Identification of Bacterial Protein O-
Oligosaccharyltransferases and Their Glycoprotein Substrates

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Abstract

O-glycosylation of proteins in Neisseria meningitidis is catalyzed by PglL, which belongs to a protein family including WaaL. O-antigen ligases. We developed two hidden Markov models that identify 31 novel candidate PglL homologs in diverse bacterial species, and describe several conserved sequence and structural features. Most of these genes are adjacent to possible novel target proteins for glycosylation. We show that in the general glycosylation system of N. meningitidis, efficient glycosylation of additional protein substrates requires local structural similarity to the pilin acceptor site. For some Neisserial PglL substrates identified by sensitive analytical approaches, only a small fraction of the total protein pool is modified in the native organism, whereas others are completely glycosylated. Our results show that bacterial protein O-glycosylation is common, and that substrate selection in the general Neisserial system is dominated by recognition of structural homology.

Introduction

Protein glycosylation occurs in all domains of life, where it is important in protein folding, stability and function. The presence of bacterial glycoproteins has long been known, but recent years have shown a dramatic increase in reports of protein glycosylation in diverse bacteria [1,2]. Genes encoding these glycoproteins are typically encoded in operons that include a glycosyltransferase and a single acceptor glycoprotein. Several recent reports have described general glycosylation systems in Gram-negative bacteria, including Neisseria meningitidis [3], Neisseria gonorrhoeae [4], Campylobacter jejuni [5,6] and Bacteroides fragilis [7]. In these general systems, a single glycosyltransferase or oligosaccharyltransferase enzyme modifies multiple different substrate proteins and the genes encoding the enzyme and substrate proteins are typically not closely linked on the genome.

The pathogenic N. meningitidis is the causative agent of meningococcal meningitis and septicaemia and is a worldwide health burden. N. meningitidis has a general system for protein O-glycosylation, which modifies PilE (Pilin), the major adhesin of N. meningitidis [8], and AnA, a surface exposed nitrite reductase [3]. A model has been developed for protein O-glycosylation in this system, which is similar to wzy-dependent O-antigen biosynthesis in Gram-negative bacteria [9]. In this model, a glycan to be transferred to protein is assembled on a diphosphate-polyprenyl lipid carrier on the cytoplasmic face of the inner membrane by the sequential action of glycosyltransferases PglB, PglA, PglE and the acetyltransferase PglI. N. meningitidis can have different repertoires of glycosyltransferases, with PglB2, PglG and PglH also present in some isolates [10,11]. Alterations in glycan structure can also occur by phase variation (the high frequency, reversible ON/OFF switching of gene expression) of the glycosyltransferases [10]. This potential diversity in the presence of glycosyltransferases leads to a corresponding diversity of potential mature glycan structures that can be transferred to protein. However, independent of the structure of the mature glycan, it is flipped to the periplasmic face of the inner membrane by PglF and then transferred to protein by the PglL O-oligosaccharyltransferase (O-OTase) [12]. This O-OTase enzyme exhibits extreme glycan substrate promiscuity, and is capable of transferring many structurally unrelated substrates from a pyrophosphate-polyprenyl carrier to protein, including the possible naturally occurring N. meningitidis glycans, C. jejuni glycan and even peptidoglycan subunits [13]. This promiscuity is presumably advantageous to allow efficient transfer of the diverse naturally occurring Neisserial glycans to facilitate immune evasion.

While the PglL O-OTase exhibits extreme glycan substrate tolerance, its acceptor protein range is not so diverse. Although N.
isoVitaleX. Media was supplemented with appropriate antibiotics. 

N. gonorrhoeae brain heart infusion medium (BHI) supplemented with Levinthal’s N. meningitidis was used to the kan resistance cassette, excised from pUC4kan with ACIAD3337). The product was cloned into the pT7Blue vector, DNA Isolation and Manipulation

**Materials and Methods**

**Identification and Alignment of Homologues of PglL**

The BLASTP programme was used to examine the NCBI non-redundant protein database (http://www.ncbi.nlm.nih.gov/BLAST/) for protein homology searches. The protein glycosylation ligase of N. meningitidis (PgL, NMA0800). 22 homologs, that were unique protein sequences from each genus, were downloaded (PIDs 15676501, 34499662, 153886317, 76809217, 50083393, 153886318, 126665137, 12161683, 91790502, 126643191, 12425256, 120613309, 86147861, 89900058, 148977877, 121609153, 12069538, 89755938, 119974919, 15981610, 150324530, 110807034, 77766347, 135294362). ClusterW alignment of these proteins identified two regions that were well conserved in the putative PgL proteins and not in the WaaL proteins (O-antigen ligases). The first region, termed PgL\_A, was 25 amino acids (equivalent to amino acid 395 to 452 of NMA0800) and the second, termed PgL\_B, was 30 amino acids (equivalent to amino acid 171 to 201 of NMA0800). A HMM was generated from a ClusterW alignment of both of these regions in the above proteins using the program hmmbuild, followed by hmmpcalibrate [14]. Membrane spanning regions of proteins were predicted using Phobius V 1.0 (http://phobius.sbc.su.se/) [15]. The graphical representation of the Phobius model was created with TMReps2d [16].

**Bacterial Strains and Culture Conditions**

*Acinetobacter baylyi* strain ADP1 and *Escherichia coli* strain DH5α, used to propagate cloned plasmids, were grown at 37°C in LB broth or on LB solid agar. *N. meningitidis* strains were grown on brain heart infusion medium (BHI) supplemented with Levinthal’s base. *N. gonorrhoeae* strains were grown on GC media with IsoVitalex. Media was supplemented with appropriate antibiotics. DNA Isolation and Manipulation

Genomic DNA of *A. baylyi* strain ADP1 was used as template in a PCR reaction to amplify the pgL homolog (accession number ACIAD3337). The product was cloned into the pT7Blue vector, linearized with restriction endonuclease Styl, blunted and ligated to the kan resistance cassette, excised from pUC4kan with Hinfl.

Transformation of ADP1 was based on previously described methods [17]. Shuttle vector pWH1266 [10] was used to complement the ADP1pgL::kan mutant. The wild type ADP1 pgL gene including 61 bp of the upstream region was amplified by PCR, digested by BamHI and inserted into vector pWH1266 at the BamHI site. The resulting plasmid, pWH1266-pgL\_A, and pWH1266 were separately transformed into the ADP1pgL::kan mutant by electroporation. Previously described plasmid encoding FLAG-tagged AniA and TetMB [3] was used as template for site-directed mutagenesis to construct AniA variants [19]. