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Vaccines to combat meningococcal disease - definitive vaccines for elusive pathogens

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Thesis

**VACCINES TO COMBAT MENINGOCOCCAL DISEASE –
DEFINITIVE VACCINES FOR ELUSIVE PATHOGENS**

by

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ABSTRACT

Neisseria meningitidis (Nm) disease occurs worldwide. Disease incidence rates can vary from 1 to 1000 cases per 100,000 with the highest incidence found in the sub-Saharan Africa meningitis belt. Nm has evolved a number of mechanisms to evade host immunity. This includes the production of genetic variants through re-combinatorial events, which is thought to have contributed to the evolution of hyper-invasive lineages that are largely responsible for meningococcal disease. Antigenic diversity of Nm surface proteins has been the main limitation in the design of broadly protective vaccines, particularly against capsular serogroup B strains. To overcome this problem, several Nm genomes have been sequenced in an effort to find highly sequence-conserved surface antigens recognized by the human immune system in order to develop a vaccine, which would be broadly protective against disease. Nm genomes contain over 2 million base pairs that contain between 2000 and 2500 open reading frames. Add to this the difficulty of identifying highly conserved recombinant antigens with strong intrinsic immunostimulatory properties, makes vaccine design and development a daunting task. Recent advances in our understanding of the interactions between innate and acquired immunity, and the discovery of pattern recognition receptors, including

Toll-like receptors (TLRs), have ushered in a new set of adjuvant compounds, TLR agonists, which invoke strong humoral and cellular responses with nominal toxicity and adverse reactions. These insights have opened up new areas of vaccine research to combat invasive Nm disease.

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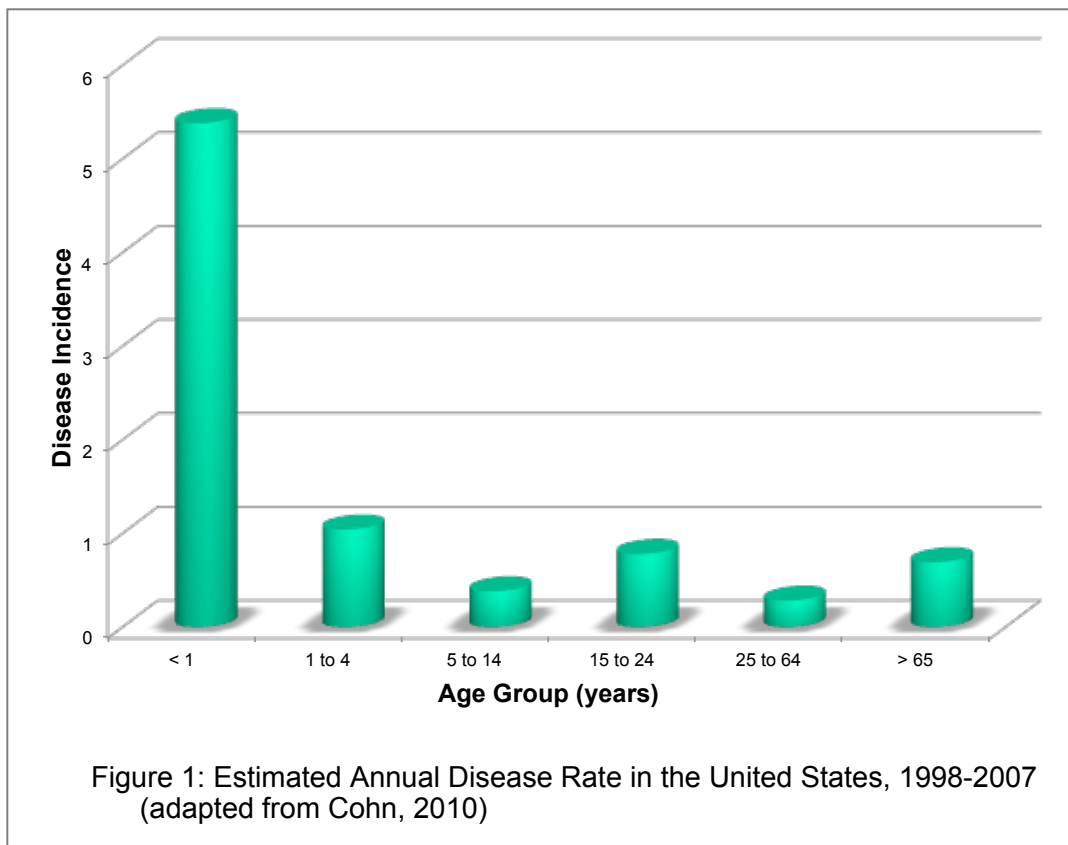
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Epidemiology of *Neisseria meningitidis* Disease

Disease caused by *Neisseria meningitidis* (Nm) is a global health problem. Nm is pathogenic only in humans. Nm infection can result in mortality within 24 to 48 hours from the onset of disease symptoms. The mortality rates associated with meningococcal infection are 10–20%, which can vary by causative strain. Of those individuals that survive infection, approximately 20% experience significant sequelae including limb loss, hearing loss, chronic pain, and loss of neurological function (Pace & Pollard, 2012; Stein-Zamir et al., 2014). Disease incidence occurs mostly within three age groups (Figure 1): the highest rate in infants under the age of 1 years, with approximately two-thirds of Nm disease occurring in the first 6



months due to absences or loss of maternal antibodies; a 2nd peak in adolescents and young adults between 15 and 24 years old; and, a 3rd peak seen in the elderly at 65 years and older shown (Thompson et al., 2006; Cohn et al., 2010; Chang et al., 2012).

