Susceptibility to Invasive Meningococcal Disease: Polymorphism of Complement System Genes and Neisseria meningitidis Factor H Binding Protein

Declan T. Bradley1,2*, Thomas W. Bourke3, Derek J. Fairley4, Raymond Borrow5,6, Michael D. Shields3, Peter F. Zipfel7,8, Anne E. Hughes9

1 Centre for Public Health, School of Medicine, Dentistry and Biomedical Sciences, Queen’s University Belfast, Belfast, United Kingdom, 2 Public Health Agency, Belfast, United Kingdom, 3 Centre for Infection and Immunity, School of Medicine, Dentistry and Biomedical Sciences, Queen’s University Belfast, Belfast, United Kingdom, 4 Regional Virus Laboratory, Belfast Health and Social Care Trust, Belfast, United Kingdom, 5 Vaccine Evaluation Unit, Public Health England, Manchester, United Kingdom, 6 Inflammation Sciences Research Group, School of Translational Medicine, University of Manchester, Manchester, United Kingdom, 7 Department of Infection Biology, Leibniz Institute for Natural Product Research and Infection Biology—Hans Knöll Institute, Jena, Germany, 8 Friedrich Schiller University, Jena, Germany, 9 Formerly of Centre for Public Health, School of Medicine, Dentistry and Biomedical Sciences, Queen’s University Belfast, Belfast, United Kingdom

* dbradley09@qub.ac.uk

Abstract

Background

Neisseria meningitidis can cause severe infection in humans. Polymorphism of Complement Factor H (CFH) is associated with altered risk of invasive meningococcal disease (IMD). We aimed to find whether polymorphism of other complement genes altered risk and whether variation of N. meningitidis factor H binding protein (fHBP) affected the risk association.

Methods

We undertook a case-control study with 309 European cases and 5,200 1958 Birth Cohort and National Blood Service cohort controls. We used additive model logistic regression, accepting P<0.05 as significant after correction for multiple testing. The effects of fHBP subfamily on the age at infection and severity of disease was tested using the independent samples median test and Student’s T test. The effect of CFH polymorphism on the N. meningitidis fHBP subfamily was investigated by logistic regression and Chi squared test.

Results

Rs12085435 A in C8B was associated with odds ratio (OR) of IMD (0.35 [95% CI 0.19–0.67]; P = 0.03 after correction). A CFH haplotype tagged by rs3753396 G was associated with IMD (OR 0.56 [95% CI 0.42–0.76], P = 1.6x10-4). There was no bacterial load (CtrA
cycle threshold) difference associated with carriage of this haplotype. Host CFH haplotype and meningococcal fHBP subfamily were not associated. Individuals infected with meningococci expressing subfamily A fHBP were younger than those with subfamily B fHBP meningococci (median 1 vs 2 years; \( P = 0.025 \)).

**Discussion**

The protective CFH haplotype alters odds of IMD without affecting bacterial load for affected heterozygotes. CFH haplotype did not affect the likelihood of infecting meningococci having either fHBP subfamily. The association between C8B rs12085435 and IMD requires independent replication. The CFH association is of interest because it is independent of known functional polymorphisms in CFH. As fHBP-containing vaccines are now in use, relationships between CFH polymorphism and vaccine effectiveness and side-effects may become important.

**Introduction**

The complement system is a fundamental part of the innate immune response. This pathway harms unprotected surfaces by a powerful positive feedback cycle that injures cells by perforating them with circular polymers (the membrane attack complex) and by activating further immune response by releasing opsonins and anaphylatoxins [1–3]. Complement activation can cause harm to both unprotected self and foreign cell surfaces [1,2].

Pathogenic bacteria evade the complement system by mimicking or binding to protective host proteins [4]. Human complement factor H (CFH) is the major inhibitory regulator of the complement system. Polymorphism of CFH and the adjacent homologous CFHR1–5 genes is associated with susceptibility to several inflammatory diseases [5–10]. A genome-wide association study of susceptibility to invasive meningococcal disease identified a major risk association at the CFH and CFHR3 locus [11]. The report noted that the associated variants are in strong linkage disequilibrium with the minor allele of rs1065489 (D936E) in the CFH gene, but evidence that this is the functional cause is lacking. Unexpectedly, the associated CFH polymorphism as one with no known functional effect and is not one associated with other inflammatory diseases.

*Neisseria meningitidis* infection causes sepsis and meningitis, with death in approximately 10% of cases [12]. Factor H-binding protein (fHBP) and Neisserial Surface Protein A bind host CFH to protect *N. meningitidis* [13–15]; *Neisserial* fHBP is critical for meningococcal survival in blood [16]. It binds short consensus repeats 6 and 7 of human CFH, which is a region of CFH that also binds to self-surface membranes [17]. It may cause its severe systemic effects by sequestering host CFH, leaving self surfaces unprotected [17,18]. The common CFH Y402H polymorphism (rs1061170), which is a major risk factor for age-related macular degeneration, is adjacent to the fHBP binding site, but does not affect binding to fHBP [17].

