant</td>
</tr>
<tr>
<td>Total CPM</td>
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<td>CPM in cell-associated phospholipids</td>
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<td>CPM in bleb-associated phospholipids</td>
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<tr>
<td>Ratio of mutant to wild type CPM</td>
</tr>
<tr>
<td>Ratio of mutant to wild type bleb-associated CPM</td>
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</table>

In each of these three experiments, *N. gonorrhoeae* strain 1291 bmr incorporated increased amounts of label compared to wild type. Both cell-associated and bleb-associated label was increased in the mutants. The increase in cell-associated counts was slight, which agrees with microscopy observations in which the mutant and wild type bacteria did not appear different except for the presence of connections between mutant diploeoei and increased level of blebbing in the mutant. As would be expected from the morphology, mutant bleb-associated counts were between two-and-four-fold higher than wild type.

Labeling experiments were also conducted using *N. meningitidis*. For unknown reasons, it proved difficult to obtain consistent bleb-associated counts with these bacteria. The micrographs suggested that the membrane alteration observed with these mutants did not involve the type of blebbing seen in the gonococcus, but instead involved cell-associated membrane changes. However, total membrane was increased as was seen in the *N. gonorrhoeae* experiments. Table II shows a comparison of total outer membrane counts from both wild type and mutant bacteria. Increased incorporation of counts in the mutants was observed.

| TABLE II |
| 14C-acetate Incorporation, Counts per Minute |
| Wild type and bmr mutant of *N. meningitidis* NMB |
| | Experiment 1 | Experiment 2 |
| Wild-Type | | |
| Total CPM | 4.0 x 10^7 | 6.0 x 10^7 |
| Total phospholipids | 1.0 x 10^7 | 5.4 x 10^7 |
| Mutant | | |
| Total CPM | 4.0 x 10^7 | 6.0 x 10^7 |
| Total phospholipids | 1.9 x 10^7 | 9.7 x 10^7 |
| Ratio of mutant to wild-type CPM | 1.5 | 1.8 |

When larger quantities of membrane are desired, the culturing and purification may be easily scaled up.

EXAMPLE 4

Use of the Neisseria bmr Mutants to Estimate Virulence of Bacteria Recovered from Clinical Samples.

Swabs from suspected Neisseria infections are cultured for meningococci or gonococci by the methods disclosed in Example 1. A laboratory strain of Neisseria and a super blebber are grown in the same manner as controls. Overnight cultures are examined for blebbing in the SEM as described in Example 2B.

Phospholipids are isolated as described in Example 1. Phospholipids are quantitated as described by the incorporation of radiouclide or by HPLC analysis of total phospholipids. A level of phospholipid close to that of the super blebber indicates infection with a virulent neisserial pathogen, indicating that therapy should be immediate and aggressive.

As seen in Table III, a quantitative estimate on a scale of 1 (no blebbing) to 3 (many blebs and filamentous connections between cells) and the phospholipid content that correlates with blebbing are made to determine virulence of the clinical sample.

| TABLE III |
| Phospholipid Blebbing CPM* |
| Diagnosis |
| *N. gonorrhoeae* strain 1291 | | |
| Super blebber | 3 | 2 x 10^6 |
| Hypothetical Sample #1 | 1 | 6 x 10^7 |
| Hypothetical Sample #2 | 2 | 1 x 10^6 |
| Hypothetical Sample #3 | 3 | >1.8 x 10^6 |

| Diagnosis |
| Not virulent, therapy not needed |
| Moderate virulence, therapy indicated |
| Highly virulent, immediate and |


EXAMPLE 5

Use of super blebbers to screen biocidal or biostatic agents.

A ninety-six well culture is set up with N. gonorrhoeae Strain 1291 and the N. gonorrhoeae super blebber, and the N. meningitidis strain NMB and the N. meningitidis super blebber. Dilutions of the potentially selective antibiotics are added to respective wells. An antibiotic is considered selective if it inhibits the mutant organisms that show excessive blebbing as indicated by no growth in the super blebber chambers at lower concentrations than those that inhibit growth in the strains 1291 and/or NMB.

An compound may affect a specific property of the bacterium without outright killing of the organism. Such a compound may be particularly useful in that it does not disturb the normal microflora of a patient while inhibiting the specific property that renders a pathogen virulent. It would be particularly useful to identify a compound that targets the Neisseria blebbing process. A ninety-six well culture is set up with a recently isolated, high-blebbing Neisseria that shows excessive outer membrane formation as indicated by blebbing. Dilutions of the potentially selective antibiotics are added to respective wells. An antibiotic is considered selective if it inhibits the blebbing at lower concentrations than those that inhibit growth. Such an antibiotic may be considered to have converted the high-blebbing, virulent bacterium to a non-virulent form.

All of the compositions and methods disclosed and claimed herein can be made and executed without undue experimentation in light of the previous disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be readily appreciated by those of skill in the art that many variations and modifications may be applied to the compositions and methods and used in the steps or in the sequence of steps of the methods described herein without departing from the concept and scope of the invention. More specifically, it will be apparent that certain agents, such as vectors, primers and bacterial strains, that are both chemically and physiologically equivalent may be substituted for the agents described herein while the same or similar results would be achieved. All such similar variations and modifications apparent to those of skill in the art are deemed to be within the scope and concept of the invention defined by the appended claims.