Classification of Nm is historically based upon the immunochemistry of its capsular polysaccharide (serogroup). There are 13 serogroups that have been identified to date, with most disease occurrences resulting from serogroups A, B, C, W-135, X, and Y. Meningococci are further classified on the basis of their class 1 outer-membrane proteins (PorA, serosubtype), class 2 or 3 outer-membrane proteins (PorB, serotype), and lipo-oligosaccharides (immunotype). Molecular subtyping with the use of pulsed-field gel electrophoresis, or DNA-sequence analysis has been helpful in identifying closely related strains responsible for disease outbreaks (Frasch et al., 1985; Maiden et al., 1998). Globally, Nm disease cases are caused primarily by serogroups A, B, and C. The geographical variations observed likely result from differences in regional population immunity, and environmental factors. The incidence of disease can vary from between 0.5 and 1000 cases per 100,000 depending on geographical region of occurrence (Stephens et al., 2007; Caugant & Maiden 2009). The majority of cases in Europe and North America involve serogroups B, C and Y, while Serogroups A and C predominating throughout Asia and Africa (Connolly & Noah, 1999; Cohn et al., 2010; Jafri et al., 2013). Fluctuations in disease dynamics have been observed recently in the Sub-Saharan "meningitis

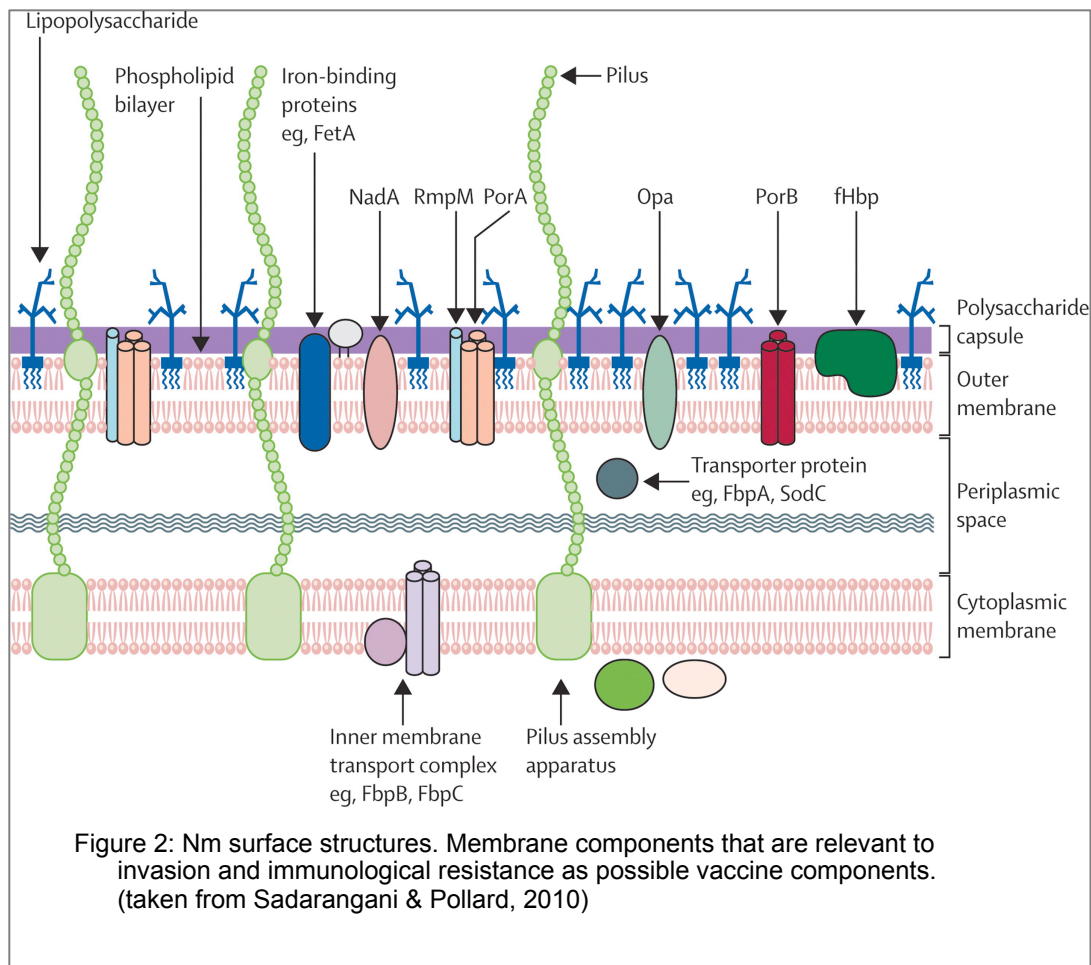
belt", where serogroup A was historically the cause of seasonal epidemics, however serogroup W-135 predominated in 2010 and 2011 (Halperin et al., 2012). In order to better understand the mechanisms underlying outbreaks, a genetics based characterization scheme referred to as Multi-locus Sequence Typing (MLST) was developed in which the sequences of seven housekeeping genes are analyzed to group disease-related isolates into sequence types and then larger clonal complexes. This strain typing system has allowed researchers and clinicians to better determine if local outbreaks and regional epidemics are due to a single strain or multiple unrelated strains circulating within the affected population (Brehony et al., 2007). This typing system has advanced the identification of disease-causing hypervirulent strains.