Factor H binding protein has been a recent focus of interest because it is now a component of vaccines against serogroup B *N. meningitidis* [19,20], one of which is already used in outbreak control [21] and is likely to be added to the UK childhood immunisation schedule [22], which might result in meningococcal disease becoming rare.

Polymorphism of fHBP can be categorized by two different systems of nomenclature. Fletcher *et al.* use a system of two subfamilies, A and B [19]. Massignani *et al.* use a system of
three variant groups (1, 2 and 3) [20]. Disease severity is associated with polymorphic variation affecting the five segments that make up the modular structure of fHBP [23–25]. Previous studies of fHBP sequenced the whole gene from cultured N. meningitidis isolates, and then defined the subfamily, variant group or modular group using only a small number of sequence features. Our study is the first to define fHBP type directly using DNA isolated from patient blood. This may avoid bias due to variation in the success in culturing different strains of N. meningitidis.

The aim of this study was to explore the relationship between invasive meningococcal disease and variation of the human complement system. We sought to refine the risk association at the CFH locus and to investigate whether variation of N. meningitidis fHBP affects this association. We explored other variations of the complement system, including terminal pathway genes where deficiency of proteins has been associated with susceptibility to recurrent meningococcal disease [26–29] and two complement inhibitors to which N. meningitidis binds: CD46, which encodes membrane cofactor protein, a membrane-bound complement inhibitor [30,31] and C4 binding protein, which inhibits the classical pathway [32].

Methods
Ethics Statement
The study was approved by the Office for Research Ethics Committees Northern Ireland (part of the UK National Research Ethics Service; study reference: 10/NIR03/24). Following formal proposal to its project advisory group, the Health Protection Agency (now part of Public Health England) provided anonymised residual clinical diagnostic DNA samples from PCR-confirmed cases of invasive meningococcal disease collected in 2009 and 2010. No identifying information was provided. Informed consent was not required for these samples because only anonymised demographic data and residual clinical DNA samples were provided. The Wellcome Trust Case Control Consortium (WTCCC) 1958 Birth Cohort and National Blood Service samples were collected with informed consent and used with permission of the WTCCC.

Study Population
The case population characteristics have been described in detail previously [33]. The cases were 309 European individuals with PCR-confirmed invasive meningococcal disease. We did not have access to details of the clinical features or demographic details other than age at time of illness. The N. meningitidis serogroups were: B, 292; C, 3; W, 4; Y 4. The ages ranged between one month and 73 years, with a median of two years. European ancestry was ascertained by using an ancestry-informative panel of polymorphisms [34] and cluster analysis, as described previously [33].

The control population comprised 5,200 individuals with European ancestry from the United Kingdom 1958 Birth Cohort and National Blood Service (NBS) cohort, for whom microarray genome-wide data were provided by the Wellcome Trust Case-Control Consortium (WTCCC). The WTCCC exclusions were applied, and validated by principal components analysis, as described previously [33]. The case population does not overlap with any group tested in the Davila et al. genome-wide association study. The control group is identical to that used in the genome-wide association study [11]. The median age of NBS participants was 45 years. The 1958 Birth Cohort participants were aged 52 years at the time of genotyping.

Detection of N. meningitidis
Confirmation of invasive meningococcal disease was based on a positive diagnostic Taqman assay for capsular transfer gene (ctrA) at the Health Protection Agency (now Public Health
England) Meningococcal Reference Unit using an Applied Biosystems 7700 sequence detection system, as described previously [35]. The cycle number at which each positive sample was detected was reported. Cycle threshold, which is inversely correlated with bacterial load, has been used as an indicator of disease severity in other studies [36,37].

Genotyping of CFH Polymorphisms

Six SNPs in CFH were genotyped by SNapshot primer extension methodology, involving PCR to amplify sequence fragments containing polymorphisms of interest, ExoSAP-IT to neutralise unincorporated dNTPs, fluorescent primer extension, further shrimp alkaline phosphatase clean-up, and analysis on an ABI 3100 genetic analyser. The SNPs genotyped were rs1061170 (Y402H), rs800292 (I62V), rs6677604 (which is in full linkage disequilibrium with the deletion of CFHR3-CFHR1), rs3753396 (which is in full linkage disequilibrium with rs1065489, D936E), rs419137, and rs2284664. SNPs were chosen on the basis of our established protocols for genotyping [8, 38]. Oligonucleotides are shown in S1 Table. Genotype calls were made using GeneMarker v1.5.1. The control dataset had been genotyped on an Illumina 1.2M duo SNP microarray. Four core CFH haplotypes were defined using four SNPs (Table 1) based our previous studies (with the very closely related haplotypes 1 and 2 in our haplotype model [38] replaced by haplotype A in the present report, defined by rs1061170) [8,38].

