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(72) **Inventeurs/Inventors:**
BAKALETZ, LAUREN O., US;
MUNSON, ROBERT S., JR., US

(73) **Propriétaire/Owner:**
NATIONWIDE CHILDREN'S HOSPITAL, INC., US

(74) **Agent:** SMART & BIGGAR

(54) **Titre : PILI D'HAEMOPHILUS INFLUENZAE DE TYPE IV**
(54) **Title: HAEMOPHILUS INFLUENZAE TYPE IV PILI**

(57) **Abrégé/Abstract:**
The invention described herein relates to a Haemophilus influenzae (H. influenzae) regulon encoding type IV pili. In particular, the invention relates to type IV pili from nontypeable H. influenzae (NTHi) and from H. influenzae strains a, b, c, e and f. The invention provides isolated H. influenzae pilus polynucleotides and polypeptides encoded by the polynucleotides as well as polynucleotides and polypeptides encoded by the polynucleotides involved in the assembly/disassembly of the structure. The invention also relates to uses of these polynucleotides and/or polypeptides including methods for eliciting an immune response to H. influenzae and methods of treating and preventing H. influenzae related pathological conditions.

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(71) Applicant *(for all designated States except US)*: **CHILDREN'S HOSPITAL, INC.** [US/US]; 700 Children's Drive, Columbus, OH 43205 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **BAKALETZ, Lauren, O.** [US/US]; 4825 Canterwood Court, Hilliard, OH 43026 (US). **MUNSON, Robert, S., Jr.** [US/US]; 4825 Canterwood Court, Hilliard, OH 43026 (US).

(74) Agent: **NOLAND, Greta, E.**; Marshall, Gerstein & Borun LLP, 6300 Sears Tower, 233 South Wacker Drive, Chicago, IL 60606 (US).

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(54) Title: HAEMOPHILUS INFLUENZAE TYPE IV PILI

(57) Abstract: The invention described herein relates to *a Haemophilus influenzae (H. influenzae)* regulon encoding type IV pili. In particular, the invention relates to type IV pili from nontypeable *H. influenzae* (NTHi) and from *H. influenzae* strains a, b, c, e and f. The invention provides isolated *H. influenzae* pilus polynucleotides and polypeptides encoded by the polynucleotides as well as polynucleotides and polypeptides encoded by the polynucleotides involved in the assembly/disassembly of the structure. The invention also relates to uses of these polynucleotides and/or polypeptides including methods for eliciting an immune response to *H. influenzae* and methods of treating and preventing *H. influenzae* related pathological conditions.

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HAEMOPHILUS INFLUENZAE TYPE IV PILI

[0001] Experimental work relating to the invention described herein was supported by grants from the U.S. National Institutes of Health (NIH)/the U.S. National Institute on Deafness and other Communication Disorders (NIDCD). The United States government may have certain rights in the invention.

Field of Invention

[0002] The invention described herein relates to a *Haemophilus influenzae* (*H. influenzae*) regulon encoding type IV pili. In particular, the invention relates to type IV pili from nontypeable *H. influenzae* (NTHi) and from *H. influenzae* strains a, b, c, e and f. The invention provides isolated *H. influenzae* pilus polynucleotides and polypeptides encoded by the polynucleotides as well as polynucleotides and polypeptides encoded by the polynucleotides involved in the assembly/disassembly of the structure. The invention also relates to uses of these polynucleotides and/or polypeptides including methods for eliciting an immune response to *H. influenzae* and methods of treating and preventing *H. influenzae* related pathological conditions.

Background

[0003] The clinical term for middle ear infections is otitis media (OM). According to Klein, *Vaccine*, 19 (Suppl. 1): S2-S8, 2000, OM is the most common reason for an ill child to obtain healthcare and for a child in the United States to receive antibiotics or undergo a general anesthetic. Statistics indicate that 24.5 million physician office visits were made for OM in 1990, representing a greater than 200% increase over those reported in the 1980s. While rarely associated with mortality, the morbidity associated with OM is significant. Hearing loss is a common problem associated with this disease, often affecting a child's behavior, education and development of language skills (Baldwin, *Am. J. Otol.*, 14: 601-604, 1993; Hunter *et al.*, *Ann. Otol. Rhinol. Laryngol. Suppl.*,163: 59-61, 1994; Teele *et al.*, *J. Infect. Dis.*, 162: 685-694, 1990). The socioeconomic impact of OM is also great, with direct and indirect costs of diagnosing and managing OM exceeding $5 billion annually in the U.S. alone (Kaplan *et al.*, *Pediatr. Infect. Dis. J.*, 16: S9-11, 1997).

[0004] OM is thought to result from infectious, environmental and host genetics factors. Bacteria such as *Haemophilus influenzae, Streptococcus pneumoniae and Moraxella catarrhalis* are the most common infectious organisms in OM. Acute OM is a disease characterized by rapid onset and short duration of signs and symptoms of

inflammation in the middle ear, while chronic OM refers to a condition that is defined by the relatively asymptomatic presence of fluid (or effusion) in the middle ear. However, in chronic OM, despite the absence of certain signs of acute infection (*i.e.*, ear pain or fever), these abnormal middle ear fluids can persist for periods exceeding three months. Treatment of acute OM by antibiotic therapy is common, but antibiotic-resistant bacteria have emerged. Surgical management of chronic OM involves the insertion of tympanostomy tubes through the tympanic membrane of the ear while a child is under general anesthesia. While this procedure is commonplace (prevalence rates are ~ 13%; Bright *et al., Am. J. Public Health*, 83(7): 1026-8, 1993) and is highly effective in terms of relieving painful symptoms by draining the middle ear of accumulated fluids, it is invasive and carries incumbent risks (Berman *et al., Pediatrics*, 93(3):353-63, 1994; Bright *et al., supra.;* Cimons, *ASM News*, 60: 527-528; Paap, *Ann. Pharmacother.,* 30(11): 1291-7, 1996). There is thus a need for additional approaches to the management and, preferably, the prevention of OM.

[0005] OM vaccine development is most advanced for *S. pneumoniae*, the primary causative agent of acute OM (AOM), as evidenced by the recent approval and release of a seven-valent capsular-conjugate vaccine, PREVNAR® (Eskola and Kilpi, *Pedriatr. Infect. Dis. J.* 16: S72-78, 2000). While PREVNAR® has been highly efficacious for invasive pneumococcal disease, coverage for OM has been disappointing (6-8%) with reports of an increased number of OM cases due to serotypes not included in the vaccine (Black *et al., Pedriatr. Infect. Dis J*, 19: 187-195, 2000; Eskola *et al., Pedriatr. Infect. Dis J.*, 19: S72-78, 2000; Eskola *et al., N. Engl. J. Med.,* 344: 403-409, 2001; Snow *et al., Otol. Neurotol.*, 23: 1-2, 2002).

[0006] *H. influenzae* is a gram-negative bacterium that, as noted above, plays a role in OM. Clinical isolates of *H. influenzae* are classified either as serotypes "a" through "f" or as non-typeable depending on the presence or absence, respectively, of type-specific polysaccharide capsules on the bacteria. A vaccine for *H. influenzae* type b has been developed. Like Prevnar®, the type b *H. influenzae* vaccines target the polysaccharide capsule of this organism and thus the vaccine is comprised of capsule polysaccharide that has been conjugated to a protein carrier. Less progress has been made for a vaccine for non-typeable *H. influenzae* (NTHi) which causes approximately 20% of acute OM in children and predominates in chronic OM with effusion (Coleman *et al., Inf and Immunity,* 59(5), 1716-1722, 1991; Klein, *Pedriatr.*

Infect. Dis J., 16, S5-8, 1997; Spinola *et al., J. Infect. Dis.*, 154, 100-109, 1986). NTHi can also cause pneumonia, sinusitis, septicemia, endocarditis, epiglottitis, septic arthritis, meningitis, postpartum and neonatal infections, postpartum and neonatal sepsis, acute and chromic salpingitis, epiglottis, pericardis, cellulitis, osteomyelitis, endocarditis, cholecystitis, intraabdominal infections, urinary tract infection, mastoiditis, aortic graft infection, conjunctitivitis, Brazilian purpuric fever, occult bacteremia and exacerbation of underlying lung diseases such as chronic bronchitis, bronchietasis and cystic fibrosis. A prototype NTHi isolate is the low passage isolate 86-028NP which was recovered from a child with chronic OM. This strain has been well characterized *in vitro* (Bakaletz *et al.*, *Infect. Immun.*, 53: 331-5, 1988; Holmes *et al., Microb. Pathog.*, 23: 157-66, 1997) as well as in a chinchilla OM model (Bakaletz *et al.*, *Vaccine*, 15: 955-61, 1997; Suzuki *et al., Infect. Immun.*, 62: 1710-8, 1994; DeMaria *et al.*, *Infect. Immun.*, 64: 5187-92, 1996). The NTHi strain 86-026NP was deposited with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110, on October 16, 2001 and assigned accession no. PTA-4764. A contig set from the genome of strain 86-028NP can be found at the Microbial-Pathogenesis.org web site of Children's Hospital, Columbus, Ohio.

[0007] Adherence and colonization are acknowledged first steps in the pathogenesis of *H. influenzae*. As such, *H. influenzae* express multiple adhesins including hemagglutinating pili, fimbriae and non-fimbrial adhesins (Gilsdorf *et al.*, *Pediatr Res* 39, 343-348, 1996; Gilsdorf ., *Infect. Immun.*, 65, 2997-3002, 1997; and St. Geme III, *Cell. Microbiol.*, 4, 191-200, 2002). Notably, none of the adhesins described have previously been associated with a motility function. Moreover, *H. influenzae* do not express flagella with are also associated with motility. Twitching motility is a flagella-independent form of bacterial translocation over moist surfaces and occurs by extension, tethering, and then retraction of polar structures known as type IV pili (Bardy ., *Microbiology*, 149, 295-304, 2003; Tonjum and Koomey, *Gene*, 192, 155-163, 1997; Wolfgang *et al., EMBO J.*, 19, 6408-6418, ; Mattick, *Annu. Rev. Microbiol.*, 56, 289-314, 2002). Type IV pili are typically 5-7 nm in diameter, several micrometers in length and comprised of a single protein subunit assembled into a helical conformation with 5 subunits per turn (Bardy *et al., Microbiology*, 149, 295-304, 2003; Wall and Kaiser, *Mol. Microbiol.*, 32, 1-10, 1999). Type IV pilin subunits are usually 145-160 amino acids in length and may be glycosylated or

phosphorylated. There are two classes of pilin subunits, type IVa and type IVb, which are distinguished from one another by the average length of the leader peptide and the mature subunit, which N-methylated amino acid occupies the N-terminal position of the mature protein, and the average length of the D-region (for disulfide region). Most of the respiratory pathogens express class IVa pilins, whereas the enteropathogens more typically express class IVb pilins. Type IVa pili are distinguished by the presence of a highly conserved, hydrophobic N-terminal methylated phenylalanine.