***Neisseria meningitidis* Disease Mechanisms**

Colonization and Carriage

Nm related invasive disease is a multi-step process, which involves colonization and carriage in the nasopharynx, invasion of the respiratory tract epithelia and migration of the underlying endothelia, entry into the microvasculature, and then systemic dissemination via the bloodstream. Nm colonization and subsequent carriage in the human nasopharynx is typically asymptomatic and can be detected in up to 40% of the population at any particular time. Carriage is transient, can last

from days to months depending on the bacterial strain, and varies by season and age group (Caugant et al., 2007; Caugant & Maiden 2009). The first steps to nasopharyngeal colonization involves the initial adhesion of meningococci to the exposed epithelium which is mediated by Type IV pili, a multimeric scaffold/pore protein complex that spans the inner and outer membranes of Nm strains (Carbonnelle et al., 2006; Brown et al., 2010). The type IV pilus has also been reported in other infection related processes including adhesion to endothelial cells, bacterial aggregation, and migration, and natural transformation of exogenous DNA (Bernard et al., 2014; Imhaus & Dumenil, 2014). Adhesion is further mediated by additional meningococcal surface receptors such as: the opacity proteins, Opa, and Opc; the trimeric autotransporter NhhA; the Adhesion and penetration protein, App; and NadA, which collectively bind to extracellular receptors and matrix components, including carcinoembryonic antigen cell adhesion molecules (CEACAMs), heparan sulfate, and laminin (Virji, 2000; Hadi et al., 2001; Comanducci et al. 2002; Serruto et al., 2003; Capecchi, et al., 2005; Scarselli et al., 2006; Coureuil et al., 2010). The assortment of adhesion receptors with different specificities suggests a high level of binding cooperatively when targeting the same cell type, as well as at other stages of infection when binding endothelium, and other cells types for entry into various host tissues. Many of these membrane structures are possible target for the development of a vaccine to protect against meningococcal disease (Figure 2), however Nm strain diversity and an inclination to circumvent immune surveillance has made use of most of these antigens impractical (Sadarangani & Pollard, 2010).



Immune Evasion by *Neisseria meningitidis*

Several strategies are used by Nm to generate genetic variants in order to evade immunity by altering antigenic structure, or acquire and maintain antibiotic resistance when selective pressures are exerted in this manner (Spratt et al., 1992; Swartley et al., 1997). One such mechanism is horizontal gene transfer, which allows Nm to obtain large segments of DNA from other commensal and invasive *Neisseria* strains or unrelated species (Feil et al., 1999; Linz et al., 2000). Capsule switching is an example of this whereby the original infectious strain can achieve

immunologic escape from natural immunity, or acquired immunity via immunization, while maintaining in essence the same genetic lineage. In the United States, a large percentage of disease-causing Nm strains appear to have arisen via capsule switching including an outbreak of serogroup B disease in Oregon in the 1990s where serogroup C isolates were found to be otherwise genetically indistinguishable from the serogroup B outbreak strain (Diermayer et al., 1999; Harrison et al., 2010). Capsule switching was also likely the cause of a serogroup W-135 outbreak in the year 2000 at the Hajj in Mecca, Saudi Arabia (Mayer et al., 2002; Mustapha et al., 2016).

The importance of the capsule and lipo-oligosaccharide structures on the surface of meningococci for immune evasion and resistance to complement-mediated lysis was demonstrated by a large scale gene disruption study which suggested that these two components were major contributors to serum resistance during invasion and widespread dissemination in the blood stream (Geoffroy et al., 2003). Additionally, it was shown that Nm have three independent RNA thermo-sensors that are activated by an increase in temperature, such as during invasion from the nasopharynx into the blood stream, or during the fever response in humans. The thermo-sensors are in the 5' untranslated regions (UTR) of genes necessary for capsule biosynthesis, sialylation of lipopolysaccharide, and the expression of the complement inhibitor factor H binding protein (fHBP). All three products are essential for resistance to host bactericidal responses (Loh et al., 2013). These

thermo-sensors form stem loop structures at the lower permissive temperatures, which obscures the ribosome-binding site (RBS) contained within the loop, and interferes with translation. When these loops are unwound at higher temperatures, the RBS becomes more accessible allowing increased expression of relevant proteins.

Recombinant gene conversion is employed by Nm to achieve antigenic variants allowing Nm to escape host immune detection without the acquisition of foreign DNA. Over 100 phase-variable genes have been identified (Moxon et al., 1994; Snyder et al., 2001) with the majority associated with meningococcal surface antigens including: the capsule (Hammerschmidt et al., 1996b); lipopolysaccharide (Jennings et al., 1995); the Pile component in Type IV pili which has in close proximity 8 truncated pseudogenes available for recombination with the pile gene (Howell-Adams & Seifert, 2000; Saunders et al., 2000; Andrews & Gojobori, 2004; and, other outer membrane proteins, such as the porins and the opacity proteins (Sarkari et al., 1994; van der Ende et al., 2000). Moreover, antigenic variation has been shown to arise from a variety of insertion sequences, transposons, and Correia elements (Hammerschmidt et al., 1996a; Packiam et al., 2006; Elias & Vogel, 2007). Nm has been shown to also bind complement negative regulators to its surface as an immune evasion strategy, which allows Nm to further mask itself and increase its resistance to lysis by the complement (Madico, et al., 2006). This propensity toward the production of genetic variants through re-combinatorial events is thought to be

a primary mechanism underlying Nm evasion of host protective immunity, as well as the evolution of hyper-invasive lineages that are largely responsible for meningococcal disease.