Sequenom iPLEX for complement gene polymorphisms

Polymorphisms of complement pathway genes were investigated using the Sequenom iPLEX platform. PCR and primer extension oligonucleotides were designed using the My Sequenom Online Tools (Sequenom Inc., San Diego, CA, USA), with a target PCR fragment length of between 80 and 120 bp and target primer extension oligonucleotide of between 15 and 30 bases, according to the manufacturer’s protocol. Oligonucleotide sequences are shown in S2 Table. Shrimp alkaline phosphatase was used to neutralise unincorporated dNTPs after the PCR reaction and the iPLEX Gold resin used for final conditioning after primer extension. The reaction product was nanodispensed onto an array chip by technical staff in the Queen’s University Belfast Genome Core using the MassARRAY nanodispenser prior to operation of the MassARRAY mass spectrometer. Genotyping was then carried out using TYPER software (Sequenom). Each SNP cluster plot was inspected individually for quality of clustering and the mass spectrometry plot examined for potentially erroneous base calls, which were recalled or set to missing if a problem was observed. Data were exported from TYPER and converted to PLINK format using Microsoft Excel 2010.

Genotyping of Neisserial fHBP

A method based on the sequence variation described by Pajon et al. [23] was developed and validated by sequencing fHBP from eight cultured isolates of N. meningitidis. We used a one-step duplex of two PCR reactions in the same experiment. Subfamily A and B fHBP were

Table 1. CFH Haplotype Definitions.

| Haplotype Name | rs1061170 | rs3753396 | rs6677604 | rs2284664 |
|----------------|-----------|-----------|-----------|-----------|
| A              | G         | A         | G         | G         |
| B              | A         | G         | G         | G         |
| C              | A         | A         | A         | G         |
| D              | A         | A         | G         | A         |

doi:10.1371/journal.pone.0120757.t001
distinguished by detection of a ten-base insertion/deletion polymorphism in module A of the gene. One pair of primers, one of which was fluorescently Fam-labelled, was used to make a product of either 157 or 167 bases in length, which was detected on the ABI 3100 Genetic Analyser. Further distinguishing between variant 2 and variant 3 was by the use of three sequence-specific primers, all paired with one common, Fam-labelled primer. The three sequence-specific primers were of different lengths, and bound to the junction between modules C and D, each of which may have one of two variants. According to Pajon et al., three variants are found, and therefore, the sequence-specific primers were designed to bind to these combinations of polymorphic modules C and D. Oligonucleotide sequences are shown in S3 Table. In addition to the subfamily and variant classifications of fHBP, the method can determine the most common modular groups described in Pajon et al. [23]. The rare (<0.5%) groups VII, VIII and IX cannot each be distinguished from closely related more common modular groups (Table 2).

Statistical Analysis

Assessment for deviation from Hardy Weinberg equilibrium was conducted using the method of Wigginton et al. [39] as implemented in PLINK v1.07 [40,41]. A P value for deviation of <0.05 in cases, controls, or overall was considered to be significant.

A minimum genotyping rate per SNP of 90% and minimum genotyping rate per individual of 90% were used. Association with individual SNPs was assessed by univariate logistic regression (additive model) in PLINK. Significance for association was accepted at \( P < 0.05 \) after Bonferroni correction for multiple testing in the study of the complement pathway. Correction for multiple testing was not used for analysis of \( CFH \) as this was a replication of a previous report.

Individuals missing genotypes for any of the four \( CFH \) haplotype-tagging SNPs were excluded from haplotype analysis. Multivariate logistic regression was conducted in SPSS v19 for case-control status using the number of copies of each \( CFH \) haplotype as covariates, omitting one haplotype (D) as a reference variable to avoid multicollinearity.

Cycle threshold was compared between \( CFH \) haplotype B carriers and non-carriers using Student’s T test in R v3.1.1. Age was compared between fHBP Subfamily A and fHBP Subfamily B using the independent samples median test in SPSS.

Results

CFH

The genotyping rate was 99.7%. No markers deviated significantly from Hardy Weinberg equilibrium. Two cases failed genotyping entirely, no other individuals were excluded for incomplete genotyping and no markers were excluded because of low genotyping.

Rs1061170 G was associated with increased risk (OR 1.26 [95% CI 1.07–1.49], \( P = 5.3 \times 10^{-3} \)) and rs3753396 G was associated with reduced risk (OR 0.56 [95% CI 0.43–0.74], \( P = 3.0 \times 10^{-5} \)) (Table 3). Multivariate logistic regression shows that haplotype B, tagged by rs3753396 G, is significantly associated with a reduced odds ratio of invasive meningococcal disease (OR 0.56

| Table 2. Subfamily, Variant and Modular fHBP groups. |
|-------------|----------------|----------------|
| **Subfamily** | **Subfamily A** | **Subfamily B** |
| **Variant** | Variant 2 | Variant 3 | Variant 1 |
| **Common Modular Groups** | III | VI | II | V |
| **Rare Modular Groups not differentiated from above by fHBP test** | VIII | IX | VII |

doi:10.1371/journal.pone.0120757.t002
[95% CI 0.42–0.76], \( P = 1.6 \times 10^{-4} \) (Table 4). Haplotype C, which carries the deletion of \( CFHR3 \) and \( CFHR1 \) [8] was not associated with the phenotype.

The cycle threshold for \( CtrA \) in haplotype B carriers was 31.4 and for ‘wild-type’ non-carriers was 31.3.