[0008] Type IV pili serve as a means of rapid colonization of new surfaces. Thus type IV pilus expression is important to both adherence and biofilm formation by many bacteria (Mattick, *Annu. Rev. Microbiol.*, 56, 289-314 2002; O'Toole and Kolter, *Mol. Microbiol.*, 30, 295-304, 1998; Klausen *et al., Mol. Microbiol.*, 50, 61-68, 2003; Jesaitis *et al., J. Immunol.*, 171, 4329-4339, 2003), as well as virulence of *Neisseria* species, *Moraxella bovis*, *Vibrio cholerae*, enteropathogenic *Escherichia coli* and *Pseudomonas aeruginosa*, among others (O'Toole and Kolter, *supra*; Klausen *et al., supra*; Klausen *et al., Mol. Microbiol.*, 48, 1511-1524, 2003; Strom and Lory, *Annu. Rev. Microbiol.*, 47, 565-596, 1993). A biofilm is a complex organization of bacteria that are anchored to a surface via a bacterially extruded exopolysaccharide matrix. The matrix envelopes the bacteria and protects it from the human immune system. Ehrlich *et al., JAMA*, 287(13), 1710-1715 (2002) describes biofilm formation by *H. influenzae*. It has been postulated that blocking the interaction between type IV pili and the human body can avoid or stop the bacterial infection (Meyer *et al.*, U.S. Patent No. 6,268,171 issued July 31, 2001).

[0009] Type IV pilus expression is a complex and highly regulated bacterial function. In *P. aeruginosa*, the biogenesis and function of type IV pili is controlled by over forty genes (Strom and Lory, *supra*). To date, only a subset of the vast number of related type IV pilus genes (Tonjum and Koomey, *supra*; Darzins and Russell, *Gene*, 192, 109-115, 1997) have been found in several members of the HAP (*Haemophilus*, *Actinobacillus* and *Pasteurella*) family (Stevenson *et al., Vet. Microbiol.*, 92, 121-134, 2003; Doughty *et al., Vet. Microbiol.*, 72, 79-90, 2000; Dougherty and Smith, *Microbiology*, 145, 401-409 1999), but neither expression of type IV pili nor twitching motility has ever been described for any *H. influenzae* isolate. In fact, *H. influenzae* is classically described as a bacterium that does not

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express these structures (Friedrich *et al. Appl. Environ. Microbiol.*, 69, 3695-3700, 2003; Fussenegger *et al., Gene*, 192, 125-134, 1997), despite the presence of a cryptic gene cluster within the strain Rd genome (Fleischmann *et al., Science*, 269, 496-512, 1995). Strain Rd is a non-encapsulated derivative of an *H. influenzae* serotype d organism (Zwahlen *et al., Infect. Immun.*, 42, 708-715, 1983; Bendler and Goodgal, *J. Microbiol.*, 70, 411-422, 1972; Risberg *et al., Eur. J. Biochem.*, 261, 171-180, 1999). Although strain Rd has some virulence properties, serotype d strains are generally considered to be commensals; they do not frequently cause disease (Daines *et al., J. Med. Microbiol.*, 52, 277-282, 2003). It is therefore important to make the distinction between disease-causing strains of *H. influenzae* and strain Rd.

Summary of the Invention

[0010] The present invention relates to Type IV pilus gene clusters of *H. influenzae*, in particular non-typeable *H. influenzae* (NTHi) and *H. influenzae* strains a, b, c, e and f.

[0010a] The present invention as claimed relates to:

- an isolated polynucleotide comprising a nucleotide sequence encoding the amino acid sequence of any one of: PilA polypeptide SEQ ID NO: 2, PilA polypeptide SEQ ID NO: 26, PilA polypeptide SEQ ID NO: 28, PilA polypeptide SEQ ID NO: 30, PilA polypeptide SEQ ID NO: 32, PilA polypeptide SEQ ID NO: 34, PilA polypeptide SEQ ID NO: 36, PilA polypeptide SEQ ID NO: 38, PilA polypeptide SEQ ID NO: 40, PilA polypeptide SEQ ID NO: 42, or PilA polypeptide SEQ ID NO: 44;

- an isolated polynucleotide comprising the nucleotide sequence of any one of: *pilA* SEQ ID NO: 1, *pilA* SEQ ID No: 25, *pilA* SEQ ID No: 27, *pilA* SEQ ID No: 29, *pilA* SEQ ID No: 31, *pilA* SEQ ID No: 33, *pilA* SEQ ID No: 35, *pilA* SEQ ID No: 37, *pilA* SEQ ID No: 39, *pilA* SEQ ID No: 41 or *pilA* SEQ ID No: 43;

- a vector comprising the polynucleotide as described herein;

- an isolated polypeptide comprising the amino acid sequence encoded by the nucleotide sequence as described herein;

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- an isolated polypeptide comprising the amino acid sequence of any one of PilA polypeptide SEQ ID NO: 2, PilA polypeptide SEQ ID NO: 26, PilA polypeptide SEQ ID NO: 28, PilA polypeptide SEQ ID NO: 30, PilA polypeptide SEQ ID NO: 32, PilA polypeptide SEQ ID NO: 34, PilA polypeptide SEQ ID NO: 36, PilA polypeptide SEQ ID NO: 38, PilA polypeptide SEQ ID NO: 40, PilA polypeptide SEQ ID NO: 42, or PilA polypeptide SEQ ID NO: 44;

- an isolated peptide fragment of the polypeptide of SEQ ID NO: 2, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, or SEQ ID NO: 44, wherein the peptide fragment elicits an immune response to *H. influenzae* pilin polypeptide;

- an isolated peptide fragment of the polypeptide of SEQ ID NO: 2, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, or SEQ ID NO: 44, wherein the peptide fragment inhibits *H. influenzae* cellular adherence;

- a composition comprising the polypeptide as described herein or the peptide fragment as described herein and a pharmaceutically acceptable carrier;

- an antibody that specifically binds to the polypeptide as described herein or the peptide fragment as described herein;

- a composition comprising the antibody as described herein and a pharmaceutically acceptable carrier;

- a method for detecting non-typeable *H. influenzae* (NTHi) bacteria in a biological sample comprising (a) contacting the polynucleotide as described herein or a polynucleotide that encodes the peptide fragment as described herein with a biological sample under stringent conditions for hybridization and washing with 0.015 M sodium chloride, 0.0015 M sodium citrate at 65-68°C or 0.015 M sodium chloride, 0.0015M sodium citrate, and 50% formamide at 42°C, and (b) detecting hybridization of the polynucleotide within the sample, wherein hybridization indicates the presence of NTHi bacteria;

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- a method for detecting non-typeable *H. influenzae* (NTHi) bacteria in a biological sample comprising: (a) contacting the antibody as described herein with a biological sample, and (b) detecting binding of the antibody within the sample, wherein binding indicates the presence of NTHi bacteria;

- use of one or more polypeptides as described herein or the peptide fragment as described herein for the preparation of a medicament for eliciting an immune response to non-typeable *H. influenza* (NTHi) bacteria;

- use of one or more polynucleotides as described herein for the preparation of a medicament for eliciting an immune response to non-typeable *H. influenzae* (NTHi) bacteria;

- use of an antisense oligonucleotide that inhibits expression of the polypeptide as described herein for the preparation of a medicament for treating or preventing non-typeable *H. influenza* (NTHi) bacterial infection; and

- use of the antibody or composition as described herein for the preparation of a medicament for treating or preventing non-typeable *H. influenza* (NTHi) bacterial infection.

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Polynucleotides and Polypeptides of the Invention

[0011] The present invention provides *H. influenzae* polynucleotides and particularly open reading frames from a regulon arranged in two gene clusters plus one other gene. The regulon includes a gene (*pilA*) that encodes the major subunit of a heretofore uncharacterized *H. influenzae* type IV pilus. The regulon includes polynucleotides from a gene cluster encoding pilin polypeptides PilA (major pilin subunit), PilD (leader peptidase), PilB and PilC (involved in the assembly/disassembly of the pilin structure); another gene cluster encoding ComA, ComB, ComC, ComD, ComE, and ComF (involved in competence for transformation and pilus expression); and a gene encoding PilF (required for type IV pilus biogenesis) (Watson *et al, Gene*, 49: 56, 1996). In one embodiment, the pilus regulon is that of NTHi *H. influenzae* strain 86-028NP.

[0012] Polynucleotides encoding the NTHi 86-028NP pilin polypeptides set out in the following SEQ ID NOs are provided by the invention: PilA polypeptide in SEQ ID NO: 2, PilB polypeptide in SEQ ID NO: 4, PilC polypeptide in SEQ ID NO: 6, PilD polypeptide in SEQ ID NO: 8, ComA polypeptide in SEQ ID NO: 10, ComB polypeptide in SEQ ID NO: 12, ComC polypeptide in SEQ ID NO: 14, ComD polypeptide in SEQ ID NO: 16, ComE polypeptide in SEQ ID NO: 18, ComF

polypeptide in SEQ ID NO: 20 and PilF polypeptide in SEQ ID NO: 22. Alternative codon usage is thus specifically contemplated by the invention. In one embodiment, the polynucleotides comprise the NTHi 86-028NP gene sequences set out in the following SEQ ID NOs which respectively encode the foregoing polypeptides: *pilA* in SEQ ID NO: 1, *pilB* in SEQ ID NO: 3, *pilC* in SEQ ID NO: 5, *pilD* in SEQ ID NO: 7, *comA* in SEQ ID NO: 9, *comB* in SEQ ID NO: 11, *comC* in SEQ ID NO: 13, *comD* in SEQ ID NO: 15, *comE* in SEQ ID NO: 17, *comF* in SEQ ID NO: 19; and *pilF* in SEQ ID NO: 21. Each of the polynucleotide sequences includes a final three nucleotides representing a stop codon.

[0013] Also provided are polynucleotides encoding PilA polypeptides from NTHi clinical isolates 1728MEE, 1729MEE, 3224A, 10548MEE, 1060MEE, 1885MEE, 1714MEE, 1236MEE, 1128MEE and 214NP. The amino acid sequences of these PilA polypeptides are set out in SEQ ID NOs: 26, 28, 30, 32, 34, 36, 38, 40, 42 and 44, respectively. Again, the possibility of alternative codon usage is specifically contemplated in polynucleotides encoding the polypeptides. In one embodiment, the polypeptides are respectively encoded by the nucleotide sequences set out in SEQ ID NOs: 25, 27, 29, 31, 33, 35, 37, 39, 41 and 43.

[0014] The invention provides for polynucleotides that hybridize under stringent conditions to (a) the complement of the nucleotide sequences set out in SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 25, 27, 29, 31, 33, 35, 37, 39, 41 or 43; (b) a polynucleotide which is an allelic variant of any polynucleotides recited above; (c) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (d) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of the present invention. Type IV pilin polynucleotides from other non-typeable *H. influenzae* strains and from *H. influenzae* strains a, b, c, e and f are specifically contemplated. These polynucleotides can be identified and isolated by techniques standard in the art such as hybridization and polymerase chain reaction using part or all of the polynucleotides of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 25, 27, 29, 31, 33, 35, 37, 39, 41 or 43 as probes or primers, respectively.

[0015] The polynucleotides of the invention also include nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least 65%, at least 70%, at least 75%, at

least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more typically at least 90%, 91%, 92%, 93%, or 94% and even more typically at least 95%, 96%, 97%, 98% or 99% sequence identity to the NTHi polynucleotides recited above.

[0016] Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to the NTHi nucleotide sequences of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 25, 27, 29, 31, 33, 35, 37, 39, 41 or 43, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, *e.g.*, 15, 17, or 20 nucleotides or more that are selective for (*i.e.*, specifically hybridize to any one of the polynucleotides of the invention) are contemplated. These nucleic acid sequence fragments capable of specifically hybridizing to a NTHi polynucleotide of the invention can be used as probes to detect NTHi polynucleotides of the invention and/or can differentiate NTHi polynucleotides of the invention from other bacterial genes, and are preferably based on unique nucleotide sequences.

[0017] The term "stringent" is used herein to refer to conditions that are commonly understood in the art as stringent. Hybridization stringency is principally determined by temperature, ionic strength, and the concentration of denaturing agents such as formamide. Examples of stringent conditions for hybridization and washing are 0.015 M sodium chloride, 0.0015 M sodium citrate at 65-68°C or 0.015 M sodium chloride, 0.0015M sodium citrate, and 50% formamide at 42°C. See Sambrook *et al.*, *Molecular Cloning*: *A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory, (Cold Spring Harbor, N.Y. 1989).

[0018] More stringent conditions (such as higher temperature, lower ionic strength, higher formamide, or other denaturing agent) may also be used, however, the rate of hybridization will be affected. In instances wherein hybridization of deoxyoligonucleotides is concerned, additional exemplary stringent hybridization conditions include washing in 6X SSC 0.05% sodium pyrophosphate at 37°C (for 14-base oligos), 48°C (for 17-base oligos), 55°C (for 20-base oligos), and 60°C (for 23-base oligos).

[0019] Other agents may be included in the hybridization and washing buffers for the purpose of reducing non-specific and/or background hybridization. Examples are

0.1% bovine serum albumin, 0.1% polyvinyl-pyrrolidone, 0.1% sodium pyrophosphate, 0.1% sodium dodecylsulfate, $NaDodSO_4$, (SDS), ficoll, Denhardt's solution, sonicated salmon sperm DNA (or other non-complementary DNA), and dextran sulfate, although other suitable agents can also be used. The concentration and types of these additives can be changed without substantially affecting the stringency of the hybridization conditions. Hybridization experiments are usually carried out at pH 6.8-7.4, however, at typical ionic strength conditions, the rate of hybridization is nearly independent of pH. *See* Anderson *et al.*, *Nucleic Acid Hybridisation*: *A Practical Approach*, Ch. 4, IRL Press Limited (Oxford, England). Hybridization conditions can be adjusted by one skilled in the art in order to accommodate these variables and allow DNAs of different sequence relatedness to form hybrids.

[0020] As noted above, polynucleotides contemplated by the present invention are not limited to the specific polynucleotides of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 25, 27, 29, 31, 33, 35, 37, 39, 41 or 43, but also include, for example, allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 25, 27, 29, 31, 33, 35, 37, 39, 41 or 43, preferably the open reading frames therein, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to the open reading frames within SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 25, 27, 29, 31, 33, 35, 37, 39, 41 or 43 with a sequence from another isolate of the same species or another species. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, the GCG program package, including GAP (Devereux *et al.*, *Nucl. Acid. Res.*, 12: 387, 1984; Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, and FASTA (Altschul *et al., J. Mol. Biol.*, 215: 403-410, 1990). The BLASTX program is publicly available from the National Center for Biotechnology Information (NCBI) and other sources (*BLAST Manual*, Altschul *et al.* NCB/NLM/NIH Bethesda, MD 20894; Altschul *et al., supra*). The well known Smith-Waterman algorithm may also be used to determine identity.

[0021] Polynucleotides of the invention may be isolated from natural sources or may be synthesized by standard chemical techniques, *e.g.*, the phosphotriester method described in Matteucci *et al., J Am Chem Soc.*, 103: 3185 (1981).

[0022] Antisense polynucleotides complementary to the polynucleotides encoding the pilus polypeptides of the invention are also provided.

[0023] Polypeptides of the invention include pilin polypeptides PilA, PilD, PilB, PilC, ComA, ComB, ComC, ComD, ComE, ComF and PilF. In one embodiment the polypeptides comprise the NTHi 86-028NP amino acid sequences respectively set out in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 or 22. Polypeptides of the invention also include PilA polypeptides set out in SEQ ID NOs: 26, 28, 30, 32, 34, 36, 38, 40, 42 or 44. In additional embodiments, the Type IV pilin polypeptides of the invention are those of other non-typeable *H. influenzae* strains and from *H. influenzae* strains a, b, c, e and f.

[0024] Polypeptides of the invention specifically include peptide fragments (*i.e.*, peptides) that retain one or more biological or immunogenic properties of a full length polypeptide of the invention. In one embodiment PilA peptide fragments provided by the invention are designated TfpQ2, TFPQ3, TfpQ4 and OLP3 and respectively comprise amino acids 35 through 68 of SEQ ID NO: 2, amino acids 69 through 102 of SEQ ID NO: 2, amino acids 103 through 137 of SEQ ID NO: 2, and amino acids 21 through 35 of SEQ ID NO: 2.

[0025] The invention also provides for polypeptides with one or more conservative amino acid substitutions that do not affect the biological and/or immunogenic activity of the polypeptide. Alternatively, the polypeptides of the invention are contemplated to have conservative amino acids substitutions which may or may not alter biological activity. The term "conservative amino acid substitution" refers to a substitution of a native amino acid residue with a nonnative residue, including naturally occurring and nonnaturally occurring amino acids, such that there is little or no effect on the polarity or charge of the amino acid residue at that position. For example, a conservative substitution results from the replacement of a non-polar residue in a polypeptide with any other non-polar residue. Further, any native residue in the polypeptide may also be substituted with alanine, according to the methods of "alanine scanning mutagenesis". Naturally occurring amino acids are characterized based on their side

chains as follows: basic: arginine, lysine, histidine; acidic: glutamic acid, aspartic acid; uncharged polar: glutamine, asparagine, serine, threonine, tyrosine; and non-polar: phenylalanine, tryptophan, cysteine, glycine, alanine, valine, proline, methionine, leucine, norleucine, isoleucine General rules for amino acid substitutions are set forth in Table 1 below.

Table 1
Amino Acid Substitutions

Original Residues	Exemplary Substitutions	Preferred Substitutions
Ala	Val, Leu, Ile	Val
Arg	Lys, Gln, Asn	Lys
Asn	Gln	Gln
Asp	Glu	Glu
Cys	Ser, Ala	Ser
Gln	Asn	Asn
Glu	Asp	Asn
Gly	Pro, Ala	Ala
His	Asn, Gln, Lys, Arg	Arg
Ile	Leu, Val, Met, Ala, Phe,	Leu
Leu	Norleucine, Ile, Val, Met,	Leu
Lys	Arg, 1,4 Diaminobutyric	Arg
Met	Leu, Phe, Ile	Leu
Phe	Leu, Val, Ile, Ala, Tyr	Arg
Pro	Ala	Gly
Ser	Thr, Ala, Cys	Thr
Thr	Ser	Ser
Trp	Tyr, Phe	Tyr
Tyr	Trp, Phe, Thr, Ser	Phe
Val	Ile, Met, Leu, Phe, Ala,	Leu

[0026] The invention also provides variants of the polypeptides of the present invention (*e.g.*, a polypeptide exhibiting at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity

to a polypeptide of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 or 22) that retain biological and/or immunogenic activity.

[0027] The invention contemplates that polynucleotides of the invention may be inserted in a vector for amplification or expression. For expression, the polynucleotides are operatively linked to appropriate expression control sequences such as promoter and polyadenylation signal sequences. Further provided are host cells comprising polynucleotides of the invention. Exemplary prokaryotic host cells include bacteria such as *E. coli*, *Bacillus*, *Streptomyces*, *Pseudomonas*, *Salmonella* and *Serratia*. Methods of producing polypeptides of the invention by growing the host cells and isolating polypeptide from the host cells or growth medium are specifically contemplated. One or more polynucleotides from the pilus regulon may be expressed in a host cell. For example, expression of the *pilA* gene alone and expression of multiple polynucleotides from the pilus regulon in order to affect assembly of the native pili structure are both specifically contemplated. Alternatively, polypeptides of the invention can be prepared by chemical synthesis using standard means. Particularly convenient are solid phase techniques (see, *e.g.*, Erikson *et al.*, *The Proteins* (1976) v. 2, Academic Press, New York, p. 255). Automated solid phase synthesizers are commercially available. In addition, modifications in the sequence are easily made by substitution, addition or omission of appropriate residues. For example, a cysteine residue may be added at the carboxy terminus to provide a sulfhydryl group for convenient linkage to a carrier protein, or spacer elements, such as an additional glycine residue, may be incorporated into the sequence between the linking amino acid at the C-terminus and the remainder of the peptide.

[0028] The term "isolated" refers to a substance removed from, and essentially free of, the other components of the environment in which it naturally exists. For example, a polypeptide is separated from other cellular proteins or a DNA is separated from other DNA flanking it in a genome in which it naturally occurs.

Antibodies

[0029] The invention provides antibodies which bind to antigenic epitopes unique to (i.e., are specific for) *H. influenzae* pilus polypeptides of the invention. Also provided are antibodies which bind to antigenic epitopes common among multiple *H.*

influenzae subtypes but unique with respect to any other antigenic epitopes. The antibodies may be polyclonal antibodies, monoclonal antibodies, antibody fragments which retain their ability to bind their unique epitope (*e.g.*, Fv, Fab and F(ab)2 fragments), single chain antibodies and human or humanized antibodies. Antibodies may be generated by techniques standard in the art using pilin polypeptide(s) of the invention or host cells expressing pilin polypeptide(s) of the invention as antigens.

[0030] The present invention provides for antibodies specific for the pilin polypeptides of the present invention and fragments thereof, which exhibit the ability to kill both *H. influenzae* bacteria and to protect humans from infection. The present invention also provides for antibodies specific for the polypeptides of the invention which reduce the virulence, inhibit adherence, inhibit biofilm formation, inhibit twitching motility, inhibit cell division, and/or inhibit penetration into the epithelium of *H. influenzae* bacteria and/or enhance phagocytosis of the *H. influenzae* bacteria.

[0031] *In vitro* complement mediated bactericidal assay systems (Musher *et al.*, *Infect. Immun.* 39: 297-304, 1983; Anderson *et al.*, *J. Clin. Invest.* 51: 31-38, 1972) may be used to measure the bactericidal activity of anti-pilus antibodies.

[0032] It is also possible to confer short-term protection to a host by passive immunotherapy via the administration of pre-formed antibody against an *H. influenzae* polypeptide of the invention. Thus, antibodies of the invention may be used in passive immunotherapy. Human immunoglobulin is preferred in human medicine because a heterologous immunoglobulin may provoke an immune response to its foreign immunogenic components. Such passive immunization could be used on an emergency basis for immediate protection of unimmunized individuals subject to special risks.

