Pro-inflammatory cytokines can act as intracellular modulators of commensal bacterial virulence

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1. Summary

Interactions between commensal pathogens and hosts are critical for disease development but the underlying mechanisms for switching between the commensal and virulent states are unknown. We show that the human pathogen Neisseria meningitidis, the leading cause of pyogenic meningitis, can modulate gene expression via uptake of host pro-inflammatory cytokines leading to increased virulence. This uptake is mediated by type IV pili (Tfp) and reliant on the PilT ATPase activity. Two Tfp subunits, PilE and PilQ, are identified as the ligands for TNF-α and IL-8 in a glycan-dependent manner, and their deletion results in decreased virulence and increased survival in a mouse model. We propose a novel mechanism by which pathogens use the twitching motility mode of the Tfp machinery for sensing and importing host elicitors, aligning with the inflamed environment and switching to the virulent state.

2. Introduction

Neisseria meningitidis (Nm), a Gram-negative diplococcus, is an obligate human pathogen that colonizes the nasopharyngeal epithelium and carried asymptotically in the nasopharynx of up to 30% of the global population at a
Nm is highly adaptable to its environment; it downregulates pilus expression and capsule production after contact with host cells [26]. Transcriptome analysis of Nm in contact with epithelial and endothelial cells has revealed altered expression levels of certain genes involved in pathogenesis, such as IgA1 protease, proteins involved in iron uptake and Tfp assembly [27]. The coordination of capsule formation and pilus gene expression maximizes the virulence and transmission of Nm.

The effects of Nm on the host and the inflammatory response caused by Nm infection have been investigated at length; what remains to be considered is how these cytokine-orchestrated immune responses influence Nm and modulate virulence gene expression and phenotype. Here, we investigate the bacterial mechanisms employed to respond to this inflammatory reaction and phenotypic change independently of any cell contact. We show that detection of environmental changes and recognition by Nm ligands, followed by uptake of cytokines, are key steps in the conversion of commensal bacteria into hypervirulent phenotypes.

3. Results

3.1. Neisseria meningitidis type IV pili bind to human cytokines

To determine the range and specificity of cytokines that bind Nm, IL-8, IL-10, IL-12, IFN-γ and TNF-α were immobilized in amino-linked enzyme-linked immunosorbent assay (ELISA) plates and incubated with digoxigenin-labelled log-phase-grown Nm strain MC58. The bacterial cells bound to different cytokines with a somewhat variable degree of binding among cytokines (figure 1a). TNF-α exhibited the highest binding signal, with the rest of the cytokines exhibiting lower signals with marginal variations. We then examined the concentration-dependent effects of cytokines (using TNF-α and IL-8) on bacterial growth. Bacteria were incubated with TNF-α or IL-8, and the growth was measured for a 24 h period. The mean average results for non-induced and cytokine-induced bacteria, collated from three independent experiments, show that TNF-α or IL-8 had no effect on bacterial growth (see electronic supplementary material, §S1a).

Our findings reveal an interaction between surface structures of the capsulated Nm serogroup B MC58 with TNF-α and IL-8. To examine whether this interaction is confined to Nm serogroup B or extends to other serogroups (different types of capsule structure classify Nm into different serogroups), five clinical isolates of serogroups B and Y were selected [28], and binding to TNF-α and IL-8 was assessed by ELISA. In all isolates from the two serogroups, the level of binding to TNF-α or IL-8 was comparable to the MC58 strain (see electronic supplementary material, §S1b).

A retagging technique [29] was used for the identification and purification of Nm TNF-α-binding adhesin(s); two subunits of the meningococcal Tfp, PilE (accession: P05431; 18.1 kDa; score: 1185.07) and PilQ (accession: Q70M91; 28.42 kDa; score: 1915), were identified as putative human cytokine receptors. To evaluate the contribution of these adhesins to bacterial binding, ΔpilQ and ΔpilE MC58 mutants were generated. The ΔpilQ mutation resulted in a significant reduction in binding to all of the examined cytokines (figure 1b). However, the ΔpilE mutation did not result in any significant reduction to cytokine binding with the exception of TNF-α.
Figure 1. Binding of *N. meningitidis* (Nm) to human cytokines. To determine the range and specificity of human cytokines that bind *Nm* strain MC58, IL-8, IL-10, IL-12, INF-γ and TNF-α were immobilized in amino-linked ELISA plates (bovine serum albumin was used as a negative control) and incubated with log-phase digoxigenin-labelled bacteria. (a) The wild-type strain MC58 bound to all the cytokines; the degree of binding varied marginally between the cytokines, except for TNF-α which was substantially higher. Data shown represent the results of four repeated ELISA tests. Error bars represent the mean ± s.e.m. of the absorbance values. (b) The binding of wild-type and mutant strains (∆*pilQ* and ∆*pilE*) was examined in the same manner. Binding of ∆*pilE* and ∆*pilQ* to all of the examined cytokines was significantly reduced compared with the wild-type strain (*p* < 0.05, t-test), with the exception of the binding of ∆*pilE/IL-12* (*p* < 0.05, t-test). Data shown represent the results of four repeated ELISA tests. Error bars represent the mean ± s.e.m. of the absorbance values. Binding of *Nm* to human cytokines is glycan dependent. (c) Glycosyl-transferase-deficient strains (∆*pglC*, ∆*pglL* and the ∆*pglC/L*) were examined to assess their binding to IL-8 and TNF-α. All mutants exhibited somewhat defective binding to TNF-α and IL-8. (d) Inhibition of *Nm* binding to human cytokines using specific lectins. The specificity of the interaction between cytokines (i.e. TNF-α and IL-8) and the surface structure of *Nm* was examined. To identify the role of glycosylated surface structures of *Nm*, the inhibition of IL-8- and TNF-binding was performed using a series of lectins with different specificities. ELISA results revealed a significant reduction in *Nm* binding to TNF-α compared with untreated *Nm* with all lectins examined except DSL and LEL. The results shown are expressed as means ± s.e.m. for three independent experiments performed in triplicate. The asterisks indicate *p*-values of <0.05, t-test. (e) The intensity of binding of *Nm* capsule-deficient ∆*siaD* mutant strain MC58 to human TNF-α and IL-8 cytokines was measured using ELISA. The level of binding of the non-capsulated mutant was significantly higher in comparison with the wild-type strain, with binding to bovine serum albumin used as a background value. This observation is consistent with a role of the capsule in masking outer-membrane structures, and suggests that the capsule and its polysaccharide structures are not involved in interactions with cytokines. The results shown are expressed as mean ± s.e.m. for three independent experiments performed in triplicate. Asterisks indicate *p*-values of <0.05, t-test.
3.2. Glycosylation of pili is crucial for binding to human cytokines