**Factor H-Binding Protein Characteristics in the Case Population**

The frequencies of the Neisserial \( fHBP \) variants are shown (Table 5). These are similar to those reported by Pajon et al. [23].

The median age of cases with subfamily A \( fHBP \) \( N. meningitidis \) was one year and that of cases with subfamily B \( fHBP \) \( N. meningitidis \) was two years (independent-samples median test \( P = 0.025 \)). The mean cycle threshold for detection of \( ctrA \) for cases with subfamily A \( fHBP \) \( N. meningitidis \) was 29.7 and that for subfamily B \( fHBP \) \( N. meningitidis \) was 29.2.

**Susceptibility to \( N. meningitidis \) with Subfamily A and Subfamily B \( fHBP \)**

\( CFH \) Haplotype B was associated with a statistically significant protective effect against the rarer subfamily A \( fHBP \)-expressing \( N. meningitidis \) infection, but was not associated with protection against the more common subfamily B \( fHBP \)-expressing \( N. meningitidis \) (Table 6). However, there was no significant difference between the distribution of \( fHBP \) subfamily \( N. meningitidis \) infection in haplotype B heterozygote cases and wild-type homozygote cases (Pearson chi-square \( P = 0.11 \); Table 7).

**Complement Pathway**

Twenty nine individuals were excluded because of a low genotyping rate, and no SNPs were excluded because of low genotyping leaving 281 cases and 5,199 controls. The remaining genotyping rate was 99.8%. Five SNPs were excluded due to significant deviation from Hardy Weinberg equilibrium in controls, all of which were in \( CD46 \).

One SNP in each of \( CD46 \) (rs2796278), \( C5 \) (rs17216529), \( C8A \) (rs17300936) and \( C8B \) (rs12085435) was associated with the phenotype before correction for multiple testing (Table 8). The association with rs12085435 in \( C8B \) was significant after Bonferroni correction.
for 21 tests \((P = 0.03)\), and the other SNP associations were non-significant. Both C8 SNPs were independently associated with the disease phenotype in multivariate logistic regression (Table 9).

**Discussion**

Our study explored the characteristics of the association between meningococcal disease and CFH polymorphism, the relationship between fHBP subfamily and this association and the effects of other polymorphisms of complement system genes on disease risk.

Our findings provide further evidence supporting the association between CFH polymorphism and invasive meningococcal disease reported by Davila et al. [11] but as we used the same control group as that study, this is not a full independent replication of the finding. Haplotypic exploration revealed that the association is due to only one haplotype (B), which does not carry any of the known major functional variants associated with AMD. The haplotypes that carry deletion of CFHR3-CFHR1 (haplotype C) and Y402H (haplotype A) were not associated in a multivariate logistic regression. The protective haplotype B was not associated with any difference in the bacterial load (measured by cycle threshold), suggesting that while disease risk is altered by carrying this variant, severity of disease is not. There was no significant difference in age of cases between carriers and non-carriers of haplotype B, suggesting that the protective mechanism does not affect the age of onset.

**Table 5. fHBP Variant Frequencies in the Case Population.**

| fHBP Module Group | Present Study Number (frequency) | Pajon[23] Number (frequency) |
|-------------------|----------------------------------|-----------------------------|
| I/VII             | 129 (0.52)                       | 126 (0.52)                  |
| II/VIII           | 7 (0.03)                         | 21 (0.09)                   |
| III               | 12 (0.05)                        | 26 (0.11)                   |
| IV                | 54 (0.22)                        | 12 (0.05)                   |
| V/IX              | 24 (0.10)                        | 32 (0.13)                   |
| VI                | 20 (0.08)                        | 25 (0.10)                   |
| Total             | 246                              | 242                         |

**Table 6. Association of CFH Haplotypes with Susceptibility to Invasive Infection with N. meningitidis expressing Subfamily A and Subfamily B fHBP.**

| Subfamily A fHBP | Odds Ratio (95% CI) | P     | Subfamily B fHBP | Odds Ratio (95% CI) | P     |
|------------------|---------------------|-------|------------------|---------------------|-------|
| Haplotype A [rs1061170 G] | 1.31 (0.83–2.05)   | 0.25  | 1.03 (0.78–1.36) | 0.83                |
| Haplotype B [rs3753396 G] | 0.46 (0.22–0.98)   | 0.046 | 0.72 (0.50–1.06) | 0.09                |
| Haplotype C [rs6677604 A] | 0.99 (0.56–1.74)   | 0.98  | 0.91 (0.65–1.28) | 0.59                |

**Table 5. fHBP Variant Frequencies in the Case Population.**

| fHBP Module Group | Present Study Number (frequency) | Pajon[23] Number (frequency) |
|-------------------|----------------------------------|-----------------------------|
| I/VII             | 129 (0.52)                       | 126 (0.52)                  |
| II/VIII           | 7 (0.03)                         | 21 (0.09)                   |
| III               | 12 (0.05)                        | 26 (0.11)                   |
| IV                | 54 (0.22)                        | 12 (0.05)                   |
| V/IX              | 24 (0.10)                        | 32 (0.13)                   |
| VI                | 20 (0.08)                        | 25 (0.10)                   |
| Total             | 246                              | 242                         |