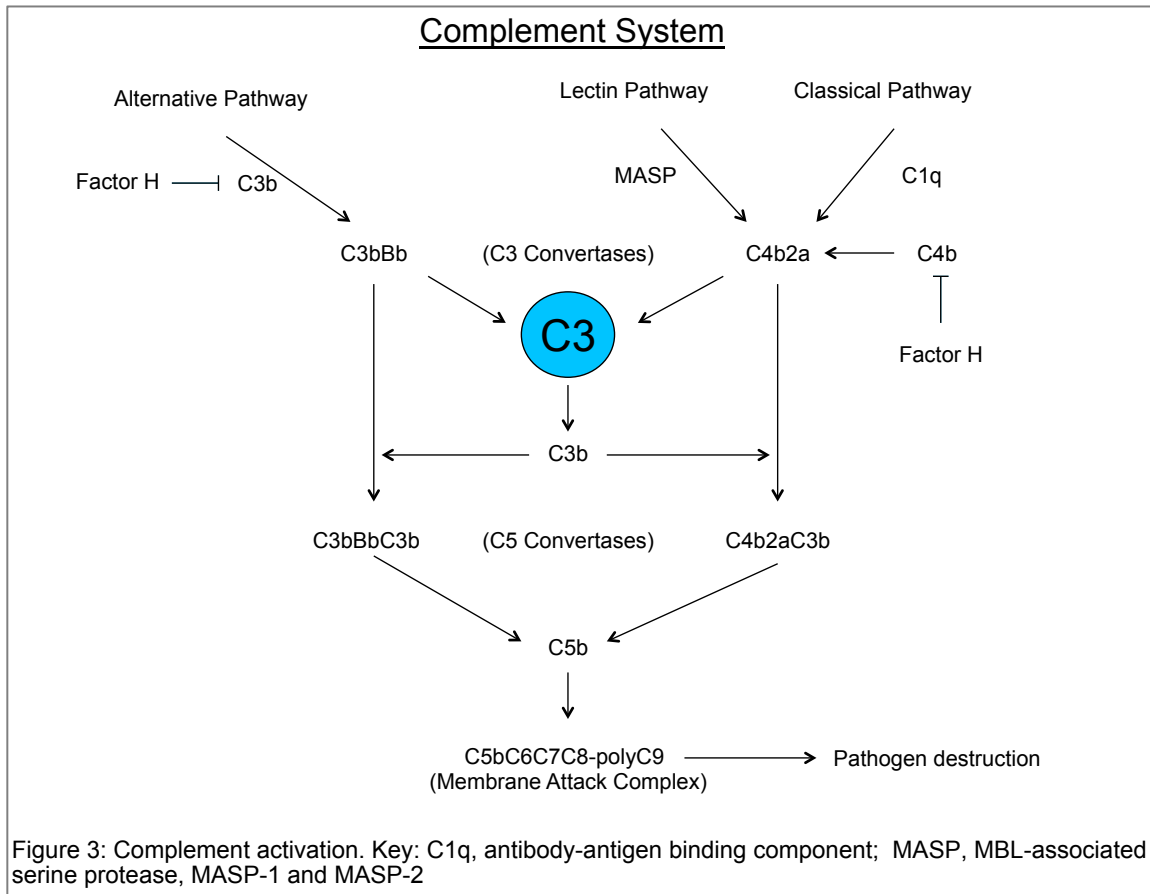
Host Defenses against *Neisseria meningitidis*

Innate immune responses are the first line of defense against Nm, especially in the immature immune systems in human infants and toddlers, who are particularly susceptible to infection following the loss of maternal antibodies. Central to this innate protective response is the complement system, consisting of over 30 fluid phase factors, and membrane-bound regulators of complement, which plays a significant role in defense against meningococcal infection. The importance of the complement system in combating Nm disease is highlighted by the increased susceptibility of patients with complement deficiencies to Nm, in particular loss of terminal complement components, reduction in levels of circulating C3, and alterations in complement regulators (Figuerola et al., 1993; Garty et al., 1993; Schneider et al., 2007; Hellerud et al., 2010).

Three complement activation pathways have been identified to date in humans: the alternative pathway, which is activated by the binding of the complement component C3b covalently to the hydroxyl or amino groups of microbial surface structures that then recruits additional complement components, factor B, factor D

and properdin (P) to further activation; the lectin pathway, which is triggered when mannose-binding lectin (MBL) or ficolins bind to carbohydrates on microbial surfaces and recruit two MBL-associated serine protease (MASP1 and MASP2); and, the classical pathway (C1q, C1r, C1s, C4, and C2 components), which is activated primarily by antibody–antigen interactions (Nesargikar et al., 2012). When triggered, all three converge to further produce C3b via two different C3-convertases, which catalyze the formation of C5-convertases, and sets off the subsequent cascade of downstream activation events (Figure 3). The end product of this cascade is the formation of the membrane attack complex (MAC) involving C5b, C6, C7, C8 and C9, which inserts pores into the surface of pathogens resulting in membrane disruption and pathogen lysis (Morgan et al., 1999; Nesargikar et al., 2012). Additional complement cleavage products, such as C3a, C4a, and C5a, are known to chemotactically recruit immune cells to sites of infections, as well as bind and opsonize microbial targets for clearance by phagocytic cells (Gasque, 2004).

In the case of Nm, the insertion of MACs into surface membranes and subsequent cell lysis has been established as the primary method of protection against disease. This was determined in a landmark study of Army recruits in the United States in the 1960s where the presence of serum bactericidal antibodies was shown to be the most important protective host factor against Nm infection (Goldschneider et al., 1969). These bactericidal antibodies are thought to be naturally acquired through carriage of commensal species, such as *Neisseria lactamica*, that express on their



surface cross-reacting epitopes, as well as from colonization of non-invasive meningococci. This acquisition then provides increased protection against meningococcal infection through early childhood and adolescence (Gold et al., 1978; Pollard & Frasch, 2001; Sanchez S, et al., 2002; Troncoso et al., 2002). Given the high rate of Nm disease in infants however, the need to induce via vaccination a strong adaptive immune response in this population is clear and apparent.