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| 2 | Leu | Met | Leu | Leu | Leu | Asp | Leu | Gly | Leu | Leu | Pro | Gly | Arg | Asp | Gly | Leu | Asp | Val | 35 | 40 | 45 |
| 3 | Leu | Ser | Glu | Ile | Arg | Ala | Ala | Gly | Cys | Thr | Val | Pro | Val | Leu | Ile | Val | 50 | 55 | 60 |
| 4 | Thr | Ala | Arg | Asp | Arg | Leu | Tyr | Ser | Arg | Leu | Asn | Gly | Leu | Asp | Gly | Gly | 65 | 70 | 75 | 80 |
| 5 | Ala | Asp | Gly | Ile | Val | Lys | Pro | Phe | Asp | Met | Ala | Glu | Phe | Lys | Ala | 85 | 90 | 95 |
| 6 | Arg | Met | Arg | Ala | Val | Leu | Arg | Arg | Gly | Ser | Gly | Gln | Ala | Glu | Ala | Cys | 100 | 105 | 110 |
| 7 | Leu | Ser | Asn | Gly | Ala | Leu | Ser | Leu | Asn | Pro | Ala | Thr | Tyr | Gln | Val | Glu | 115 | 120 | 125 |
| 8 | Ile | Ile | Ala | Glu | Gly | Arg | Gln | Val | Ala | Leu | Ser | Asn | Gln | Glu | Phe | Ser | 130 | 135 | 140 |
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| 10 | Asp | Ser | Glu | Asp | Lys | Val | Tyr | Gly | Trp | Gly | Gly | Val | Glu | Ser | Asn | 165 | 170 | 175 |
| 11 | Ala | Val | Asp | Phe | Leu | Ile | His | Gly | Leu | Cys | Lys | Leu | Gly | Lys | Glu | 180 | 185 | 190 |
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| 5 | Leu | Met | Leu | Leu | Leu | Asp | Leu | Gly | Leu | Leu | Pro | Gly | Arg | Asp | Gly | Leu | Asp | Val | 35 | 40 | 45 |
| 6 | Leu | Ser | Glu | Ile | Arg | Ala | Ala | Gly | Cys | Thr | Val | Pro | Val | Leu | Ile | Val | 50 | 55 | 60 |
| 7 | Thr | Ala | Arg | Asp | Arg | Leu | Tyr | Ser | Arg | Leu | Asn | Gly | Leu | Asp | Gly | Gly | 65 | 70 | 75 | 80 |
| 8 | Ala | Asp | Gly | Ile | Val | Lys | Pro | Phe | Asp | Met | Ala | Glu | Phe | Lys | Ala | 85 | 90 | 95 |
| 9 | Arg | Met | Arg | Ala | Val | Leu | Arg | Arg | Gly | Ser | Gly | Gln | Ala | Glu | Ala | Cys | 100 | 105 | 110 |
| 10 | Leu | Ser | Asn | Gly | Ala | Leu | Ser | Leu | Asn | Pro | Ala | Thr | Tyr | Gln | Val | Glu | 115 | 120 | 125 |
| 11 | Ile | Ile | Ala | Glu | Gly | Arg | Gln | Val | Ala | Leu | Ser | Asn | Gln | Glu | Phe | Ser | 130 | 135 | 140 |
| 12 | Val | Leu | Gln | Ala | Leu | Leu | Ala | Arg | Pro | Gly | Val | Ile | Leu | Ser | Arg | Ser | 145 | 150 | 155 | 160 |
| 13 | Asp | Ser | Glu | Asp | Lys | Val | Tyr | Gly | Trp | Gly | Gly | Val | Glu | Ser | Asn | 165 | 170 | 175 |
| 14 | Ala | Val | Asp | Phe | Leu | Ile | His | Gly | Leu | Cys | Lys | Leu | Gly | Lys | Glu | 180 | 185 | 190 |
| 15 | Ser | Ile | Gln | Asn | Val | Arg | Gly | Val | Gly | Trp | Leu | Met | Pro | Arg | Gln | Asp | 195 | 200 | 205 |
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Leu Ser Ala Leu Ser Val Asp Asn Ile Pro Ser Gin Ile Arg Gly Phe 165 170 175
Val Thr Ala Ile Asn Leu Leu Leu Lys Arg Ala Asp Glu Asp Ile Arg 180 185 190
His Arg Gin Arg Phe Val Ala Asp Ala Ala His Glu Leu Arg Thr Pro 195 200 205
Met Thr Ala Leu Ser Leu Gin Ala Glu Arg Leu Asn Met Ser Leu 210 215 220
Pro Pro Asp Ala Ala Arg Gin Pro Ala Val Leu Gin Gin Ser Ile Arg 225 230 235 240
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Pro Asp Ala Leu Pro Glu Gly Asp Gly Thr Arg Ile Leu Val Gin 70 75 80
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Gly Leu His Thr Leu Arg Ala Asp Glu Asp Asp Tyr Tyr Arg Val 100 105 110
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Thr His Gln Ala Met Arg Pro Val Arg Ile Leu Ser Gin Asn Leu Glu 165 170 175
Gln Arg Arg Leu Asp Asp Leu Ser Ala Leu Aan Thr Asp Asn Ile Pro 180 185 190
We claim:

1. A Neisseria bacterium comprising a mutant two-component regulatory (2CR) system that controls super-blebbing, wherein said system comprises DNA encoding a BmrR open reading frame (ORF) and a BmrS ORF, wherein the BmrR ORF or the BmrS ORF contains an insertion or a deletion as compared to corresponding wild-type BmrR ORF or BmrS ORF.

2. The bacterium of claim 1 which is Neisseria gonorrhoeae.

3. The bacterium of claim 1 which is Neisseria meningitidis.

4. The bacterium of claim 2 which has been deposited with the American Type Culture Collection under accession number PTA-801.

5. The bacterium of claim 3 which has been deposited with the American Type Culture Collection under accession number PTA-800.

* * * * *