[0033] In another embodiment, antibodies of the invention may be used in the production of anti-idiotypic antibody, which in turn can be used as an antigen to stimulate an immune response against pilin epitopes.

Methods for Eliciting an Immune Response and Compositions Therefor

[0034] The invention contemplates methods of eliciting in an individual an immune response to one or more *H. influenzae* type IV pilus polypeptides. In certain embodiments, the methods elicit an immune response to the PilA protein. These methods elicit one or more immune responses, including but not limited to, immune

responses which inhibit bacterial replication, immune responses which block *H. influenzae* adherence to cells, immune responses which prevent *H. influenzae* twitching and immune responses which prevent biofilm formation. In one embodiment, the methods comprise a step of administering an immunogenic dose of a composition comprising one or more polypeptides of the invention. In another embodiment, the methods comprise administering an immunogenic dose of a composition comprising a cell expressing one or more polypeptides of the invention. In yet another embodiment, the methods comprise administering an immunogenic dose of a composition comprising one or more polynucleotides encoding one or more polypeptides of the invention. The polynucleotide may be a naked polynucleotide not associated with any other nucleic acid or may be in a vector such as a plasmid or viral vector (*e.g.*, adeno-associated virus vector or adenovirus vector). The methods may be used in combination in a single individual. The methods may be used prior or subsequent to *H. influenzae* infection of an individual.

[0035] In one embodiment of methods of the invention, a composition of the invention is administered as a priming dose followed by one or more booster doses. Co-administration of proteins or polypeptides that beneficially enhance the immune response such as cytokines (*e.g.*, IL-2, IL-12, GM-CSF), cytokine-inducing molecules (*e.g.* Leaf) or costimulatory molecules is also contemplated.

[0036] An "immunogenic dose" of a composition of the invention is one that generates, after administration, a detectable humoral (antibody) and/or cellular (T cell) immune response in comparison to the immune response detectable before administration or in comparison to a standard immune response before administration. The invention contemplates that the immune response resulting from the methods may be protective and/or therapeutic. In a preferred embodiment, the antibody and/or T cell immune response protects the individual from *H. influenzae* infection, particularly infection of the middle ear and/or the nasopharynx or lower airway. In this use, the precise dose depends on the patient's state of health and weight, the mode of administration, the nature of the formulation, etc., but generally ranges from about 1.0 μg to about 5000 μg per 70 kilogram patient, more commonly from about 10 to about 500 μg per 70 kg of body weight.

[0037] Humoral immune response may be measured by many well known methods, such as Single Radial Immunodiffussion Assay (SRID), Enzyme Immunoassay (EIA)

and Hemagglutination Inhibition Assay (HAI). In particular, SRID utilizes a layer of a gel, such as agarose, containing the immunogen being tested. A well is cut in the gel and the serum being tested is placed in the well. Diffusion of the antibody out into the gel leads to the formation of a precipitation ring whose area is proportional to the concentration of the antibody in the serum being tested. EIA, also known as ELISA (Enzyme Linked Immunoassay), is used to determine total antibodies in the sample. The immunogen is adsorbed to the surface of a microtiter plate. The test serum is exposed to the plate followed by an enzyme linked immunoglobulin, such as IgG. The enzyme activity adherent to the plate is quantified by any convenient means such as spectrophotometry and is proportional to the concentration of antibody directed against the immunogen present in the test sample. HAI utilizes the capability of an immunogen such as viral proteins to agglutinate chicken red blood cells (or the like). The assay detects neutralizing antibodies, *i.e.*, those antibodies able to inhibit hemagglutination. Dilutions of the test serum are incubated with a standard concentration of immunogen, followed by the addition of the red blood cells. The presence of neutralizing antibodies will inhibit the agglutination of the red blood cells by the immunogen. Tests to measure cellular immune response include determination of delayed-type hypersensitivity or measuring the proliferative response of lymphocytes to target immunogen.

[0038] The invention correspondingly provides compositions suitable for eliciting an immune response to pilus polypeptides of the invention. As noted above, the compositions comprise one or more pilus polypeptides, cells expressing one or more polypeptides, or one or more polynucleotides encoding one or more pilus polypeptides. The compositions may also comprise other ingredients such as carriers and adjuvants.

[0039] In compositions of the invention, a pilus polypeptide may be fused to another protein when produced by recombinant methods. In one embodiment, the other protein may not, by itself, elicit antibodies, but it stabilizes the first protein and forms a fusion protein retaining immunogenic activity. In another embodiment, the fusion protein comprises another protein that is immunogenic, such as Glutathione-S-transferase (GST) or beta-galactosidase, relatively large co-proteins which solubilize the fusion protein and facilitate production and purification thereof. The other protein may act as an adjuvant in the sense of providing a generalized stimulation of the

immune system. The other protein may be fused to either the amino or carboxy terminus of the NTHi protein of the invention.

[0040] In other compositions of the invention, pilus polypeptides may be otherwise linked to carrier substances. Any method of creating such linkages known in the art may be used. Linkages can be formed with heterobifunctional agents that generate a disulfide link at one functional group end and a peptide link at the other, such as a disulfide amide forming agent, *e.g.*, N-succidimidyl-3-(2-pyridyldithio) proprionate (SPDP) (See, *e.g.*, Jansen *et al.*, *Immun. Rev.* 62:185, 1982) and bifunctional coupling agents that form a thioether rather than a disulfide linkage such as reactive esters of 6-maleimidocaproic acid, 2-bromoacetic acid, 2-iodoacetic acid, 4-(N-maleimido-methyl) cyclohexane-1-carboxylic acid and the like, and coupling agent which activate carboxyl groups by combining them with succinimide or 1-hydroxy-2-nitro-4-sulfonic acid, for sodium salt such as succinimmidyl 4-(N-maleimido-methyl) cyclohexane-1-carobxylate (SMCC).

[0041] The pilus polypeptides may be formulated as neutral or salt forms. Pharmaceutically acceptable salts, include the acid addition salts (formed with the free amino groups of the peptide) and which are formed with inorganic acids such as, *e.g.*, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic. Salts formed with the free carboxyl groups may also be derived from inorganic bases such as, *e.g.*, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, and procaine.

[0042] Compositions of the invention may further comprise adjuvants. Known adjuvants include, for example, emulsions such as Freund's Adjuvants and other oil emulsions, *Bordetella pertussis*, MF59, purified saponin from *Quillaja saponaria* (QS21), aluminum salts such as hydroxide, phosphate and alum, calcium phosphate, (and other metal salts), gels such as aluminum hydroxide salts, mycobacterial products including muramyl dipeptides, solid materials, particles such as liposomes and virosomes. Examples of natural and bacterial products known to be used as adjuvants include monophosphoryl lipid A (MPL), RC-529 (synthetic MPL-like acylated monosaccharide), OM-174 which is a lipid A derivative from *E. coli*, holotoxins such as cholera toxin (CT) or one of its derivatives, pertussis toxin (PT) and heat-labile toxin (LT) of *E. coli* or one of its derivatives, and CpG

oligonucleotides. Adjuvant activity can be affected by a number of factors, such as carrier effect, depot formation, altered lymphocyte recirculation, stimulation of T-lymphocytes, direct stimulation of B-lymphocytes and stimulation of macrophages.

[0043] Compositions of the invention are typically formulated as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection may also be prepared. The preparation may also be emulsified. The active immunogenic ingredient is often mixed with excipients, which are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, *e.g.*, water, saline, dextrose, glycerol, ethanol, or the like and combinations thereof. In addition, if desired, the vaccine may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, or adjuvants, which enhance the effectiveness of the vaccine. The vaccines are conventionally administered parenterally, by injection, for example, either subcutaneously or intramuscularly.

[0044] Additional formulations which are suitable for other modes of administration include suppositories and, in some cases, oral formulations. For suppositories, traditional binders and carriers may include, for example, polyalkalene glycols or triglycerides; such suppositories may be formed from mixtures containing the active ingredient in the range of 0.5% to 10%, preferably 1-2%. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate and the like. These compositions take the form of solutions, suspensions, tablets, pills, capsules, sustained release formulations or powders and contain 10%-95% of active ingredient, preferably 25-70%.

[0045] Compositions may also be administered through transdermal routes utilizing jet injectors, microneedles, electroporation, sonoporation, microencapsulation, polymers or liposomes, transmucosal routes and intranasal routes using nebulizers, aerosols and nasal sprays. Microencapsulation using natural or synthetic polymers such as starch, alginate and chitosan, D-poly L-lactate (PLA), D-poly DL-lactic-coglycolic microspheres, polycaprolactones, polyorthoesters, polyanhydrides and polyphosphazenes polyphosphatazanes are useful for both transdermal and transmucosal administration. Polymeric complexes comprising synthetic poly-ornithate, poly-lysine and poly-arginine or amphipathic peptides are useful for

transdermal delivery systems. In addition, due to their amphipathic nature, liposomes are contemplated for transdermal, transmucosal and intranasal vaccine delivery systems. Common lipids used for vaccine delivery include N-(1)2,3-(dioleyl-dihydroxypropyl)-N,N,N, - trimethylammonium-methyl sulfate (DOTAP), dioleyloxy-propyl - trimethylammonium chloride DOTMA, dimystyloxypropyl-3-dimethyl-hydroxyethyl ammonium (DMRIE), dimethyldioctadecyl ammonium bromide (DDAB) and 9N(N',N-dimethylaminoethane) carbamoyl) cholesterol (DC-Chol). The combination of helper lipids and liposomes will enhance up-take of the liposomes through the skin. These helper lipids include, dioleoyl phosphatidylethanolamine (DOPE), dilauroylphosphatidylethanolamine (DLPE), dimyristoyl phosphatidylethanolamine (DMPE), dipalmitoylphosphatidylethanolamine (DPPE). In addition, triterpenoid glycosides or saponins derived from the Chilean soap tree bark (*Quillaja saponaria*) and chitosan (deacetylated chitan) have been contemplated as useful adjuvants for intranasal and transmucosal vaccine delivery.

[0046] Formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use.

Methods of Inhibiting *H. influenzae*

[0047] Alternatively, the invention includes methods of inhibiting *H. influenzae* type IV pili function in an individual. The methods comprise administering to the individual, for example, one or more antibodies of the invention; one or more polypeptides of the invention; one or more antisense polynucleotides of the invention; one or more RNAi molecules; and/or one or more small molecules, in an amount that inhibits function of the pili. *In vitro* assays may be used to demonstrate the ability to inhibit pili function. Embodiments of these methods include, for example, methods using inhibitors of pilus polyepeptide synthesis and/or pilus assembly, inhibitors of adherence mediated via type IV pili, inhibitors that disrupt existing biofilms mediated by type IV pili, and inhibitors of twitching.