Correlates of Protection

In the seminal study in the 1960s, the importance of bactericidal antibody for protection against Nm disease was shown using baseline serum samples from military recruits who were at high risk of acquiring serogroup C disease during training camp. A baseline serum bactericidal titer of $\geq 1:4$ was a strong predictor of protection whereas individuals with baseline titers $< 1:4$ were at highest risk to contract disease. A titer of 1:4 indicates that a dilution of serum down to 25% by volume, for use in the standard bactericidal assay, will result in a $\geq 50\%$ reduction in bacterial colonies compared to the number of colonies measured at time zero. Furthering this link was data on age-specific incidence of meningococcal disease in the United States, which demonstrated that the proportion of individuals lacking serum bactericidal activity to serogroups A, B, and C was inversely related to the incidence of disease (Goldschneider et al., 1969; Frasch CE, 2009). These data established the bactericidal assay, with normal human serum as the complement source, as the immunologic correlate of protection against meningococcal disease. For serogroup B, a correlation between protection after vaccination and the level of bactericidal antibody was reported following the use of an Outer Membrane Vesicle (OMV) vaccine during a meningococcal epidemic in Norway (Holst et al., 2003).

Finding normal human serum lacking naturally acquired antibodies to Nm from adults is not trivial, as sera from many healthy adults often contain antibodies to group-specific polysaccharide, lipopolysaccharide, or outer membrane proteins that

can activate complement and interfere with assay results. In order to accurately model these early studies, serum complement from an untreated agammaglobulinemia patient, which is now rare in the population due to medical management, or from healthy adults who lacks intrinsic bactericidal activity against specific strains of interest, would be required. Because of the perceived challenges in obtaining human complement, infant rabbit sera that lack intrinsic bactericidal activity was selected for use in the standardization of the bactericidal assay (World Health Organization, 1976; Wong et al., 1977; Maslanka et al., 1997).⁶⁵⁻⁶⁷ It was later reported that the use of rabbit complement resulted in much higher bactericidal titers for serogroup B and C meningococcal strains than the use of human complement (Zollinger & Mandrell, 1983; Mandrell, et al., 1995). Since the clinical relevance of higher bactericidal titers as measured in the standardized assay with rabbit complement was unknown, a direct comparison of the two complement sources using serogroup C post vaccination human sera after 1 dose determined that a threshold titer of approximately 1:128 when using rabbit complement was equivalent to 1:4 when using human complement (Santos et al., 2001).⁷⁰ This observation was confirmed and extended to serogroups A, W-135, and Y in a follow-up study (Gill et al., 2011).

The apparent difference in titer when using the two complement sources has been attributed at least in part to the species specificity of binding of human factor H, a complement regulatory molecule that down-regulates complement activation. Nm

binds human factor H to its surface as an immune evasion strategy, which allows Nm to mask itself and increase its resistance to bactericidal activity. Rabbit factor H does not bind Nm allowing unrestricted complement deposition onto its surface and bacteriolysis at significantly lower anti-Nm antibody concentrations (Schneider et al., 2007; Granoff et al., 2009). For serogroup B strains, species specificity regarding the source of exogenous complement for clinical assay use was not an issue because the lack of compatibility of baby rabbit complement in the assay system eliminated it as a viable option. Despite the perceived limitations, sufficient volumes of human complement were obtained for a four-site interlaboratory standardization of the bactericidal assay for Nm serogroup B (Borrow et al., 2005), as well as ongoing clinical trials.

As a correlate of protection, the utility of the bactericidal assay in assessing vaccine responses to new and novel antigen-adjuvant combinations is evident. There is an ongoing need however, to better understand the mechanisms underlying meningococcal disease, and develop additional laboratory correlates for testing the effectiveness of meningococcal vaccines in both pre-clinical studies and future human clinical trials. Among the model systems that have come forward, the ex vivo human blood bacteremia model, the infant rat model, the humanized mouse infection assay, and the meningococcal antigen typing system (MATS) are some of the in vitro systems showing early promise for the evaluation of protective immunity against Nm (Granoff et al., 1998; Toropainen et al., 1999; Gorringer et al.,

2005; Plested et al., 2009, Donnelly et al., 2010). The need for streamlined assays for use during clinical trials is especially apparent given that volumes of test samples are limiting, particularly in infants, and breadth of bacterial strains to be tested are large. Many normal human donors have intrinsic bactericidal activity that is strain specific, hence a specific complement donor or donor set must be found for each isolate. Assay miniaturization is an important issue for both trial specimen and complement reagent conservation with the aim of maintaining the established protective correlation (Mountzouros & Howell, 2000; Rodríguez et al., 2003; Mak et al., 2011).

Developments in *Neisseria meningitidis* Capsular Antigen Vaccines

Despite the prompt use of antibiotic to combat meningococcal infection upon clinical presentation, vaccination is clearly the best strategy to prevent the high fatality rate and significant sequelae associated with meningococcal disease. This is primarily due to the rapid onset of disease with death occurring often within 24 to 48 hours. Early vaccines developed against Nm were based upon purified capsular polysaccharide antigens targeting serogroups A and C (Gotschlich et al., 1969). This was subsequently followed by a four-component polysaccharide vaccine, which covered serogroups A, C, W-135, and Y vaccine, licensed in the United States in the 1980s. Although these vaccines were safe and immunogenic and greater than 85% efficacious for the A and C components, polysaccharide vaccines in general were