**Table 6. Association of CFH Haplotypes with Susceptibility to Invasive Infection with N. meningitidis expressing Subfamily A and Subfamily B fHBP.**

| Subfamily A fHBP | Odds Ratio (95% CI) | P     | Subfamily B fHBP | Odds Ratio (95% CI) | P     |
|------------------|---------------------|-------|------------------|---------------------|-------|
| Haplotype A [rs1061170 G] | 1.31 (0.83–2.05)   | 0.25  | 1.03 (0.78–1.36) | 0.83                |
| Haplotype B [rs3753396 G] | 0.46 (0.22–0.98)   | 0.046 | 0.72 (0.50–1.06) | 0.09                |
| Haplotype C [rs6677604 A] | 0.99 (0.56–1.74)   | 0.98  | 0.91 (0.65–1.28) | 0.59                |

doi:10.1371/journal.pone.0120757.t006
There was no significant difference between the distribution of the fHBP subfamilies in individuals who have a copy of CFH haplotype B and those who do not, which suggests that CFH haplotype variation does not alter the risk of infection with meningococci with fHBP subfamilies A and B differently.

The patients affected by N. meningitidis with fHBP subfamily A were significantly younger than those who had infection with N. meningitidis with fHBP subfamily B.

Our investigation of other complement pathway polymorphisms suggests that a coding polymorphism in C8B may be associated with susceptibility to invasive meningococcal disease. This is consistent with the observation that terminal complement component deficiencies increase risk of invasive meningococcal disease [42]. This possibility requires replication in an independent cohort.

Our study is unique in integrating human and bacteriological genomic information to assess the effects of variation of genes that produce interacting proteins. The most important limitation of this study is the lack of an independent replication group to confirm the association at C8B. Our study used the same control group as Davila et al. [11], meaning that we have not reported a full independent replication of the association at CFH. We conducted our own laboratory experiments to genotype meningococcal disease cases and compared them to controls that

| Subfamily A | Subfamily B |
|-------------|-------------|
| Haplotype B Heterozygote | 9 | 42 |
| Wild-type Homozygote | 49 | 120 |

Table 7. Direct Comparison of Subfamily of Haplotype B Heterozygotes and Non-Heterozygotes (Wild-type).

doi:10.1371/journal.pone.0120757.t007

| Chromosome | Position(NCBI b37) | SNP Name | Gene | Change | Allele 1 | Allele 2 | Odds Ratio (95% CI) | P |
|------------|---------------------|----------|------|--------|----------|----------|---------------------|---|
| 1          | 57064136            | rs947636 | C8A  | C      | 0.32     | 0.29     | 1.15 (0.96–1.38)    | 0.14 |
| 1          | 57113315            | rs652785 | C8A  | Q>K    | 0.42     | 0.38     | 1.19 (1.00–1.41)    | 0.06 |
| 1          | 57155946            | rs17300936 | C8A | P>L    | 0.09     | 0.13     | 0.67 (0.50–0.89)    | 6.2x10⁻³ |
| 1          | 57180072            | rs626457 | C8B  | A      | 0.34     | 0.33     | 1.04 (0.87–1.25)    | 0.67 |
| 1          | 57187898            | rs12085435 | C8B | P>L    | 0.02     | 0.05     | 0.35 (0.19–0.67)    | 1.3x10⁻³ |
| 1          | 57195072            | rs1013579 | C8B | G>R    | 0.03     | 0.03     | 0.96 (0.58–1.61)    | 0.89 |
| 1          | 57195099            | rs12067507 | C8B | E>K    | 0.04     | 0.05     | 0.71 (0.46–1.10)    | 0.13 |
| 1          | 205356059           | rs2842704 | C4BPA | C     | 0.14     | 0.14     | 1.03 (0.80–1.32)    | 0.83 |
| 1          | 205360403           | rs4425986 | C4BPA | C     | 0.44     | 0.43     | 1.05 (0.88–1.25)    | 0.58 |
| 1          | 205364303           | rs1126618 | C4BPA | G>G    | 0.17     | 0.16     | 1.06 (0.84–1.33)    | 0.61 |
| 1          | 205371523           | rs4844573 | C4BPA | I>T    | 0.32     | 0.35     | 0.90 (0.75–1.08)    | 0.26 |
| 1          | 205372211           | rs4571969 | C4BPA | T     | 0.24     | 0.24     | 1.00 (0.82–1.23)    | 0.99 |
| 1          | 206022446           | rs2796278 | CD46  | C     | 0.54     | 0.49     | 1.25 (1.05–1.48)    | 0.01 |
| 5          | 39285479            | rs155375 | C9    | T      | 0.43     | 0.44     | 0.96 (0.81–1.13)    | 0.61 |
| 5          | 39400311            | rs700233 | C9    | R>W    | 0.37     | 0.40     | 0.88 (0.74–1.05)    | 0.16 |
| 5          | 40998620            | rs10941528 | C7 | A      | 0.23     | 0.23     | 1.01 (0.83–1.24)    | 0.90 |
| 5          | 41001075            | rs3805221 | C7    | T      | 0.23     | 0.24     | 0.99 (0.81–1.21)    | 0.89 |
| 5          | 41021361            | rs4957361 | C7    | T      | 0.35     | 0.36     | 0.98 (0.82–1.17)    | 0.79 |
| 5          | 41235716            | rs1801033 | C8    | A>E    | 0.35     | 0.37     | 0.94 (0.79–1.13)    | 0.52 |
| 9          | 122765747           | rs17612 | C5    | E>D    | 0.06     | 0.08     | 0.74 (0.51–1.06)    | 0.10 |
| 9          | 122840039           | rs17216529 | C5 | V>I    | 0.04     | 0.07     | 0.55 (0.36–0.84)    | 5.6x10⁻³ |