Many cytokines possess lectin-like activity that may be essential for the expression of their full biological activities. For example, pili are post-translationally modified (see electronic supplementary material, S2) and the surface accessibility of phosphorylcholine on pili is affected by changes to the structure of the pilin-linked glycan [15]. Here, we focused on the relevance of the lectin-like activity of cytokines in mediating Nm binding, using TNF-α and IL-8 as examples.

Three oligosaccharyltransferase (O-OTase) mutants (ΔpgIL, ΔpgLC and a double mutant) of the MC58 strain were generated and examined for binding to IL-8 and TNF-α. All three mutants exhibited significant reductions in binding to both cytokines (figure 1c). By contrast, a ΔqsF mutant of the MC58 strain (defective for the synthesis of the polysialic acid capsule or LOS) [30] did not exhibit defective bacterial binding to IL-8 (see electronic supplementary material, figure S3).

To investigate further the nature of the interaction between cytokines and the surface structure of Nm, and to identify the role of glycosylated surface structures of Nm, the inhibition of IL-8 and TNF-α-binding were examined using a series of lectins—Griffonia (Bandeiraea) simplicifolia lectin II (GSL-II); Datura stramonium lectin (DSL); Erythrina cristagalli lectin (ECL); Lycopersicon esculentum (tomato) lectin (LEL); Solanum tuberosum (potato) lectin (STL); Vicia villosa agglutinin (VVA); Artocarpus integrifolia (lacatin)—with all lectins representing activity against different Gly copolymers (i.e. Galb1,3GlcNAc, Galβ1,4GalNAc, and GaINAc). In addition, the binding of IL-8 was significantly reduced with ECL and VVA, suggesting that the IL-8 and TNF-α interactions are mediated by different PilE protein glycan moieties (figure 1d).

3.3. IL-8 and TNF-α induce changes in Nm gene expression

To investigate whether the bacterial interaction with human cytokines affects Nm gene expression, the transcriptional profiles were compared in non-induced and both IL-8 and TNF-α-induced cultures using deep-sequencing analysis. The RNA integrity of deep-sequencing samples was examined as explained in electronic supplementary material, §S6. In the IL-8 and TNF-α-induced cultures, the expression of 473 (approx. 20%) and 1080 (approx. 45%) Nm genes were altered, respectively (figure 2a; electronic supplementary material, §S7, separate Excel file (S2)). The genes with modified expression were categorized using the Genome Properties System (http://cmr.jcvi.org/tigr-scripts/CMR/CmrHomePage.cgi). A Log2 ratio of read counts higher than 0.5 was considered to indicate significant differences between induced and non-induced conditions.

Among the known genes, the expression of those coding for adhesion (S2a), energy metabolism (S2d), transport and binding proteins (S2e), cell envelope (S2f), bacterial survival (S2g), regulatory function (S2h) and amino acid synthesis (S2i) were altered. A significant portion of the regulated genes were of unknown function (i.e. hypothetical genes; electronic supplementary material, §S7, separate Excel file and Deep seq figures).

The comparison of the gene activation profiles in Nm led to the identification of genes that were down- or upregulated in cytokine-treated organisms and genes that were inversely regulated, such as those encoding PilE, cytochrome c, Iron ABC transporter, H8 outer-membrane protein, MarR (AraC-family transcription regulator), Adhesion and Penetration Protein (APP) [31] and Meningococcal Serine Protease A (MSPA) [32] (electronic supplementary material, §S7, separate Excel file). Our study also showed that SiaD (NMB0067) and LipA (NMB0082), which are involved in LPS production, are highly upregulated by TNF-α exposure.

All these genes probably play an important role in virulence and pathogenicity once bacteria are exposed to hyperinflammatory conditions. Furthermore, the prominence of regulated surface proteins and/or structures in the cytokine-treated bacteria indicates that host-secreted cytokines induce a profound remodelling of the bacterial cell membrane.

3.4. The effect of human cytokines on Nm gene expression using the reporter gene lacZ

In batch culture, it is unlikely that the level of expression at the beginning of growth is the same as the steady-state level [33], because the cultures are usually inoculated with cells from the stationary growth phase (‘overnight’) or with ‘uninduced’ cells. In the latter case, the β-galactosidase concentration in the inoculum was zero. Therefore, β-galactosidase activity was assayed using the method of Miller [34], after growth of Nm strains for up to 9 h (middle of log-phase) in DMEM in the presence or the absence of cytokines IL-8 or TNF-α (both 100 ng ml⁻¹). The β-galactosidase activity measurements from strains of Nm bearing the promoter NMB0750 (bacterioferritin co-migratory protein, bcp), NMB0946 (peroxiredoxin, prx) and NMB1998 (mspa)-lacZ fusions confirmed that gene expression of prx and bcp is significantly regulated following the treatment with cytokines (figure 2b). The expression of mspa, however, was increased by 22% compared with uninduced bacteria.
3.5. Cytokines-induced *Nm* resistance to complement-mediated lysis

Resistance to complement-mediated lysis is a key virulence attribute of *Nm*. Meningococcus displays a vast repertoire of genes, often involved in virulence, whose expression is controlled by inflammatory cytokines mediated through reversible changes in the TfP structure. The phenotypes observed here can therefore be due to variation in expression of genes involved in *Nm* surface structure. A functional study was carried out to validate the deep-sequencing data and differences in the transcriptional profiles observed to assess their role in *Nm* pathogenicity and/or virulence. To assess whether different cytokine treatments of wild-type (wt) MC58 and its isogenic mutants differ in sensitivity towards bactericidal activity, experiments were performed at the initial log-phase (9 h) of the *Nm* growth in the presence and the absence of cytokines (figure 2c). The rabbit antibody against recombinant PilQ in the presence of rabbit complement was capable of inducing 67% cell death in the untreated wt MC58 strain (i.e. 33% survived), whereas in the case of TNF-α-induced bacteria 31% cell death was induced (i.e. 69% survived). This is equivalent to a doubling of survival. By comparison, in the isogenic (Δ*pilQ*, Δ*pilE* and Δ*gplC/L*) mutants, there was no significant difference between cytokine-treated and non-treated bacteria. IL-8-treated bacteria did not exhibit any significant resistance to complement-mediated lysis (figure 2c). These data confirm the significance of modulation of surface structures (hence pathogenicity) and validate the results from deep sequencing.

### 3.6. *Nm* can ingest human cytokines, in vivo

To analyse the intracellular uptake of cytokines by *Nm*, wild-type bacteria and related mutants (Δ*pilQ*, Δ*pilE* and Δ*gplC/L*) were grown in DMEM and induced with either TNF-α or IL-8 (40 ng ml⁻¹) for 9 h at 37°C. Cells were then extensively washed and fixed for transmission electron microscopy. The cytokines were detected with monoclonal antibodies, followed by secondary antibody conjugated with 10 nm colloidal gold particles. The majority of the TNF-α and IL-8-gold labelling was localized in the cytoplasm of wt *Nm* (figure 3, red arrowhead).

No TNF-α or IL-8 uptake was seen in the cytoplasm of the Δ*pilQ*, Δ*pilE*, Δ*pilT* or Δ*gplC/L* mutants. Mutations in the *gpl* or *pilT* (lacking pilus retraction ability) had no effect on normal piliation phenotype [35], also confirmed by this study (figure 3).

The intracellular uptake of labelled TNF-α by *Nm* wild-type MC58 bacteria was confirmed by confocal imaging, whereas in control experiments there was no uptake of labelled Gal-3 (galectin 3), confirming the specificity of the uptake (figure 4a). Furthermore, pre-treatment of the bacteria with non-labelled TNF-α inhibited the uptake of labelled TNF-α (figure 4a), further confirming uptake specificity. In addition, MC58 *Nm* isolated directly from the peritoneum and blood of mice 4 h post-infection exhibited TNF-α uptake, whereas Δ*gplC/L* mutant *Nm* did not in EM experiments (figure 4b). Immunogold staining demonstrated 66% and 50% of the wt MC58 bacterial population in peritoneum and blood, respectively, showing uptake of TNF-α, but none of the examined samples from the Δ*gplC/L* mutant showed any signs of TNF-α binding and/or uptake. Collectively, our data confirmed the specific uptake of TNF-α in *in vivo*.

### 3.7. Cytokines bind to the genomic DNA of *Nm in vivo*

We hypothesized that human cytokines may bind across the *Nm* genome, acting as transcription modulators for the expression of virulence genes such as autotransporter proteins MSPA and APP, in addition to the PptB transferase...
that adds phosphoglycerol onto Tfp [20]. Qualitative chromatin immunoprecipitation [36] was used to investigate the binding of cytokines to intergenic (promoter-containing) regions of these virulence genes.