largely ineffective in the population most susceptible to Nm disease, namely children under 2 years of age (Cadoz, 1998). Because polysaccharides are T-cell independent antigens that induce only short-lived humoral immunity with no memory response, a new generation of protein-conjugated polysaccharide vaccines emerged that largely remedied these limitations (Bilukha & Rosenstein, 2005; Pollard et al., 2009). Protein-conjugated polysaccharides elicit both B-cell and T-cell responses along with immunologic memory in all age groups including children under 2 years of age (Harrison, 2006). Polysaccharide–protein conjugate vaccines were first introduced into the United Kingdom in 1999 to protect against Nm serogroup C strains in the ST11 clonal complex (ET37 complex C2a) that had spread there following appearances in Canada, Spain, and the Czech Republic (Miller et al., 2001). These vaccines were shown to elicit bactericidal antibodies in all age groups including infants under 2 years old, and resulted in a significant decline in the incidence of serogroup C disease in the UK (Borrow et al., 2013). Serogroup C polysaccharide–protein conjugate vaccines were subsequently included into the schedule for routine infant immunizations. The success of this campaign later resulted in the development of quadrivalent polysaccharide–protein conjugate vaccines that protected against serogroups A, C, W-135, and Y by also inducing serum bactericidal antibodies, interrupting carriage transmission, and providing herd immunity against strains in the other 3 serogroups (Baltimore, 2006). Because of the high cost of the quadrivalent conjugate vaccine in the developed countries, to combat serogroup A disease in the meningitis belt in sub-Saharan Africa a low cost

conjugated serogroup A vaccine was developed in India. The serogroup A vaccine was launched in Burkina Faso and Chad starting in 2010, and resulted in a significant reduction of the incidence of disease along with a concurrent decline in serogroup A carriage (Daugla et al., 2013; Kupferschmidt, 2014; Gamougam et al., 2015; Meyer et al., 2015).

The Challenges of Vaccines Development against Serogroup B

Capsular polysaccharide conjugation to protein carriers has greatly improved the overall effectiveness of meningococcal vaccines against disease caused by serogroups A, C, W-135, and Y. The development of capsule based vaccines to protect against Nm serogroup B disease did not move forward however, due to the structural identity between the serogroup B capsule, an α 2-8-linked polysialic acid, and the human neural-cell adhesion molecules NCAM, particularly the embryonic form (Finne et al., 1983; Finne et al., 1987; Nedelec et al., 1990).

A different strategy was undertaken to confront this problem, which led to the development of outer membrane vesicles (OMVs) as an antigen vehicle for vaccines against serogroup B disease. OMVs were used to control outbreaks of group B disease for many years however, the breadth of protection they offered was limited (Bjune et al., 1991; Sierra et al., 1991; de Moraes et al., 1992; Boslego et al., 1995; O'Hallahan et al., 2009).

OMVs contain a mixture of immunogenic outer-membrane antigens including the porins, PorA and porB, and the iron-regulated membrane protein, FetA, in a lipid based structure derived from deoxycholate detergent preparations of Nm cultures (van der Ley et al., 1991; Feavers et al., 1996; Thompson et al., 2003). The primary protein component that drives the initial immune response to OMVs, PorA, contains two immunodominant hyper-variable loops VR1 and VR2, which effectively limit protective immunity mainly to the epidemic/outbreak, strain PorA-type. By one estimate, a vaccine would have to contain 20 different PorA types in order to cover 80% of strains that cause endemic disease in the United States alone (Sacchi et al., 2000). Although OMV vaccines have been effective in outbreak type situations caused by a single PorA-type strain, the number of PorA variants globally makes this approach impractical in the long-term against a pathogen with an inherent propensity towards antigenic diversity (Harrison et al., 2006).¹⁰⁶

Reverse Vaccinology and Serogroup B

Traditional biochemical methods of purifying and identifying membrane bound antigens for the purposes of developing a broadly protective vaccine against Nm serogroup B had been largely unsuccessful. An alternative strategy coined “reverse vaccinology” was launched in 2000 which involved the sequencing of the entire genome of the disease causing serogroup B strain, MC-58, in order to identify highly conserved outer membranes bound antigens for use in the next generation serogroup B vaccine. From the sequencing of a 2,272,351-base pair genome, 2158

predicted coding regions were identified (Tettelin et al., 2000). Over 300 candidate antigen sequences were expressed in *E. coli* and used to immunize mice, which resulted in the identification of proteins that were surface exposed, sequence conserved across a diverse collection of disease causing strains, and induced a bactericidal antibody response (Pizza et al., 2000). From this work five antigens were formulated: two protein-protein fusions, fHbp(GNA2091)-GNA1870 and NHBA(GNA2132)-GNA1030; and; NadA for use in human clinical trials.

The three target antigens fHbp, NHBA, and NadA, were selected due to their ability induced serum bactericidal antibodies against a diverse strain set. The two carrier proteins, GNA 2091 and GNA 1030, improved the immunogenicity of the coupled target antigens when fused with them. When tested in mice, this vaccine induced bactericidal antibodies against 78% of a globally diverse panel of 85 meningococcal strains. Interestingly, the addition of CpG oligonucleotides to an aluminum hydroxide based formulation, known to stimulate immune responses via toll-like receptor (TLR) activation, increased strain coverage to 90% (Giuliani et al., 2006).

The antigen fHbp, is an important virulence factor that allows Nm to bind soluble human factor H, down-regulate the complement amplification loop, and inhibit the insertion of the membrane attack complex on its surface. This makes fHbp a significant vaccine target given that antibodies raised against it can potentially block the binding of human factor H rendering strains more susceptible to the action of complement. The 2nd vaccine antigen is NadA which is an important target given its

role in Nm adhesion and invasion. Though highly sequence conserved, it is not universally expressed on all strains. Expression of NadA is known to be phase variable, and completely absent from the disease causing sequence type 41/44 serogroup B lineage. The 3rd vaccine antigen, NHBA, is expressed by most meningococcal strains, and shown to bind heparin, which is thought to aid the adhesion/invasion process. The vaccine includes the most common variant of NHBA, which induce antibodies that results in cross-reactivity with many of the other variants (Wang et al., 2011).