Table 8. Sequenom iPLEX of Complement Pathway Genes in IMD.

doi:10.1371/journal.pone.0120757.t008
were genotyped using a different method, at a different time. This presents risk of a systematic genotyping error that could result in a false association. Independent replication is therefore vital. The exploration of the effect of CFH haplotype on disease severity (indicated by CtrA cycle threshold) and of fHBP on severity and age, are not affected by these limitations because these are analyses of cases only.

The functional basis for the relationship between CFH polymorphism and susceptibility to invasive meningococcal disease is not yet understood: It is likely that it relates to the interaction between CFH or CFH-related proteins and N. meningitidis. As meningococcal disease becomes less common, the focus of research may change to questions of immunity and vaccination: It would be most interesting to understand whether vaccine fHBP interacts differently with different variants in host CFH and CFHR proteins following vaccination in humans, and whether vaccination results in complement activation through transient sequestration of CFH. Costa et al. recently suggested that fHBP with low affinity for CFH should be explored in future development of fHBP-based vaccines to increase immunogenicity and reduce the chance of auto-antibody formation to CFH [43]. It is conceivable that carriage of the protective CFH haplotype could influence the effectiveness or side-effects of the vaccine, such as fever, which is common following meningococcal B vaccination [44].

The association between C8B rs12085435 and risk of meningococcal disease in our study is in keeping with the effect of inherited terminal complement deficiencies on susceptibility to meningococcal disease [42]. Independent replication will be key to establishing whether C8B is a second complement gene associated with meningococcal disease risk.

### Supporting Information

S1 Table. CFH PCR and SNaPshot Oligonucleotides.
(DOCX)

S2 Table. Sequenom iPLEX Oligonucleotides.
(DOCX)

S3 Table. fHBP Oligonucleotides.
(DOCX)

### Acknowledgments

We thank Dr Steve Gray for preparation of samples.

This study makes use of data generated by the Wellcome Trust Case Control Consortium. A full list of the investigators who contributed to the generation of the data is available from www.wtccc.org.uk.

### Author Contributions

Conceived and designed the experiments: DTB TWB DJF PFZ AEH. Performed the experiments: DTB TWB DJF AEH. Analyzed the data: DTB AEH. Contributed reagents/materials/analysis tools: DTB TWB DJF AEH. Wrote the paper: DTB TWB DJF RB MDS PFZ AEH.
References

1. Zipfel PF. Complement and immune defense: From innate immunity to human diseases. Immunol Lett. 2009; 126: 1–7. doi: 10.1016/j.imlet.2009.07.005 PMID: 19616581

2. Zipfel PF, Skerka C. Complement regulators and inhibitory proteins. Nat Rev Immunol. 2009; 9: 729–740. doi: 10.1038/nri2620 PMID: 19730437

3. Bradley DT, Zipfel PF, Hughes AE. Complement in age-related macular degeneration: A focus on function. Eye. 2011; 25: 683–693. doi: 10.1038/eye.2011.37 PMID: 21394116

4. Zipfel PF, Hallstrom T, Hammerschmidt S, Skerka C. The complement fitness factor H: Role in human diseases and for immune escape of pathogens, like pneumococci. Vaccine. 2008; 26: 67–74.

5. Klein RJ, Zeiss C, Chew EY, Tsai JY, Sackler RS, Haynes C, et al. Complement factor H polymorphism in age-related macular degeneration. Science. 2005; 308: 385–389. PMID: 15761122

6. Haines JL, Hauser MA, Schmidt S, Scott WK, Olson LM, Gallins P, et al. Complement factor H variant increases the risk of age-related macular degeneration. Science. 2005; 308: 419–421. PMID: 15761120

7. Hageman GS, Anderson DH, Johnson LV, Hancox LS, Taiber AJ, Hardisty LI, et al. A common haplotype in the complement regulatory gene factor H (HF1/CFH) predisposes individuals to age-related macular degeneration. Proc Natl Acad Sci U S A. 2005; 102: 7227–7232. PMID: 15870199