The wt MC58 strain and the ΔpilE, ΔpilQ and ΔpglC/L mutants were grown in the presence or the absence of TNF-α or IL-8, and antibodies directed against TNF-α were used to select protein cross-linked DNA fragments that were further purified using magnetic beads coated with a secondary antibody. Q-PCR was carried out using primers specific for the app, mspA and pptB promoter regions. The app, pptB and mspA immunoprecipitated DNA fragments from the TNF-α-induced wt strain were more than four- to fivefold enriched compared with the equivalent non-induced samples (figure 5a). These data confirm the uptake of TNF-α by wt Nm and suggest that TNF-α binds to genomic DNA sites within the app, mspA and pptB genes.

A gel-shift assay was used to study the direct binding of TNF-α to three partially overlapping fragments (70–84 bp) from the intergenic (promoter-containing) and one from the intragenic (non-promoter containing) regions of the app gene. Specific binding was detected with two fragments from the intergenic region immediately upstream from the app gene, but not with the other two fragments (figure 5b–e). The alignment of the two binding fragments suggests several conserved binding sites, which require further study to exquisitely define the precise sequence of the DNA-binding site (figure 5f).

3.8. Direct comparison of the mortality rates of wild-type and isogenic mutant Nm strains in an animal model

The pili of Nm interact with CD46, a human cell-surface protein involved in the regulation of complement activation. CD46, with the cytoplasmic tail Cyt-2, regulates T-cell-mediated inflammatory responses [37], is preferentially expressed in brain tissue and is tyrosine-phosphorylated by

![Figure 3](https://rsob.royalsocietypublishing.org/6)
Neisseria [38]. The interaction with human CD46 represents a critical step for the onset of bacterial meningitis [39]. Transgenic mice expressing human CD46 are susceptible to meningococcal disease because bacteria can cross the blood–brain barrier in these mice [39].

Figure 4. Confocal images of Nm uptake of human cytokines. (a) Detection of intracellular TNF-α into the meningococcal cytoplasm. Nm live cells were induced with Atto680-labelled recombinant proteins (TNF-α or Galactin-3). Cells were stained with anti-PorA monoclonal antibody and DPI. Merged images depict co-localization of Atto680 (red) and monoclonal anti-PorA antibody (green), DPI (blue) and +TNF-α680 induced (yellow). Non-induced Nm MC58 (CT) or Gal-3680 labelled was used as negative control. In addition, the uptake of labelled TNF-α680 was inhibited by using non-labelled TNF-α. Insets shown are at 2.5 times magnification. Images are single sections (300 nm) and data were collected from different fluorophores in separate channels. (b) Transmission electron micrograph of Nm TNF-α uptake in mice peritoneum and blood. TEM macrograph analysis of TNF-α uptake by Nm wild-type strain and ΔpglC/L mutant isolated from peritoneum and blood at 4 h post-infected mice. Treated samples with only secondary antibody were used as negative control (CT). Wild-type MC58 strain shows accumulation of gold particles inside or on the surface of the bacteria (red arrow). The cells shown in this image are representative of approximately 66% and 50% of the analysed bacterial population in peritoneum and blood, respectively. No uptake was observed in images of TNF-α ΔpglC/L mutants, indicating that uptake of cytokines requires the glycosylated form of PilE protein. The scale bar represents 500 nm and the insets represent two times magnification.

The impact of the Nm surface structures required for binding to human cytokines on bacteraemia and meningitis progression was investigated in CD46 transgenic mice. Eight mice in each group were intraperitoneally infected with wt or one of the isogenic mutants (ΔpilQ, ΔpilE and...
and examined for 72 h. All of the mice developed bacteraemia (see electronic supplementary material, figure S9 and table S9), but lethal instances of disease occurred only in mice that were infected with MC58 or the \( \Delta p i lE \) mutant. Mice that were infected with \( \Delta p i lQ \) and \( \Delta p g lC/L \) mutants exhibited significantly less mortality and enhanced survival rates (figure 6a). These results further confirmed the importance of PilQ and surface glycans for Nm virulence.

In addition, blood samples were collected at 2, 6, 24 and 48 h post-infection to analyse the production of inflammatory...