This set of antigens were taken into human trials, alone and also in combination with a PorA serosubtype P1.4 OMV, successfully used to combat an epidemic outbreak in New Zealand (Toneatto et al., 2011; Gossger et al., 2012). Concurrent to this work, a second research and development effort using more traditional antigen identification methods, independently identified fHbp as a potent antigen. In this case, a bivalent vaccine was developed containing elements of two Nm fHbp subfamilies shown to be effective in animal studies against 87% of strains tested (Jiang et al., 2010). Currently, both of these vaccines are independently licensed for use around the world including the United States, Europe, Canada, and Australia, selectively for infant through adults in varying countries.

Tweaking What's Innate - Toll-like Receptor Agonists as Adjuvants

Vertebrates have evolved an immune defense with two interacting branches, innate and acquired immunity, that function cooperatively to eliminate invasive pathogens. Innate immunity is an evolutionarily conserved system consisting of complement, chemokines, cytokines, and a variety of immune cells including neutrophils, phagocytes, natural killer cells, and dendritic cells that all act as a first line of defense against microbial organisms. Acquired immunity is characterized by an exquisite diversity of epitope recognition and specificity. This is made possible by somatic gene rearrangement, and subsequent clonal expansion of lymphocytes that express receptors to the vast array of epitopes in the environment. Innate immunity was long regarded as an ancient and relatively nonspecific system of immunity whose central function was the direct destruction of infectious microorganisms. The underlying complexity of the innate immune system was uncovered recently, in studies that revealed an intricate system of specific receptors coupled to signal transduction mechanisms. These innate pathways are responsible for initiating early danger signals that function to launch the cascade of initial host defenses against foreign substances, in particular invasive pathogens. A key component to this system are pattern-recognition receptors (PRRs), such as Toll-like receptors (TLRs), that detect pathogen-associated molecular patterns (PAMPs), and are found on a variety of immune cells including macrophages, dendritic cells, B and T cells, as

well as non-immune cells such as fibroblasts and epithelial cells (Janeway Jr & Medzhitov, 2002).

To date, 10 human and 13 mouse TLRs have been identified. Each TLR detects distinct PAMPs derived from viruses, bacteria, mycobacteria, fungi, and parasites (Table 1), which include: peptidoglycans (TLR1 and TLR2), viral double-stranded RNA (TLR3), lipopolysaccharides (TLR4), flagellin (TLR5), bacterial lipoproteins (TLR2 and TLR6), viral single-stranded RNA (TLR7 and TLR8), and bacterial and viral CpG (cytosine-phosphate-guanine dinucleotide) oligodeoxynucleotides (TLR9) (Akira et al., 2006). Meningococcal porB was also identified as having MyD88-dependent TLR2 stimulatory effects (Massari et al., 2002). Many TLRs are localized to the cell surface and associated with the extracellular membrane, such as TLRs 1, 2, 4, 5, and 6. However several that are localized internally, TLRs 3, 7, 8, and 9, require internalization of associated ligand before signal transduction events will occur (Akira et al., 2006).

Table 1: Recognition of Microorganisms by TLRs

<u>Bacteria</u>	<u>Species</u>	<u>Associated TLR</u>
LPS	Gram-negative bacteria	TLR4
Peptidoglycans	Gram-positive bacteria	TLR1/TLR2
Porins	<i>Neisseria</i>	TLR2
Flagellin	Flagellated bacteria	TLR5
CpG-DNA	Bacteria and mycobacteria	TLR9
<u>Viruses</u>		
DNA	Viruses	TLR9
dsRNA	Viruses	TLR3
ssRNA	RNA viruses	TLR7 and TLR8
Envelope proteins	RSV, MMTV	TLR4
Hemagglutinin protein	Measles virus	TLR2
<u>Fungus</u>		
Zymosan	<i>Saccharomyces cerevisiae</i>	TLR6/TLR2
Mannan	<i>Candida albicans</i>	TLR4
<u>Parasites</u>		
Glycoinositolphospholipids	<i>Trypanosoma</i>	TLR4
Hemozoin	<i>Plasmodium</i>	TLR9
Profilin-like molecule	<i>Toxoplasma gondii</i>	TLR11

TLRs are classified as type 1 integral membrane glycoproteins, which consist of a leucine-repeat rich extracellular N-terminal domain, and an intracellular C-terminal Toll/interleukin 1 receptor (TIR) domain. Upon dimerization, TLR monomers take on a M-shaped structure (Choe et al., 2005; Jin et al., 2007; Kang et al., 2009; Park et al., 2009), which then allows the intracellular TIR domains to recruit adaptor molecules that activate signaling pathways that up-regulate transcription factors, such as nuclear factor-kB and interferon regulatory factors. Known adaptor

molecules include myeloid differentiation primary response protein 88 (MyD88), TIR domain-containing adaptor protein (TIRAP), TIRAP inducing interferon β (TRIF), and TRIF-related adaptor molecule (TRAM) (Akira & Takeda, 2004). Current evidence provides support for the requirement of activation of innate immunity for the induction of acquired immunity. Transfection of a constitutively active mutant of a human Toll into human cell lines was shown to induce NF- κ B expression and the genes controlled by NF- κ B. TLR activation stimulates the production of the inflammatory cytokines IL-1, IL-6 and IL-8, along with the co-stimulatory molecule B7.1, required for the activation of naive T cells (Medzhitov et al., 1997; Akira et al., 2001; Medzhitov, 2001).