8. Hughes AE, Orr N, Esfandiary H, Diaz-Torres M, Goodship T, Chakravarthy U. A common CFH haplotype, with deletion of CFHR1 and CFHR3, is associated with lower risk of age-related macular degeneration. Nat Genet. 2006; 38: 1173–1177. PMID: 16998489

9. Zipfel PF, Edery M, Heinen S, Jozsi M, Richter H, Misselwitz J, et al. Deletion of complement factor H-related genes CFHR1 and CFHR3 is associated with atypical hemolytic uremic syndrome. PLoS Genet. 2007; 3: e41. PMID: 17367211

10. Zhao J, Wu H, Khosravi M, Cui H, Qian X, Kelly JA, et al. Association of genetic variants in complement factor H and factor H-related genes with systemic lupus erythematosus susceptibility. PLoS Genet. 2011; 7: e1002079. doi: 10.1371/journal.pgen.1002079 PMID: 21637784

11. Davila S, Wright VJ, Khor CC, Sim KS, Binder A, Breunis WB, et al. Genome-wide association study identifies variants in the CFH region associated with host susceptibility to meningococcal disease. Nat Genet. 2010; 42: 772–776. doi: 10.1038/ng.640 PMID: 20694013

12. Ramsay M, Kaczmarski E, Rush M, Mallard R, Farrington P, White J. Changing patterns of case ascertainment and trends in meningococcal disease in England and Wales. Commun Dis Rep CDR Rev. 1997; 7: R49–54. PMID: 9127510

13. Madico G, Welsch JA, Lewis LA, McNaughton A, Perlman DH, Costello CE, et al. The meningococcal vaccine candidate GNA1870 binds the complement regulatory protein factor H and enhances serum resistance. J Immunol. 2006; 177: 501–510. PMID: 16785547

14. Lewis LA, Ngampasutadol J, Wallace R, Reid JEA, Vogel U, Ram S. The meningococcal vaccine candidate neisserial surface protein A (NspA) binds to factor H and enhances meningococcal resistance to complement. PLoS Pathog. 2010; 6: e1001027. doi: 10.1371/journal.ppat.1001027 PMID: 20686663

15. Lewis LA, Carter M, Ram S. The relative roles of factor H binding protein, neisserial surface protein A, and lipooligosaccharide sialylation in regulation of the alternative pathway of complement on meningococci. J Immunol. 2012; 188: 5063–5072. doi: 10.4049/jimmunol.1103748 PMID: 22504643

16. Dunphy KY, Beernink PT, Brogioni B, Granoff DM. Effect of factor H-binding protein sequence variation on factor H binding and survival of neisseria meningitidis in human blood. Infect Immun. 2011; 79: 353–359. doi: 10.1128/IAI.00849-10 PMID: 21041484

17. Schneider MC, Prosser BE, Caesar JJ, Kugelberg E, Li S, Zhang Q, et al. Neisseria meningitidis recruits factor H using protein mimicry of host carbohydrates. Nature. 2009; 458: 890–893. doi: 10.1038/ nature07769 PMID: 19225461

18. Markiewski MM, DeAngelis RA, Lambris JD. Complexity of complement activation in sepsis. J Cell Mol Med. 2008; 12: 2245–2254. doi: 10.1111/j.1582-4934.2008.00504.x PMID: 18798865

19. Fletcher LD, Bernfield L, Barniak V, Farley JE, Howell A, Knauf M, et al. Vaccine potential of the neisseria meningitidis 2086 lipoprotein. Infect Immun. 2004; 72: 2088 Infection and Immunity-2100. PMID: 15039331

20. Masignani V, Comanducci M, Giuliani MM, Bambini S, Adu-Bobie J, Aricò B, et al. Vaccination against neisseria meningitidis using three variants of the lipoprotein GNA1870. J Exp Med. 2003; 197: 789–799. PMID: 12642606

21. Ladhani SN, Cordery R, Mandal S, Christensen H, Campbell H, Borrow R, et al. Preventing secondary cases of invasive meningococcal capsular group B (MenB) disease: Benefits of offering vaccination in addition to antibiotic chemoprophylaxis to close contacts of cases in the household, educational setting,
Complement Polymorphisms and Invasive Meningococcal Disease

22. Joint Committee on Vaccination and Immunisation. JCVI position statement on use of Bexsero meningococcal B vaccine in the UK. 2014; Available: https://www.gov.uk/government/publications/meningococcal-b-vaccine-jcvi-position-statement

23. Pajon R, Beernink PT, Harrison LH, Granoff DM. Frequency of factor H-binding protein modular groups and susceptibility to cross-reactive bactericidal activity in invasive meningococcal isolates. Vaccine. 2010; 28: 2122–2129. doi:10.1016/j.vaccine.2009.12.027 PMID: 20044056

24. Beernink PT, Granoff DM. The modular architecture of meningococcal factor H-binding protein. Microbiology. 2009; 155: 2873–2883. doi: 10.1099/mic.0.029876-0 PMID: 19574307

25. Piet JR, Brouwer MC, Exley R, van der Veen S, van de Beek D, van der Ende A. Meningococcal factor H binding protein fHbpd184 polymorphism influences clinical course of meningococcal meningitis. PLoS One. 2012; 7: e47973. doi:10.1371/journal.pone.0047973 PMID: 23110143