Figure 5. Chromatin immunoprecipitation. (a) An immunoprecipitation experiment to monitor the uptake and binding of TNF-\( \alpha \) to the Nm genomic DNA. The wild-type strain MC58 was cultured and induced with TNF-\( \alpha \) (100 \( \mu \)g ml\(^{-1} \)) for 4 h. The panel depicts qPCR results, generated with primers designed to detect the intergenic regions of \( a p p \) or \( m s pA \) and the open reading frame of \( p p tB \) in each sample; (i) \( a p p \), (ii) \( m s pA \) and (iii) \( p p tB \). Five independent experiments are shown and non-induced strains were considered as negative controls. Binding of TNF-\( \alpha \) to different \( a p p \) oligonucleotides of defined sequence was studied using a gel-shift assay. (b–e) Four DNA fragments (70–80 bp), three partially overlapping fragments from the intergenic region immediately upstream from the \( a p p \) gene (b,c,e) and one from the intragenic \( a p p \) gene region (d), were tested for TNF-\( \alpha \) binding. Binding reactions were carried out at different concentrations of TNF-\( \alpha \) (5, 10 and 20 \( \mu \)M). The control lane (DNA probe without protein present, 0 \( \mu \)M) contains a single band corresponding to the unbound DNA fragments (C1, C2, C3 and C4). Gel-shift complexes were resolved by electrophoresis and visualized by autoradiography. Red arrows indicate migration of the shifted TNF-\( \alpha \)– DNA-binding complexes. (f) Alignment of two fragments from the intergenic region (b and c) suggesting potential DNA-sequences as TNF-\( \alpha \) binding site(s).
cytokines such as TNF-α, IFN-γ, IL-6, keratinocyte chemotactrant (KC or CXCL-1, equivalent to human IL-8) and anti-inflammatory cytokine IL-10 (see electronic supplementary material, figure S9). The results showed that the ΔpilQ and ΔpglC/L Nm mutants can still activate immune cells to secrete inflammatory cytokines just like the wt strain. Collectively, our data suggest that although the Nm mutants can still activate cytokine secretion they are at the same time less responsive to cytokines (because they are lacking the specific adhesins); therefore, animal survival is enhanced.

Furthermore, the total RNA was purified from all collected blood (6 h post-infection) from each group of mice and pooled in one sample, in order to examine the expression of virulence genes such as app, mspA and pptB using Q-PCR. The results clearly showed that mice infected with wt MC58 were expressing these genes significantly higher than the isogenic mutants (figure 6b).

### 4. Discussion

Nm is usually a commensal bacterium of the nasopharynx. During the commensal state, most of the dividing bacteria belong to the same antigenic type and express low levels of virulence genes. Most probably, a peak of pathogenic status (bacteraemia followed by meningitis) is reached when the bacteria sense danger caused by a hyperinflamed environment. Here, we propose that host elicitors in response to microbes are engaged by commensal Nm and control the patterns of pathogenesis. Progression towards pathogenic states requires monitoring of long-term changes of bacterial behaviour to understand how this cycle varies across a broad inflammatory status. Our data provide novel insights into the changes taking place as inflammation continues to rise, and the extent and duration of inflammatory markers change.

TNF-α and IL-8 are pro-inflammatory cytokines that have numerous biological activities [40] and play important roles not only in host defence [40,41] but also in some of the pathological sequelae associated with various bacterial infections [42,43]. Here, we show that bacteria use human cytokines to sense the host environment.

Nm probably employs two mechanisms for binding to IL-8 and TNF-α. Cytokines contain lectin-like carbohydrate domains which are spatially distinct from cytokine-receptor binding sites [44]. The lectin-like domains of cytokines represent pathogen-specific recognition sites that can contribute to the elimination of pathogens via opsonization and/or leukocyte activation [44–46]. Nm might use this strategy to facilitate the neutralization and/or inactivation of human cytokines and the modulation of its own gene expression in response to environmental alterations.

Our data, with a series of glycosyltransferase-deficient mutants (ΔpglC/L, ΔpglC and a ΔpglC/L double mutant), indeed suggest that Nm-cytokine binding is mediated partially by glycan moieties and by protein–protein interactions. This observation is consistent with the findings of Estabrook et al., who showed that mannose-binding lectin binds to the non-glycosylated Nm outer-membrane proteins Opa and Forb in a carbohydrate-independent manner [47]. Here, we show that binding of TNF-α or IL-8 to Nm is mediated by pilus assembly proteins (i.e. PilQ and PilE proteins) and that the virulence properties of Nm are enhanced as a consequence of TNF-α or IL-8 binding and uptake. The ingested cytokines directly bind to genomic DNA, and consequently regulate the expression of several genes.
TNF-α was shown to exhibit DNA-binding activity (figure 5d,e). This is consistent with a previous report showing that IL-8 binding to neutrophil receptors can be prevented by anionic polymers, such as DNA and actin [48]. The available crystal structures in the PDB (Protein Data Bank) show a single well-folded domain with mainly β sheets and no obvious DNA-binding motifs. It is not a requisite that all DNA-binding proteins possess standard recognized motifs, as several proteins can still bind DNA using other structural features.

Furthermore, we show that TNF-α is able to regulate bacterial gene expression. There is a variety of mechanisms that bacteria use to modulate gene expression in response to environmental stimuli. DNA binding by cytokines may change promoter architecture, which could then change the preference (negatively or positively) of RNA polymerase for certain promoters, physically prevent direct binding of RNA polymerase to promoters or prevent binding of transcription factors (gene enhancers or silencers). Indeed, many combinations of these mechanisms may work for different promoters of different virulent (and other) genes to affect global transcription. In addition, in bacteria there are several non-specific DNA-binding proteins, known as nucleoid-associated proteins (NAPs), that bind globally to the bacterial genome (nucleoid), and affect both its structure and its transcriptional activity at the global level (often by changing pervasive DNA superhelicity, which then affects gene expression, or bind directly at specific promoters working in concert with dedicated transcription factors to regulate gene expression in response to growth phase and environmental changes [49–51]). In one specific example from the literature, the off-to-on switching of cell-surface structures such as pyelonephritis-associated pilus [52] in many enteric bacteria is environmentally regulated by a number of factors including the CpxAR two-component regulatory system, the Histone-like nucleoid structuring protein H-NS (a non-specific NAP) and cAMP-catabolite gene activator protein [53]. Hence, binding of cytokines to the bacterial genome could potentially elicit a variety of different structural/transcriptional global effects via any combination of the above mechanisms.