Recent advances in the identification of pattern-recognition receptors have opened up a new line of study on the therapeutic possibilities of PRR activation in the treatment of infectious, allergic, and immune diseases, as well as cancer. In the field of vaccine research, a growing number of compounds with immunopotential properties have been brought into use in an effort to exploit the variety of TLRs discovered in recent years. This has allowed for the development of safe and potent vaccine adjuvants and delivery systems for both prophylactic and therapeutic uses. This advance is particularly important as the use of recombinant protein subunits in vaccines, which may lack inherent immunostimulatory properties, continues to move forward. Investigations continue into novel TLR stimulating compounds alone or in combination with aluminum salts (alum), the vaccine adjuvant first

approved for human use (Lindblad, 2004). Alum itself principally stimulates T helper type 2 (Th2) biased immunity and is thought to dampen the production of protective immunity when using recombinant antigens against pathogenic microorganisms. The success of these compounds is based largely upon their abilities to skew immune responses more toward a T helper type 1 (Th1) biased response, and promote the interaction of the innate and adaptive immune pathways without raising serious adverse events (Lahiri et al., 2008).

Some of the compounds developed to date include: Monophosphoryl lipid A (MPL), a detoxified lipid A derivative of lipopolysaccharide from *Salmonella enterica*, and the AS04 adjuvant system consisting of MPL adsorbed on either aluminium hydroxide or aluminium phosphate, which minimizes the proinflammatory MyD88-dependent signalling pathway while stimulating Th1 and cell-mediated responses (Garçon, et al., 2007; Mata-Haro, et al., 2007; Casella & Mitchell, 2008); RC-529 (Ribi.529; Corixa, Seattle, WA, USA), a fully synthetic MPL mimetic and TLR4 agonist that has been used as a potent adjuvant in both preclinical and clinical studies (Mason et al., 2004; Dupont et al., 2006; Zhu et al., 2006); E6020, a synthetic molecule with a hexa-acylated acyclic backbone with the ability to promote Th1-biased antibody production (Hawkins et al., 2002; Przetak, et al., 2003; unmethylated CpG oligodeoxynucleotides, which elicit potent immunostimulatory responses through TLR9, primarily expressed on B cells and dendritic cells, and induce antigen-specific humoral and Th1-mediated cellular responses (Krieg et al.,

1995; Vabulas et al., 2000; Hornung, et al., 2002); polyribonucleosinic polyribocytidylic acid (poly[I:C]) which is a synthetic analogue of viral double-stranded RNA molecules and targets TLR3 (Asahi-Ozaki et al., 2006); the imidazoquinolines, imiquimod (R-837) and resiquimod (R-848), which are synthetic small molecules recognized by TLR7, and TLR7 and TLR8, respectively, both shown to be potent Th1 adjuvants in mice and non-human primates (Vasilakos et al., 2000; Zuber et al., 2004; Wille-Reece et al., 2005); and, the protein Flagellin, a potent activator of the NF- κ B signaling pathway through TLR5 which induces robust antibody responses even without supplemental adjuvants against a variety pathogens including influenza, *Yersinia pestis*, *Plasmodium vivax*, and *L. monocytogenes* antigens (Tallant et al., 2004; Honko et al., 2006; Huleatt et al., 2007; Bargieri et al., 2008; Huleatt et al., 2008; Mizel et al., 2009; Skountzou et al., 2010).

Alternative approaches to this problem involved the use of an OMV vaccine prepared from recombinant strains that over-express recombinant factor H binding protein (fHbp) as the target antigen, and attenuated endotoxin, designed to target TLR4, was shown to stimulate broad serum bactericidal antibody responses (Koeberling et al., 2011); and the direct coupling of a TLR7 agonist to a serogroup C polysaccharide-conjugate vaccine (Donadei et al., 2016). Efforts to engage multiple TLR receptors and/or other pattern-recognition receptors in order to gain synergistic immune responses with little or no reactogenicity are of continuing interest (Lahiri et al., 2008; Chen et al., 2010; Hajishengallis & Lambris, 2016).

Similar approaches, such as combining immune evasion surface proteins as target antigens with compounds that possess strong immune agonist properties, may be instrumental in the eradication of other difficult to treat infections including gonorrhea, tuberculosis, HCV, and potentially HIV.

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Professional Positions:

- 1982 - 1983** *Research Assistant I, Yale University* - Investigated effects of chemotherapeutic agents on RNA expression and steroid receptor metabolism.
- 1983 - 1987** *Research Associate I/II, University of California San Francisco (UCSF)* - Investigated the transcriptional regulation of proto-oncogenes by anti-steroidal agents.
- 1988 - 1992** *Research Associate II, UCSF* - Investigated fibronectin structural domain requirements in the regulation of metalloproteinases and cytoskeletal organization.
- 1993** *Research Associate, Children's Hospital Oakland Research Institute (CHORI)* - Investigated the regulation Cystic Fibrosis Transmembrane Conductance Regulator (CFTR).
- 1994** *Research Associate II, CHORI* - Investigated the role of the cytoskeleton in the regulation of platelet activation.
- 1995 - 2000** *Research Specialist, Chiron Vaccines* - Preclinical and clinical studies in support of vaccine development to protect against meningococcal group C disease.
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PATENTS

1. Publication number: 20110312510. High-Throughput Complement-Mediated Antibody-Dependent and Opsonic Bactericidal Assays. Filed: June 16, 2010, Publication date: December 22, 2011. Inventors: Puiying Annie Mak, George Santos, Jeffrey Eugene Janes, John J. Donnelly, III.
2. Publication number: 20100035234. Vaccine Assays. Filed: May 19, 2009. Publication date: February 11, 2010. Inventors: John Donnelly, Ping Wu, George Santos, Marzia Monica Giuliani, William Andrews, Jie Chen.

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ABSTRACTS AND CONFERENCE PRESENTATIONS

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