26. Brouwer MC, Read RC, van de Beek D. Host genetics and outcome in meningococcal disease: A systematic review and meta-analysis. Lancet Infect Dis. 2010; 10: 262–274. doi:10.1016/S1473-3099(10)70045-1 PMID: 20334849

27. Brouwer MC, de Gans J, Heckenberg SG, Zwinderman AH, van der Poll T, van de Beek D. Host genetic susceptibility to pneumococcal and meningococcal disease: A systematic review and meta-analysis. Lancet Infect Dis. 2009; 9: 31–44. doi: 10.1016/S1473-3099(08)70261-5 PMID: 19036641

28. Dale AP, Read RC. Genetic susceptibility to meningococcal infection. Expert Rev Anti Infect Ther. 2013; 11: 187–199. doi: 10.1586/eri.12.161 PMID: 23409824

29. Ram S, Lewis LA, Rice PA. Infections of people with complement deficiencies and patients who have undergone splenectomy. Clin Microbiol Rev. 2010; 23: 740–780. doi: 10.1128/CMR.00048-09 PMID: 20930072

30. Johansson L, Rytkonen A, Bergman P, Albigger B, Kallstrom H, Hokfelt T, et al. CD46 in meningococcal disease. Science. 2003; 301: 373–375. PMID: 12869763

31. Källström H, Liszewski MK, Atkinson JP, Jonsson A. Membrane cofactor protein (MCP or CD46) is a cellular pilus receptor for pathogenic neisseria. Mol Microbiol. 1997; 25: 639–647. PMID: 9379894

32. Jarva H, Ram S, Vogel U, Blom AM, Mert S. Binding of the complement inhibitor C4bp to serogroup B neisseria meningitidis. J Immunol. 2005; 174: 6299–6307. PMID: 15879129

33. Bradley DT, Bourke TW, Fairley DJ, Borrow R, Shields MD, Young IS, et al. Genetic susceptibility to invasive meningococcal disease: MBL2 structural polymorphisms revisited in a large case-control study and a systematic review. Int J Immunogenet. 2012; 39: 328–337. doi: 10.1111/j.1744-313X.2012.01095.x PMID: 22296677

34. Phillips C, Salas A, Sanchez JJ, Fondevila M, Gomez-Tato A, Alvarez-Dios J, et al. Inferring ancestral origin using a single multiplex assay of ancestry-informative marker SNPs. Forensic Sci Int Genet. 2007; 1: 273–280. doi: 10.1016/j.fsigen.2007.06.008 PMID: 19083773

35. Guiver M, Borrow R, Marsh J, Gray SJ, Kaczmarski EB, Howells D, et al. Evaluation of the applied biosystems automated taqman polymerase chain reaction system for the detection of meningococcal DNA. FEMS Immunol Med Microbiol. 2000; 28: 173–179. PMID: 10799809

36. Darton T, Guiver M, Naylor S, Jack DL, Kaczmarski EB, Borrow R, et al. Severity of meningococcal disease associated with genomic bacterial load. Clin Infect Dis. 2009; 48: 587–594. doi: 10.1086/596707 PMID: 19191644

37. Hackett SJ, Guiver M, Marsh J, Sills JA, Thomson APJ, Kaczmarski EB, et al. Meningococcal bacterial DNA load at presentation correlates with disease severity. Arch Dis Child. 2002; 86: 44–46. PMID: 11806883

38. Hughes AE, Orr N, Patterson C, Esfandiary H, Hogg R, McConnell V, et al. Neovascular age-related macular degeneration risk based on CFH, LOC387715/HTRA1, and smoking. PLoS Med. 2007; 4: e355. PMID: 18162041

39. Wigginton JE, Cutler DJ, Abecasis GR. A note on exact tests of hardy-weinberg equilibrium. Am J Hum Genet. 2005; 76: 887–893. PMID: 15789306

40. Purcell S. PLINK. 2009; v1.07.

41. Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MA, Bender D, et al. PLINK: A tool set for whole-genome association and population-based linkage analyses. Am J Hum Genet. 2007; 81: 559–575. PMID: 17701901

42. Tedesco F. Inherited complement deficiencies and bacterial infections. Vaccine. 2008; 26: I3–I8. PMID: 19388157
43. Costa I, Pajon R, Granoff DM. Human factor H (FH) impairs protective meningococcal anti-FHbp antibody responses and the antibodies enhance FH binding. MBio. 2014; 5: e01625–14. doi: 10.1128/mBio.01625-14 PMID: 25161192

44. Prymula R, Esposito S, Zuccotti GV, Xie F, Toneatto D, Kohl I, et al. A phase 2 randomised controlled trial of a multicomponent meningococcal serogroup B vaccine (I): Effects of prophylactic paracetamol on immunogenicity and reactogenicity of routine infant vaccines and 4CMenB. Hum Vaccin Immunother. 2014; 10: 2005–2014. doi: 10.4161/hv.29218 PMID: 25424810