[0048] Inhibition is contemplated for any pathological condition involving *H. influenzae*, for example, OM, pneumonia, sinusitis, septicemia, endocarditis, epiglottitis, septic arthritis, meningitis, postpartum and neonatal infections,

postpartum and neonatal sepsis, acute and chromic salpingitis, epiglottis, pericardis, cellulitis, osteomyelitis, endocarditis, cholecystitis, intraabdominal infections, urinary tract infection, mastoiditis, aortic graft infection, conjunctitivitis, Brazilian purpuric fever, occult bacteremia and exacerbation of underlying lung diseases such as chronic bronchitis, bronchietasis and cystic fibrosis.

[0049] Compositions comprising inhibitors of *H. influenzae* type IV pili function are provided. The compositions may consist of one of the foregoing active ingredients alone, may comprise combinations of the foregoing active ingredients or may comprise additional active ingredients used to treat bacterial infections. As discussed above, the compositions may comprise one or more additional ingredients such as pharmaceutically effective carriers. Also as discussed above, dosage and frequency of the administration of the compositions are determined by standard techniques and depend, for example, on the weight and age of the individual, the route of administration, and the severity of symptoms. Administration of the pharmaceutical compositions may be by routes standard in the art, for example, parenteral, intravenous, oral, buccal, nasal, pulmonary, rectal, intranasal, or vaginal.

Animal Model

[0050] Methods of the invention may be demonstrated in a chinchilla model widely accepted as an experimental model for OM. In particular, a chinchilla model of NTHi-induced OM has been well characterized (Bakaletz *et al.*, *J. Infect. Dis.*, 168: 865-872, 1993; Bakaletz and Holmes, *Clin. Diagn. Lab. Immunol.*,4: 223-225, 1997; Suzuki and Bakaletz, *Infect. Immun.*, 62: 1710-1718, 1994; Mason *et al.*, *Infect. Immun.*, 71:3454-3462, 2003), and has been used to determine the protective efficacy of several NTHi outer membrane proteins, combinations of outer membrane proteins, chimeric synthetic peptide vaccine components, and adjuvant formulations against OM (Bakaletz *et al.*, *Vaccine*, 15: 955-961, 1997; Bakaletz *et al.*, *Infect. Immun.*, 67: 2746-2762, 1999; Kennedy *et al.*, *Infect. Immun.*, 68: 2756-2765, 2000; Kyd *et al.*, *Infect. Immun.*, 66:2272-2278, 2003; Novotny and Bakaletz, *J. Immunol.*, 171, 1978-1983, 2003).

[0051] In the model, adenovirus predisposes chinchillas to *H. influenzae*-induced OM media, which allowed for the establishment of relevant cell, tissue and organ culture systems for the biological assessment of NTHi (Bakaletz *et al.*, *J. Infect. Dis.*,

168: 865-72, 1993; Suzuki *et al., Infect. Immunity* 62: 1710-8, 1994). Adenovirus infection alone has been used to assess the transudation of induced serum antibodies into the tympanum (Bakaletz *et al., Clin. Diagnostic Lab Immunol.*, 4(2): 223-5, 1997) and has been used as a co-pathogen with NTHi, to determine the protective efficacy of several active and passive immunization regimens targeting various NTHi outer membrane proteins, combinations of OMPs, chimeric synthetic peptide vaccine components, and adjuvant formulations as vaccinogens against otitis media (Bakaletz *et al., Infect Immunity*, 67(6): 2746-62, 1999; Kennedy *et al., Infect. Immun.*, 68(5): 2756-65, 2000; Novotny *et al., Infect Immunity* 68(4): 2119-28, 2000; Poolman *et al., Vaccine* 19 (Suppl. 1): S108-15, 2000).

Methods of Detecting *H. influenzae* bacteria

[0052] Also provided by the invention are methods for detecting bacteria in an individual. In one embodiment, the methods comprise detecting pili polynucleotides of the invention in a biological sample using primers or probes that specifically bind to the polynucleotides. Detection of the polynucleotide may be accomplished by numerous techniques routine in the art involving, for example, hybridization and/or PCR. In another embodiment, the methods comprise detecting pili polypeptides of the invention in a biological sample using antibodies of the invention that specifically bind to the polypeptides. The antibodies may be used in any immunoassay system known in the art including, but not limited to, radioimmunoassays, ELISA assays, sandwich assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, fluorescent immunoassays, protein A immunoassays and immunoelectrophoresis assays. Biological samples to be utilized in the methods include, but are not limited to, blood, serum, ear fluid, spinal fluid, sputum, urine, lymphatic fluid and cerebrospinal fluid.

Brief Description of the Drawing

[0053] Figure 1 is an alignment of amino acid sequences of the PilA polypeptides of NTHi Rd, 86-028NP (SEQ ID NO: 2), 1728MEE (SEQ ID NO: 26), 1729MEE (SEQ ID NO: 28), 3224A (SEQ ID NO: 30), 10548MEE (SEQ ID NO: 32), 1060MEE (SEQ ID NO: 34), 1885MEE (SEQ ID NO: 36), 1714MEE (SEQ ID NO: 38), 1236MEE (SEQ ID NO: 40), 1128MEE (SEQ ID NO: 42), 214NP (SEQ ID NO: 44).

Detailed Description of the Invention

[0054] The following examples illustrate the invention wherein Example 1 describes sequences of NTHi strain 86-028NP type IV pilus genes of the invention and detection of the *pilA* gene in thirteen clinical *H. influenzae* isolates, Example 2 demonstrates classical type IV pilus-dependent aggregate formation by NTHi strain 86-028NP, Example 3 demonstrates twitching motility in NTHi strain 86-028NP, Example 4 describes observation of type IV pili on NTHi strain 86-928NP by negative staining and transmission electron microscopy, Example 5 describes the generation of a *pilA* mutant, Example 6 describes experiments in a chinchilla model of infection with NTHi and *pilA* mutant NTHi, Example 7 describes *pilA* genes from ten NTHi clinical isolates, Example 8 describes experiments demonstrating an immune response to NTHi pilli in children and Example 9 describes the identification of NTHi peptide fragments for use as immunogens.

Example 1

[0055] A type IV pilus regulon was identified in an OM isolate of NTHi.

[0056] Many strains of NTHi, including strain 86-028NP, do not possess the *hif* locus required for the expression of hemagglutinating LKP pili (Mhlanga-Mutangadura *et al., J. Bacteriol.*, 180(17), 4693-4703, 1988), yet most form biofilms. Because pili are important to biofilm formation in other bacterial systems, the contig set from the NTHi strain 86-028NP genomic sequencing effort (see Microbial-Pathogenesis.org web site of Children's Hospital, Columbus, Ohio or co-owned U.S.S.N. 60/453,134) was analyzed for genes potentially encoding another type of pilus. The dataset was BLASTed using the tblasn algorithm with default parameters using the *Pseudomonas aeruginosa* proteins annotated as related to the type IV pilus or twitching motility for *P. aeruginosa* including PilQ and PilT. The translated polypeptide for the *P. multocida* PilA protein was also used in this search (Doughty *et al., Vet. Microbiol.*, 72, 79-90, 2000).

[0057] What initially appeared to be a cryptic type IV pilus gene locus was identified. Specifically, in strain 86-028NP, there are four genes that are highly homologous to those in *H. influenzae* strain Rd, *A. pleuropneumoniae* and *P. multocida* (Stevenson *et al., Vet. Microbiol.*, 92, 121-134, 2003; Doughty *et al., supra*; Zhang *et al., FEMS Microbiol Lett*, 189, 15-18, 2000; and Ruffolo *et al.*,

Infect. Immun., 65, 339-343, 1997). These genes encode PilA, PilB, PilC and PilD in strain Rd (Dougherty and Smith, *Microbiology*, 145(2), 401-409, 1999).

[0058] The NTHi strain 86-028NP regulon includes a gene cluster of polynucleotides encoding pilin polypeptides PilA (major pilin subunit), PilD (leader peptidase), PilB and PilC (contemplated to be transcribed from the same mRNA and to be involved in the assembly/disassembly of the pilin structure); a gene cluster of polynucleotides encoding pilin polypeptides ComA, ComB, ComC, ComD, ComE, and ComF (involved in competence for transformation and pilus expression); and another gene encoding PilF (required for type IV pilus biogenesis). The amino acid sequences of the pilin polypeptides set out in the following SEQ ID NOs: PilA in SEQ ID NO: 2, PilB in SEQ ID NO: 4, PilC in SEQ ID NO: 6, PilD in SEQ ID NO: 8, ComA in SEQ ID NO: 10, ComB in SEQ ID NO: 12, ComC in SEQ ID NO: 14, ComD in SEQ ID NO: 16, ComE in SEQ ID NO: 18, ComF in SEQ ID NO: 20 and PilF in SEQ ID NO: 22. The gene sequences encoding the polypeptides are set out in the following SEQ ID NOs which respectively encode the foregoing polypeptides: *pilA* in SEQ ID NO: 1, *pilB* in SEQ ID NO: 3, *pilC* in SEQ ID NO: 5, *pilD* in SEQ ID NO: 7, *comA* in SEQ ID NO: 9, *comB* in SEQ ID NO: 11, *comC* in SEQ ID NO: 13, *comD* in SEQ ID NO: 15, *comE* in SEQ ID NO: 17, *comF* in SEQ ID NO: 19; and *pilF* in SEQ ID NO: 21. Each of the polynucleotides sequences includes a final three nucleotides representing a stop codon.

[0059] In gene expression profiling studies employing cDNA microarrays to characterize the regulation of NTHi genes during the development of competence (*i.e.*, the natural ability of NTHi to take up foreign DNA potentially enhancing or expanding its genetic diversity), the *com* genes as well as the *pil* genes are up-regulated during competence development.

[0060] In a Southern blot experiment using *pilA* sequences as a probe, thirteen low-passage clinical NTHi OM isolates recovered from patients undergoing tympanostomy and tube insertion for chronic otitis media and one clinical isolate recovered from a patient with cystic fibrosis had a single copy of *pilA* within their genome. These fourteen total isolates were designated by the following strain numbers, respectively: 86-028NP; 1728MEE; 1729MEE; 1714MEE; 214NP; 1236MEE; 165NP; 1060MEE; 1128MEE; 10548MEE; 3224A; 3185A, 1885MEE and 27W11679INI.

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[0061] In the experiment, bacterial chromosomal DNA was isolated using a PUREGENE DNA isolation kit from Gentra Systems (Minneapolis, MN), digested with *Mfe*I and the digests run on a 0.8% agarose gel. DNA was transferred to a Nytran SuPerCharge membrane using the Turbo Blotter kit (Schleicher & Schuell, Keene, NH). The probe was generated by PCR amplification of the coding sequence of the 86-028NP *pilA* gene using the primers 5'tgtgacacttccgcaaaaa (SEQ ID NO: 23) and 5'taataaaaggaaaatgaatga (SEQ ID NO: 24). The amplicon was purified using a QIAquick PCR purification kit (Qiagen* Inc., Valencia, CA). Following the manufacturer's directions, 100 ng of purified PCR product was labeled with horseradish peroxidase using the ECL Direct Nucleic Acid Labeling and Detection System (Amersham* Biosciences UK Ltd., Little Chalfont, Bucks, UK). Developed blots were exposed to Fuji Super Rx X-ray film (Fuji Photo Film Co., Tokyo, Japan).