The fact that mice infected with the ΔpgaC/L double mutant, expressing both PilQ and PilE proteins but lacking glycan moieties, developed significantly less disease, revealed its reduced virulence in vivo. The expression of virulence genes was still significantly higher in wt MC58-infected mice, showing that strains lacking pili appendages or glycans are less prone to adapt to the inflamed environment (i.e. less virulent). This was consistent with EM analysis of isolated bacteria from the peritoneum and blood samples of post-infected mice. Four hours post-infection inflammation is increased in the peritoneum and 66% of wt MC58 show TNF-α uptake compared with no uptake in the ΔpgaC/L mutant (figure 4b). This is significant considering that in vivo many different cytokines could potentially interact with Nm in a complex manner, causing a wide range of changes in bacterial behaviour. Despite this complexity, we still see a considerable number of bacteria specifically interacting with TNF-α in the wt MC58 but not in the ΔpgaC/L mutant isolated from infected animals.

However, no significant difference in bacterial levels and cytokine levels in the blood from infected mice were observed between the examined strains (see electronic supplementary material, §S9), showing that survival of the animals is not related to bacteraemia.

In the case of the ΔpilE mutant, no gold particle uptake was observed (i.e. no cytokine uptake; figure 3), but the survival of infected mice was only 32% (figure 6a). However, the negative staining indicated that there was another form of pili-like surface appendages in the ΔpilE mutant, which could potentially be an alternative entry point for cytokines in vivo, which could affect survival (illustrated in figure 7a).

The Tfp system is widely distributed across many different bacteria species (more than 150 species), which suggests that cytokine entry into bacteria may be of wide applicability across many species. The binding of *Pseudomonas aeruginosa*, *Helicobacter pylori* and entero-pathogenic *E. coli* to a broad range of human cytokines was studied in parallel and the corresponding adhesins were identified (RM Delahay, H Wilkerson, P-J Royer, T Self, J Stoof, K Kong, J Notinger, P Soulantas, DAA Ala’Aldeen, J Mahdavi 2013, unpublished data). However, the detailed mechanisms of how these opportunistic pathogens actively sense alterations in the host and respond by enhancing their virulence phenotype remain to be studied.

Taken together, the proposed mechanism potentially has general applicability and the fundamental knowledge gained from investigations of the uptake system of this bacterium with biochemical analyses should yield substantial insights that will help to unlock more of the secrets of the lifestyle and pathogenic potential of this organism and, potentially, other pathogenic bacteria (illustrated in figure 7b). Our findings also provide a mechanism to explain the frequent development of meningitis in patients with an intense and protracted inflammatory response. Further research comparing the nature of hypervirulent lineages may elucidate the extent to which this feature contributes to the epidemiological distinctiveness of meningococcal infections.

In the future, our approach will focus on the identification of compounds structurally similar to cytokines that modulate the expression of bacterial virulence genes and reprogramme the bacterial behaviour towards less pathogenic and more commensal states. This knowledge could be directed towards the study of drugs and existing inhibitors, such as lectins, to assess their suitability as novel therapeutic agents. By exploiting knowledge of their modes and sites of action to combat bacterial infections, we could develop powerful novel arsenals against the serious problem of antibiotic resistance.

5. Material and methods

5.1. Enzyme-linked immunosorbent assay

Washes were performed at room temperature in PBS/T (0.1%) (phosphate-buffered saline/tween).

Purified, human recombinant IL-10, IL-12, IL-8 (aa 1–77), TNF-α (aa 77–233), (Super family, Member 2) and INF-γ (3 μg ml⁻¹) (Sino Biological Inc, Beijing, China) were coupled to 96-well plates by adding 100 μl of cytokine solution (3 μg ml⁻¹) diluted in sodium carbonate buffer (pH = 9) to each well. The bacterial strains MC58, ΔpilQ, and ΔpilE, ΔpgaC/L were labelled with 10 μg ml⁻¹ digoxigenin in PBS for 2 h at room temperature. A total of 100 μl of labelled bacteria (OD₂₆₀ 0.02) were added to each well, and the plates were incubated overnight at 4°C.

The plate was incubated with a polyclonal anti-digoxigenin (alkaline phosphatase, 1 : 5000) in 1% BSA/PBS. Then, 100 μl of ABTS solution (5 mg ml⁻¹; Roche) was added to each well. The
absorbance at 405nm was measured at different time points. For inhibition assay, the bacterial cells were pre-incubated with a series of lectins (see the electronic supplementary material, material and methods) for 2h followed by several washes, then the bacterial cells were added to coated plates with various cytokines. The following steps were similar to ELISA.