[0062] The PilA polypeptide of NTHi strain 86-028NP has a predicted and apparent molecular mass of approximately 14 kDa, contains an N-terminal methylated phenylalanine.

Example 2

[0063] NTHi strain 86-028NP formed classic aggregates in a sub-agar surface translocation assay and a surface growth assay when grown under conditions of nutrient depletion.

[0064] NTHi strain 86-028NP was grown on chocolate agar for 18-20 hours (37°C, 5% CO_2, in a humidified atmosphere) prior to all experiments. Subsequently, this organism was inoculated onto either sBHI, a rich medium on which the NTHi grows very well, or a chemically defined medium which supports the growth of *H. influenzae* (Coleman *et al. J. Clin. Micro.*, 41:4408-4410, 2003) that comprised 83% RPMI1640 media (Gibco* BRL, Rockville, MD), sodium pyruvate (87.3 mM) (Gibco BRL), β-NAD (0.0087 mg/ml) (Sigma* Chemical Co., St Louis, MO), HEME-histidine (0.0175 mg/ml) (Sigma), Uracil (0.087 mg/ml) (Sigma), and inosine (1.75 mg/ml) (Sigma).

[0065] Both agars were poured into one of two formats, in sterile 8-well chamber slides (Lab-tech, Naperville, IL) or into sterile 35 mm glass petri dishes (Fisher Scientific, location). When the glass slide was separated from the 8-well chamber slides, the agar remained within the chambers, thus enabling use of the "bottom"

*Trade-mark

surface of the agar for inoculation, which is optimal for assay of twitching motility due to the relative smoothness of this surface (Semmler *et al., Microbiology*, 145, 2863-2873, 1999 and Mattick, *Ann. Rev. Microbiol.*, 56, 289-314, 2002). Whereas agars cast into 8-well chamber slides were used to demonstrate a surface growth phenotype, agars poured into the petri dishes were used for demonstration of sub-surface agar translocation (Semmler *et al., supra*) whereas agars cast into 8-well chamber slides were used to demonstrate agar surface growth phenotype. All assays were repeated a minimum of three times, on separate days.

[0066] Agars that had been poured into sterile glass petri dishes were inoculated subsurface with 0.5 µl of a suspension of NTHi grown as described above, using a sterile micropipet tip. Plates were observed after 24 hours incubation (37°C, 5% CO_2) and were then held at room temperature (25°C) for an additional 24 hours prior to re-reading for signs of bacterial translocation between the bottom surface of the agar and the glass petri dish.

[0067] On sBHI medium, 24 hours post-inoculation, NTHi was observed to have grown in a small area (~ 0.5 mm radius) surrounding the inoculation site between the agar and the glass petri dish bottom. After an additional 24 hours, the growth pattern remained similar to that observed at 24 hours. On the chemically defined medium after 24 hours of incubation, growth of NTHi was observed between the agar surface and the glass petri dish bottom, at a distance 2 to 5 mm from the inoculation site. The bacteria had also aggregated into small colonies in a halo-like pattern surrounding the inoculation site. After 48 hours, NTHi had formed a very distinct array of micro-colonies with many occurring at a distance > 5 mm from the inoculation site. The formation of micro-satellites up to 5 mm distance from original site of inoculation was a hallmark finding of growth on chemically defined medium and was never seen when strain 86-028NP was grown on rich agar.

[0068] Chamber slides were either inoculated with 0.5 ul of a suspension of 18-20 hour chocolate agar-grown NTHi [suspended in sterile pyrogen free saline (American Pharmaceutical Partners Inc., Schaumburg, IL)], or a single colony was stabbed for transfer to the surface of the agar with a sterile toothpick.

[0069] On sBHI medium, thirty minutes post-inoculation, NTHi appeared in close association with the agar surface and was growing in a sheet-like pattern. At 2.5

hours, approximately 80-90% of the surface area was covered with a thin sheet of bacteria. Also at this time, micro-aggregates of NTHi began to appear. At 6 - 7 hours post-inoculation, these micro-aggregates were discernable with the naked eye and there were approximately 3-5 micro-aggregates per well. In addition, NTHi were still observed to be growing as a sheet that covered approximately 50-70% of the agar surface. Twenty-four hours after inoculation, NTHi appeared as large single colonies at each inoculation site.

[0070] On chemically defined medium, like that observed on sBHI, thirty minutes post-inoculation, NTHi appeared to be growing in sheet, however the density of the bacteria appeared much less than that observed on sBHI agar. At 2.5 hours after inoculation, numerous micro-aggregates were evident throughout the agar surface. In contrast to those noted when NTHi was inoculated onto sBHI agar, these micro-aggregates were larger and much more dense in appearance. Approximately 30-40 micro-aggregates could be seen on each well. There was still a large area of sheet like growth of NTHi at this time point, with approximately 80% of the surface area covered by bacteria. At 6-7 hours post inoculation, the micro-aggregates were larger, denser, and easily seen with the naked eye. Also, areas of radial growth or halos were seen radiating outward from large colonies, similar to the growth patterns described for Neisseria and Pseudomonas sp. (refs). By this time period, most of the bacteria appeared to be arranged in small clusters or micro-aggregates with a very small proportion seen covering the agar surface as a sheet or monolayer. After 24 hours, there were large single colonies at each inoculation site, however there were also many small satellite colonies present over the entire agar surface, including sites remote from the points of inoculation.

[0071] Thus, NTHi strain 86-028NP demonstrates classic aggregate formation, similar to that reported for type IV pilus-expressing *P. aeruginosa* (Semmler *et al.*, *Microbiology*, 145(10), 2863-2873, 1999), when grown under conditions of nutrient depletion.

Example 3

[0072] The movement of individual NTHi cells between a glass coverslip and a smooth agar surface was traced by video microscopy. The cells moved at approximately 0.42 μm/sec, consistent with that reported for twitching *P. aeruginosa*

(Skerker and Berg, *Proc. Natl. Acad., Sci. USA*, 98, 6901-6904, 2001) and *Neisseria gonorrhoeae* (Merz *et al., Nature,* 207, 98-102, 2000).

[0073] A loopful of NTHi stain 86-028NP, grown on chocolate agar at 37°C and 5% CO_2 for 20 hours and then held at ambient temperature for an additional 24 hours, was suspended in sterile water and 0.5 µl of the resulting suspension was placed onto a sterile glass slide. To provide contrast and thus aid visualization, 0.5 µl of trypan blue (0.4%, Sigma, St. Louis MO) was added to the bacterial suspension. The droplet was then covered with a sterile coverslip and viewed via light microscope (Axioskope 40, Zeiss, Thornwood, NY). Specimens were observed at room temperature over a period of approximately 15-20 minutes. The bacteria were readily observable and directional movement of several, although not all, cells or microaggregates of cells was noted. In order to stimulate activity, we added 0.5 µl of a heme solution (1 mg/ml) (Sigma, St. Louis, MO) to one side of the sterile coverslip. Twitching activity was documented by the capture of both video [video otoscopy system ($MEDR_X$ Inc, Seminole, FL) attached to a VCR] and still images in order to determine length and rate of excursions.

[0074] Individual cells, or microaggregates of cells, traveled a total linear distance of approximately 11.0 µm over a period of 51 seconds (rate approximately 0.22 µm/sec). However, over the entire period of observation, the rate of twitching motility observed ranged from 0.14 to 0.48 µm/sec.

Example 4

[0075] Type IV pili were visualized by negative staining and transmission electron microscopy.

[0076] Overnight cultures of NTHi strain 86-028NP were inoculated onto sBHI and defined agar plates and incubated for 2, 6 or 24 hours at 37°C, 5% CO_2. Additionally, cultures were inoculated into sBHI broth and defined broth and incubated for 2.5 or 5.5 hours. These latter time points represent entry into exponential and lag phases of growth, respectively. Bacteria were then negatively stained using a Whatman-filtered solution containing 2.0% ammonium acetate w/v (Sigma) and 2.0% ammonium molybdate w/v (Sigma) in sterile water (Bakaletz *et al. Infect Immun*, 1988 56:331-5). Formvar- and carbon-coated copper grids, 300 mesh, (Electron Microscopy Sciences) were touched to individual colonies grown on agar plates, and then floated on a

droplet of the negative stain solution. Broth-grown cultures were pelleted, the bacteria resuspended in sterile water and grids were floated on equal volumes of bacterial suspension and negative stain. After 5 minutes, grids were blotted and allowed to air dry prior to viewing in an Hitachi Model H-600 transmission electron microscope with attached video monitor (Gatan, Inc., Pleasanton, CA) and digital imaging system (Gatan, Inc.).

[0077] When NTHi were grown on sBHI, no type IV pilus-like structures were observed. Conversely, when grown under defined nutrient conditions, NTHi was seen to express structures of approximately 6 - 7 nm diameter. Many of these structures were also found free on the grid surface. There were approximately 5 to 6 pili per bacterial cell and these were polar in location.

Example 5

[0078] A mutant deficient in the expression of PilA was generated to further characterize components of the structures observed when strain 86-028NP was grown in alkaline conditions on chemically defined media.

[0079] The *pilA* gene and approximately 1kb 5′ and 3′ of the gene from strain 86-028NP was amplified by PCR, cloned into pGEM-T Easy (Promega) and the DNA sequence determined to verify that there were no changes in the sequence in the clone as a result of the PCR amplification. As there was no convenient restriction site in the *pilA* gene, a *Bam*HI site was engineered into the gene using the Stratagene QuikChange Site-Directed Mutagenesis Kit. The resulting construct was linearized with *Bam*HI and the gene was insertionally inactivated with the ΩKn-2 cassette (Perez-Casal *et al., J. Bacteriol.*, 173: 2617-2624, 1991). The resulting construct was linearized and transformed into strain 86-028NP using the MIV method (Poje and Redfield, p. 57-70 in Herbert *et al.* (Eds.), *Haemophilus influenzae* Protocols, Humana Press Inc., Toronto, 2003). Kanamycin-resistant clones were selected and insertional inactivation of the 86-028NP *pilA* gene was verified in selected clones by Southern hybridization.

[0080] When the *pilA* mutant was evaluated for expression of type IV pili after growth under conditions that induced the increased expression of type IV pili in the parental isolate (Example 4), no cell-associated or free type IV pili were observed confirming that the *pilA* gene product (and/or the *pilBCD* gene products since the

mutation is *pilA* is likely to disrupt the downstream gene products) are required for pilus expression.

Example 6

[0081] To determine whether type IV pili are necessary for colonization of the nasopharynx, as well as survival in and/or ability to form a biofilm in the middle ear, we challenged fourteen adult chinchillas both intranasally and transbullarly with either the parent strain 86-028NP or with an isogenic *pilA* mutant (Example 5). On days 2, 5, 10, 15 and 20 post-challenge, nasopharyngeal lavages and epitympanic taps were performed, and both nasal and middle ear mucosae were retrieved from 1-2 chinchillas per cohort to determine cfu of NTHi in each of these anatomic sites. Both the parent and *pilA* mutant were able to survive in the chinchilla host for twenty days. However, whereas both strains were present in equivalent amounts in lavage and tap fluids, when assayed for an adherent subpopulation in tissue homogenates of nasal mucosae, the *pilA* mutant was absent from, or below our ability to detect, in 80% of the homogenates recovered after day 5 whereas 87% of similar nasal mucosae recovered from animals challenged with the parental isolate were culture positive.