5.2. Immunogold labelling and electron microscopy

Wild-type and mutants (ΔpilQ, ΔpilE and Δpg1L/C) Nm were treated with either TNF-α or IL-8 for 4–9 h, with untreated replicates included for each strain/treatment combination. Bacteria were then fixed in 3% paraformaldehyde and 0.1% glutaraldehyde in phosphate buffer for 2h at room temperature and processed for transmission electron microscopy. The samples were subsequently washed, dehydrated and processed into Araldite resin blocks (TAAB Laboratories), before being sectioned and mounted onto nickel grids. For the immunogold labelling, samples were washed (in a 1% BSA and 5% goat serum solution) and incubated overnight at 4°C with either anti-TNF-α or anti-IL-8 monoclonal antibodies at 2 μg ml⁻¹ (Thermo Scientific), followed by labelling with goat anti-mouse IgG : 10 nm gold (BB International) at 0.2 μg ml⁻¹ for 4h at 4°C. To prevent non-specific binding with both primary and secondary antibodies, BSA and goat serum were used at appropriate stages in the procedure. Imaging was performed on an FEI Technai 12 Biotwin transmission electron microscope at 100 kV.

5.3. Chromatin IP

The IP protocol used in this study was the same as described in Grainger et al. with slight modifications [66,67].
leading to the conclusion that PilQ is non-essential for pilus fibre formation and functions specifically in Tfp biogenesis by facilitating the translocation of the fibre to release of IL-8, IL-6, TNF-α, IL-1β and other cytokines [59,60]. (ii) Tfp from a wild-type strain exhibits a natural occurrence of pili formation and retraction machinery. (iii) Formation of alternative pili in a ΔpilQ mutant. A study by Wolfgang et al. [61] using TEM showed that the membranous protrusions in PilQ/T mutants in N. gonorrhoeae contained pilus fibres. The pilus fibres were indistinguishable in diameter and morphology from those observed on the surface of wild-type cells, leading to the conclusion that PilQ is non-essential for pilus fibre formation and functions specifically in Tfp biogenesis by facilitating the translocation of the fibre to the cell surface [61]. (iv) ΔpilE mutant lacking Tfp pili. However, in absence of PilE, projection of PilX (unknown pilus) results in unusual pili, which may not be fully functional as Tfp, but may still be somewhat responsive to environmental alterations through the PilQ protein. (v) Non-glycosylated Tfp on a ΔpilQ mutant. This strain produces non-glycosylated pilin variants. (b) Tipping the balance towards inflammatory disease. A proposed homeostatic mechanism showing the delicate balance between host and microbe that determines commensalism or virulence in response to the environment. The immune system is conventionally viewed as a means of fighting infection. It has become clear, however, that what is considered as the ‘immune’ system has also evolved to maintain homeostasis and regulate commensal microbes that normally inhabit the body [62]. The shared evolutionary fate of humans and their symbiotic bacteria resulted in mutualistic interactions that are essential for human health [63]. Therefore, the recognition of the immune elicitors by bacterial cells provides a key to understanding disease processes. We propose that host responses to microbes are engaged by commensal Nm and control the patterns of pathogenesis. This hypothesis broadly serves as the conceptual foundation for understanding the interrelationships between microbes and humans. Symbiotic bacteria typically do not cause serious health problems to the host [64] and live in an equilibrated environment. This asymptomatic presence can even be beneficial to the human host because it allows antibodies to develop which can be useful in fighting a more serious subsequent infection [64]. However, Nm can sense (and respond to) the threat caused by an overreacted immune response to other pathogens, such as virus infections that can destabilize the balanced interrelationship between bacteria and host. Symbiotic bacteria either have degenerate genomes that retain only the most essential functions [65] and lack genes required for the ingestion of elicitors or eliminate the genes that proceed in response to host elicitors, thus maintaining the symbiotic interaction within their host. Our discovery paves the way to investigate novel ecological and evolutionary principles that may provide new strategies for restoring and maintaining human health. LPS, lipopolysaccharide; SP, secreted bacterial proteins; CP, cell envelope proteins.

5.4. DNA-binding studies

Electrophoretic mobility shift assays (EMSAs) were performed essentially as described [68]. Briefly, synthetic oligonucleotides from the app gene (NMB1985 APP) and its promoter region were isolated by PCR. Overlapping regions used here are: Pro.1–2: TTT CGG TGG TCC TGT CGG TGG TTT TCA TTA TTC TCT CCT ACG TGA CGG AGT GGG AT, Pro. 3–4: CGG GAT TCG GGT TTG TTT GGG CTT CCG CTT CCG GGC GGC GGC GGC GAT GTC CCT ATA TAT GCG GGT GGC CG, Pro. 5–6: TAT GTG CGG TTC GGC GGC GAT CGT AGG AAC CAC GCA GTA TTA GTC ATT ATT GTA TCG CCT GCG TCG TTC CCC, Internal region of app gene itself: GTT TTC TAC CAA CAG GAC GAT CTT TGC ATG ACG GCT CAC CAA TTA TCT ATG ATG CCC AAA AGG AAA AGT G. These were amplified and radioactively labelled using 32P-γ-ATP and T4 polynucleotide kinase (New England Biolabs). Binding reactions were carried out with 50,000 cpm (approx. 0.1 ng) of 32P-end-labelled oligonucleotide for 20–30 min at room temperature in 10 or 20 μl reaction volumes containing 12% glycerol, 12 mM HEPES-NaOH (pH 7.9), 60 mM KCl, 5 mM MgCl2, 4 mM Tris–Cl (pH 7.9), 0.6 mM EDTA (pH 7.9) and 0.6 mM dithiothreitol.