[0082] Confocal microscopy was performed on snap-frozen tissue to determine whether a biofilm was present. The biomass formed by the *pilA* mutant in the middle ear was of a different character than the well-structured biofilm characteristic of the parental isolate. The data indicate that NTHi type IV pili play a key role in the disease course of OM.

Example 7

[0083] The *pilA* gene of ten clinical isolates of NTHi have been sequenced. The nucleotide and amino acid sequences from the isolates are respectively set out as follows: 1728MEE in SEQ ID NOs: 25 and 26, 1729MEE in SEQ ID NOs: 27 and 28, 3224A in SEQ ID NOs: 29 and 30, 10548MEE in SEQ ID NOs: 31 and 32, 1060MEE in SEQ ID NOs: 33 and 34, 1885MEE in SEQ ID NOs: 35 and 36, 1714MEE in SEQ ID NOs: 37 and 38, 1236MEE in SEQ ID NOs: 39 and 40, 1128MEE in SEQ ID NOs: 41 and 42, and 214NP in SEQ ID NOs: 43 and 44. An alignment of the amino acid sequences with those of the *pilA* polypeptides from Rd and 86-028NP is presented in Figure 1.

[0084] The *pilA* genes of all isolates encode a 12-residue leader peptide that is largely invariant save a Q to L substitution at position 6 in two isolates as well as in strain Rd. Mature PilA contains 137 residues and is predicted to contain a characteristic methylated phenylalanine at position +1. Tyrosine residues at positions +24 and +27, and believed to be involved in subunit-subunit interactions, are highly conserved as are four Cys residues at positions +50, +60, +119 and +132. Interestingly, the NTHi PilA proteins appear to represent a new class of type IV pili. The leader peptide is larger than that characteristic for type IVa pilins (typically 5-6 residues in length), yet shorter than the typical IVb leader peptide (15-30 residues). At 137 residues, the mature NTHi pilin is shorter than either class IVa or IVb pilins (150 and 190 residues, respectively). Since the NTHi PilA proteins begin with an N-methylated phenylalanine, they are more like class IVa pilins however in electron micrographs, free NTHi type IV pili always appear in laterally associated bundles, a phenotype more classically associated with class IVb pilins due to their ability to self-associate through anti-parallel interactions.

[0085] In terms of NTHi PilA sequence diversity, overall these sequences are highly homologous. See Figure 1. Two areas of potentially important diversity, if surface accessible and also targeted for vaccine development due to protective immunodominance or adhesin-binding function, exist at positions 55-64 and 79-87. Within the first region, amongst the clinical isolates, there appears to be two major variants, one representing the majority (seven of eleven isolates, 64%) and characterized by the following sequence: NET/ITNCT/MGGK and the other representing the minority (four of eleven isolates, 36%) and characterized by the sequence: GKP/LST/SCSGGS. There are however some additional minor variations at positions +57 and +61 in the majority grouping and at positions +57 and +59 for the minority grouping. The diversity noted at position +61 is only seen in one isolate to date (strain #1885), wherein there is a T to M substitution. Within the second focused region of diversity (position 79-87), there appears to be two equally distributed variants among the clinical NTHi isolates. The sequence ASVKTQSGG is present in five of eleven clinical isolates (~45%), whereas the sequence KSVTTSNGA is present in six of eleven clinical isolates (~55%).

[0086] Overall, of the seven isolates with the majority sequence at position 55-64, five isolates also have the KSVTTSNGA motif at region 79-87, with the remaining

two isolates having the ASVKTQSGG motif in this region. Of the four remaining clinical isolates with the minority sequence at position 55-64, three of these also have the ASVKTQSGG motif at region 79-87, with only one isolate having the KSVTTSNGA sequence in this domain. Thereby, depending on whether or not these are conservative substitutions or not and if the sequences reside within surface accessible, hydrophilic areas of high antigenic index and thus are targets for vaccine development, they may or may not need to be included as type IV pili-based components for inducing an immune response to NTHi.

Example 8

[0087] To examine the role of type IV pili in NTHi-induced OM and determine if antibodies from children during natural disease recognize type IV pili, four sequential synthetic peptides were synthesized representing amino acids 21-137 of SEQ ID NO: 2 of the mature PilA of NTHi strain 86-028NP and assayed via biosensor versus a panel of pediatric sera and middle ear effusions obtained from children with OM. Serum from children at 2, 6-7, or 18-19 mos and 4-6 yrs of age with OM due to NTHi were segregated into low and high incidence groups, as determined by the number of episodes of OM.

[0088] To date, antibodies in sera obtained from children 2 and 6-7 mos of age of either high or low incidence of OM demonstrated limited reactivity with any of the type IV pili peptides, with values of 3-38 and 4-61 resonance units (RU), respectively. However, a striking difference between these groups was seen with serum obtained at 18-19 mos of age. Whereas values obtained with sera from the low incidence 18-19 mos group were 44-105 RU, sera from the high incidence panel recognized the type IV pili peptides up to five-fold greater (81-528 RU). At 4-6 yrs of age, as children naturally resolve OM, reactivity to the type IV pili peptides was again similar between the two incidence groups. To confirm that the reactivity observed here was specific for disease due to NTHi, sera from children with OM due to *S. pneumoniae* were also assayed. In all cases, RU values of 16-120 were obtained versus all type IV pili peptides. To assay for the presence of antibodies directed against type IV pili in effusions obtained from the middle ears, we also assayed these fluids via biosensor. Whereas effusions from children with OM due to *Streptococcus* were unreactive, those recovered from children with OM due to NTHi were highly reactive with type IV pili peptides. Collectively, the data strongly suggests that NTHi type IV pili are

expressed *in vivo*, during the disease course of OM and that these structures are immunogenic.

Example 9

[0089] Identification of immunogens that confer broad cross-protective immune responses against NTHi may be carried out as follows.

Synthesis of NTHi pilin peptides

[0090] In order to map both immunodominant and adhesin-binding domains of PilA, a panel of overlapping sequential peptides as well as peptides derived from two focused areas of known diversity (see Example 6 above) are synthesized. For example, thirteen 15-mer peptides with a 5-residue overlap will be synthesized to map the entire 137 residue mature pilin protein. The final C-terminal peptide will actually be a 17-mer spanning residues 121-137 in order to incorporate the final two amino acids of mature PilA. To accommodate the two described regions of diversity, two variants of the peptide that spans residues 51-65 and two variants of the peptide that spans residues 79-95 will be synthesized. In order to fully accommodate this latter region of diversity, two peptides are made varying in length by one amino acid at the N-terminus since the region of diversity actually spans residues 79-87. Due to the additional residue, each of these latter two peptides will be 16-mers in length. Thus a total of fifteen peptides will be synthesized: twelve will be 15-mers, one will be a 17-mer and two will be 16-mer peptides. The peptides are set out in Table 2 below wherein amino acid residue numbers correspond to amino acids in SEQ ID No: 2.

Table 2

Peptide	Sequence
OLP1 [Residues 1 – 15]	FTLIELMIVIAIIAI
OLP2 [Residues 11 – 25]	AIIAILATIAIPSYQ
OLP3[Residues 21 – 35]	IPSYQNYTKKAAVSE
OLP4 [Residues 31 – 45]	AAVSELLQASAPYKA
OLP5 [Residues 41 – 55]	APYKADVELCVYSTN
OLP6vA [Residues 51 – 65]	VYSTNETTNCTGGKN
OLP6vB [Residues 51 – 65]	VYSTGKPSTCSGGSN
OLP7 [Residues 61 – 75]	TGGKNGIAADITTAK
OLP8 [Residues 71 – 85]	ITTAKGYVKSVTTSN
OLP9vA [Residues 79 –94] 77- 95	YVKSVTTSNGAITVKGDGT
OLP9vB [Residues 79 –94] 77- 95	YVASVKTQSGGITVKGNGT
OLP10 [Residues 91 – 105]	KGDGTLANMEYILQA

OLP11 [Residues 101– 115]	YILQATGNAATGVTW
OLP12 [Residues 111–125]	TGVTWTTTCKGTDAS
OLP13 [Residues 121–137]	GTDASLFPANFCGSVTQ

Generation of recombinant NTHi pilin (rPilA)

[0091] Recombinant PilA protein (rPilA) may be generated to serve as a more readily renewable product for use in assays to represent the entire pilin subunit protein. To do this, the published protocol of Keizer *et al.* (*J. Biol. Chem.*, 276: 24186-14193, 2001), who studied a pilin which also had four Cys residues as it will be critical that rPilA similarly be properly folded so as to possess functional qualities of the native pilin subunit, is utilized. Briefly, a truncated pilin is engineered wherein the first 28 residues are removed from the N-terminus to prevent aggregation, and this truncated pilin will be further engineered to be transported to the periplasm by means of the incorporation of an OmpA leader sequence in the construct. Using this strategy Keizer *et al.* generated a recombinant soluble monomeric *P. aeruginosa* pilin protein that was able to bind to its receptor (asialo GM1) in *in vitro* assays and decrease morbidity and mortality in mice when the peptide was delivered 15 mins. prior to heterologous challenge. This soluble, monomeric, truncated form of NTHi PilA will be useful in the studies described below.

Mapping immunodominant domains of PilA

[0092] The peptides and native and recombinant PilA proteins are used in concert with both acute and convalescent chinchilla and pediatric sera in addition to middle ear fluids from chinchillas and children experiencing either experimental or natural OM due to NTHi (all available within our current specimen collection or planned for collection as part of a separate initiative) to map immunodominant domains of PilA via ELISA and also biosensor assays. Briefly, PilA peptides, rPilA and native pili are bound to 96-well microtiter plates or to a biosensor chip surface, then assayed for the relative amount of antibody within serum or middle ear fluid samples that binds to each peptide.

[0093] These studies identify those regions of the pilin subunit that are relatively more immunodominant than others as recognized by both the chinchilla host and the human child. Due to the fact that the N-terminal-most synthetic peptide is comprised of highly non-polar (hydrophobic) amino acids and is thus likely buried within the pilus fiber and inaccessible to antibody, this 15-mer peptide is anticipated to serve as

an internal *negative* control for the assays described here. Normal pediatric sera and naïve chinchilla sera will serve as negative serum controls and middle ear lavage fluids recovered from a naïve animal will be used as a negative control for effusions recovered during NTHi infection of the middle ear.

Mapping adhesin binding domains of PilA

[0094] In order to map the eukaryotic cell binding domains of PilA, competitive ELISA assays are conducted as well as evaluations of the ability of the synthetic pilin peptides to inhibit NTHi binding to eukaryotic cells in cell culture via confocal microscopy. For initial screening assays, relevant eukaryotic target cells are grown within 96-well microtiter dishes. Cells will be washed, then pre-incubated with synthetic pilin peptides, rPilA or native NTHi pili [0.2 μg in PBS] to determine their relative ability to block binding of NTHi strain 86-028NP (grown under conditions known to promote pilin expression) to these eukaryotic cells. Relative adherence of NTHi will be determined using polyclonal antisera directed against a homologous whole NTHi OMP preparation and HRP-conjugated protein A with color developed with tetramethylbenzidine (TMB). For these assays relevant epithelial target cells [i.e. chinchilla middle ear epithelial cells (CMEEs), normal human bronchial/tracheal cells (NHuBr), human type II alveolar epithelial cell line (A549s)], a clinically irrelevant epithelial target cell to which NTHi do not adhere (CHOs) as well as an *endothelial* target cells [human umbilical vein endothelial cells (HUVECs)] will be used.

[0095] For those peptides that show inhibitory activity (typically the cut-off is at ≥ 15% inhibition of adherence relative to controls), any dose-dependence to the observed bacterial adherence blocking capability is determined. The interaction may be further evaluated by conducting adherence-blockade assays using a Transwell system wherein respiratory tract epithelial cells (CMEEs and NHuBrs) are grown at the air-fluid interface. These cells are incubated with first synthetic peptides of interest (or appropriate controls, i.e. isolated OMP P5 and P2 as positive and negative controls for NTHi surface proteins involved or not in adherence, respectively and rPilA) to attempt to block available Tfp receptors, then they will be washed 5X with fresh growth medium followed by inoculation with ~2-5 x 107 NTHi grown under conditions we know will promote expression of Tfp. Cultures will be washed to remove non-adherent bacteria, then fixed with methanol on ice for 5 min, air dried,

rinsed with PBS and the membranes removed from the Transwell and placed on glass coverslips for imaging via confocal microscopy. To detect adherent NTHi, chinchilla hyperimmune anti-NTHi OMP serum and FITC-Protein A will be used to document the interaction of NTHi with its epithelial target cell, or conversely the blocking of this interaction by peptides that represent putative adhesin binding domains of PilA.

Choice of immunogen

[0096] Based on the data acquired in above, immunogenic peptides are chosen based on both relative immunodominance as well as ability to inhibit adherence of NTHi to respiratory epithelial target cells. Depending on the biochemical and structural characteristics of the regions of interest, the peptides will be produced as either synthetic peptide(s) or recombinant peptide(s).

[0097] Immunogenicity and protective efficacy of the PilA immunogens is evaluated initially in the chinchilla animal model disclosed herein and in human trials.

Example Summary

[0098] The foregoing evidence indicates that NTHi express functional type IV pili on their surface. The proteins encoded by these genes are known to be important for transformation competence in typeable *H. influenzae* and are contemplated herein to be important for biofilm formation by NTHi as well. Collectively, these observations indicate that NTHi is likely to up-regulate expression of type IV pili in the nutrient restricted environment of the human host. Thus, type IV pili represent an excellent target for a vaccine and/or for an antimicrobial strategy for pathogenic conditions caused by NTHi as well as *H. influenzae* strains a, b, c, e and f.

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JUMBO APPLICATIONS / PATENTS

THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE THAN ONE VOLUME.

THIS IS VOLUME __1___ OF __2___

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CLAIMS:

1. An isolated polynucleotide comprising a nucleotide sequence encoding the amino acid sequence of any one of: PilA polypeptide SEQ ID NO: 2, PilA polypeptide SEQ ID NO: 26, PilA polypeptide SEQ ID NO: 28, PilA polypeptide SEQ ID NO: 30, PilA polypeptide SEQ ID NO: 32, PilA polypeptide SEQ ID NO: 34, PilA polypeptide SEQ ID NO: 36, PilA polypeptide SEQ ID NO: 38, PilA polypeptide SEQ ID NO: 40, PilA polypeptide SEQ ID NO: 42, or PilA polypeptide SEQ ID NO: 44.

2. An isolated polynucleotide comprising the nucleotide sequence of any one of: *pilA* SEQ ID NO: 1, *pilA* SEQ ID No: 25, *pilA* SEQ ID No: 27, *pilA* SEQ ID No: 29, *pilA* SEQ ID No: 31, *pilA* SEQ ID No: 33, *pilA* SEQ ID No: 35, *pilA* SEQ ID No: 37, *pilA* SEQ ID No: 39, *pilA* SEQ ID No: 41 or *pilA* SEQ ID No: 43.

3. A vector comprising the polynucleotide of claim 1 or 2.

4. An isolated polypeptide comprising the amino acid sequence encoded by the nucleotide sequence of claim 1.

5. An isolated polypeptide comprising the amino acid sequence of any one of PilA polypeptide SEQ ID NO: 2, PilA polypeptide SEQ ID NO: 26, PilA polypeptide SEQ ID NO: 28, PilA polypeptide SEQ ID NO: 30, PilA polypeptide SEQ ID NO: 32, PilA polypeptide SEQ ID NO: 34, PilA polypeptide SEQ ID NO: 36, PilA polypeptide SEQ ID NO: 38, PilA polypeptide SEQ ID NO: 40, PilA polypeptide SEQ ID NO: 42, or PilA polypeptide SEQ ID NO: 44.

6. An isolated peptide fragment of the polypeptide of SEQ ID NO: 2, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, or SEQ ID NO: 44, wherein the peptide fragment elicits an immune response to *H. influenzae* pilin polypeptide.

7. An isolated peptide fragment of the polypeptide of SEQ ID NO: 2, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36,

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SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, or SEQ ID NO: 44, wherein the peptide fragment inhibits *H. influenzae* cellular adherence.

8. An isolated peptide fragment of the polypeptide of claim 4 or 5, wherein the peptide fragment comprises amino acids 35 through 68 of SEQ ID NO: 2.

9. An isolated peptide fragment of the polypeptide of claim 4 or 5, wherein the peptide fragment comprises amino acids 69 through 102 of SEQ ID NO: 2.

10. An isolated peptide fragment of the polypeptide of claim 4 or 5, wherein the peptide fragment comprises amino acids 103 through 137 of SEQ ID NO: 2.

11. An isolated peptide fragment of the polypeptide of claim 4 or 5, wherein the peptide fragment comprises amino acids 21 through 35 of SEQ ID NO: 2.

12. A composition comprising the polypeptide of claim 4 or 5 or the peptide fragment of any one of claims 6-11 and a pharmaceutically acceptable carrier.

13. An antibody that specifically binds to the polypeptide of claim 4 or 5 or the peptide fragment of any one of claims 6-11.

14. A composition comprising the antibody of claim 13 and a pharmaceutically acceptable carrier.

15. A method for detecting non-typeable *H. influenzae* (NTHi) bacteria in a biological sample comprising

(a) contacting the polynucleotide of claim 1 or 2 or a polynucleotide that encodes the peptide fragment of any one of claims 6-11 with a biological sample under stringent conditions for hybridization and washing with 0.015 M sodium chloride, 0.0015 M sodium citrate at 65-68°C or 0.015 M sodium chloride, 0.0015M sodium citrate, and 50% formamide at 42°C, and

(b) detecting hybridization of the polynucleotide within the sample, wherein hybridization indicates the presence of NTHi bacteria.

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16. A method for detecting non-typeable *H. influenzae* (NTHi) bacteria in a biological sample comprising:

(a) contacting the antibody of claim 13 with a biological sample, and

(b) detecting binding of the antibody within the sample, wherein binding indicates the presence of NTHi bacteria.

17. The method of claim 15 or 16 wherein the biological sample is selected from the group consisting of serum, sputum, ear fluid, blood, urine, lymphatic fluid, and cerebrospinal fluid.

18. Use of one or more polypeptides of claim 4 or 5 or the peptide fragment of any one of claims 6 and 8-11 for the preparation of a medicament for eliciting an immune response to non-typeable *H. influenza* (NTHi) bacteria.

19. Use of one or more polynucleotides of claim 1 or 2 for the preparation of a medicament for eliciting an immune response to non-typeable *H. influenzae* (NTHi) bacteria.

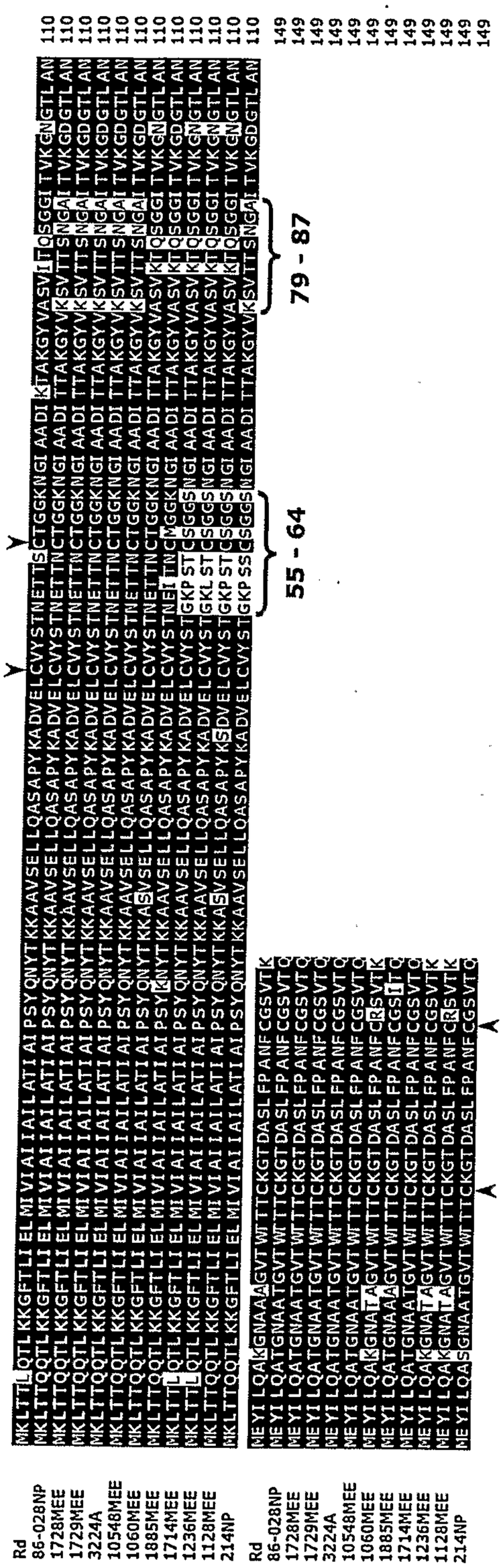
20. The use of claim 19 wherein the polynucleotide is in a plasmid or viral vector.

21. Use of an antisense oligonucleotide that inhibits expression of the polypeptide of claim 4 or 5 for the preparation of a medicament for treating or preventing non-typeable *H. influenza* (NTHi) bacterial infection.

22. Use of the antibody of claim 13 or composition of claim 14 for the preparation of a medicament for treating or preventing non-typeable *H. influenza* (NTHi) bacterial infection.

23. The use of claim 21 or 22 wherein the NTHi infection is in the middle ear.

Figure 1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