Protein–DNA complexes were resolved in 6% polyacrylamide gels pre-electrophoresed for 30 min at room temperature in 0.25 × TBE buffer (22.5 mM Tris borate and 0.5 mM EDTA, pH 8.3). Gels were dried and visualized using a phosphorimager.

5.5. Deep sequencing

Total RNA was enriched via two rounds of ribo depletion using a MICROBExpress kit (Ambion). Barcoded RNA-seq libraries were then constructed from each enriched RNA sample using a Total RNA-seq kit (Ambion) and sequenced using a SOLiD 4 genome analyser (Applied Biosystems).

The SOLiD reads were mapped to the reference genome (Nm MC58) using BioScope v. 1.3.1 software. The htsq-count script from the HTSEQ PYTHON package (http://www-huber.embld.de/users/anders/HTSeq/doc/count.html) was used to count the number of reads that were mapped to each gene. The total number of reads per kilobase per million mapped reads were also calculated [69]. Differential expression analysis between the samples was performed using the R package DESeq [70].

5.6. Reporter gene lacZ assay

Promoter–lacZ fusions were constructed by inserting Nm promoter regions upstream of lacZ, creating promoter–lacZ translational fusions, using the BamHI site upstream of lacZ in pLAS94 [71]. For gene NMB0946 (preoxiredoxin, prx), the promoter was amplified with primers 5’AAAAAGGATCC AGCACAATCCAC-3’ and 5’AAAAAGGATCCGGGCTTTC-3’ for gene NMB0780 (bacterioli teritin co-migratory protein, bcp), the promoter was amplified with primers 5’AAAAAGGATCCCATCCATGCTCTAC-3’ and 5’AAAAAGGATCCGTGGAGGAGAATCC-3’.

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For gene NMB1998 (mspA), the promoter was amplified with 5'-CCGGAGATCCGGATGATGATTATCGCTGTGAT-3' and 5'-CCGGATCCAAACAGCGAAAGCCCCGCCAG-3' by these sets of primers. Derivatives of pLES94 containing the promoter region were checked by sequencing and transformed into Nm MC58, and verified by PCR. β-galactosidase activity was assayed by the method of Miller [34], after growth of Nm strains for 0–12 h in DMEM medium in the presence or the absence of cytokines IL-8 or TNF-α, both at a concentration of 100 ng ml⁻¹.

5.7. Mouse model of infection

Previous studies have shown that the hCD46Ge transgenic mouse line (CD46[2/2]) can develop meningococcal disease [39,72,73]. Serogroup B meningococcal strains were suspended in GC liquid, and each mouse was challenged intraperitoneally (i.p.) with 1.2 × 10⁹ CFU in 100 µl of GC liquid medium. Experiments were performed with 6–8-week-old mice (n = 8 mice per group). In the control group, mice were challenged i.p. with 100 µl GC liquid. The health condition of all mice was closely monitored for 7 days. At the indicated time points, whole blood samples were collected from the tail vein for the measurement of cytokines, chemokines and bacterial levels. Bacterial strains MC58 and ΔpilG/C/L mutant were isolated from blood of five i.p.-infected mice (1.2 × 10⁹ cfu mouse⁻¹). Whole blood anticoagulated with heparan sulfate was collected by retro-orbital bleeding at 4 h post-infecation. Blood cells were removed by gentle centrifugation; bacteria in plasma were washed once with PBS following fixation with 3% PFA, 0.1% glutaraldehyde in phosphate buffer.

Ethical statement. The mouse experiments described in this study were performed at the animal facility of the Wenner-Grens Institute, Stockholm University. Animal care and experiments were conducted according to the institution's guidelines for animal husbandry. All protocols were approved by the Swedish Ethical Committee on Animal Experiments (Approval ID: N316/10).

Acknowledgements. We thank Dr Vladimir Pelicic (Imperial College London) for the IgF construct, Dr Neil Oldfield (University of Nottingham) for providing a pgC mutant, Dr Noha Aboaseuda (University of Alexandria) for providing bacterial data, Prof. Christopher M. Tang (Imperial College London) for providing saib, pilT and pilE mutants, Dr Karin Heurlier for providing lcp and prx reporter gene lacZ constructs and Mrs Denise Christie for preparation and the analysis of TEM samples. We also thank the Proteomics Core Facility at Sahlgrenska Academy, Gothenburg University. Author contributions. P.J.R. and S.A. provided input into the conceptual development as well as preparation of the manuscript. J.S. and K.B. provided technical assistance and input into data analyses. T.S. provided the TEM data. L.M.W. provided some of the EM pictures and confocal images. C.S. provided the glycosylation analysis of the PilQ protein. R.W. performed the deep sequencing and J. Moreton performed the bioinformatics analysis of deep-sequencing data. J.W.B.M. performed the reporter gene lacZ analysis. H.S.S. performed the animal study. P.S. performed the EMSA experiments. A.B.J. and T.B. participated in discussion and review of the manuscript. J. Mahdavi, P.S. and D.A.A.A. conceived the project, wrote the manuscript and coordinated the investigations.

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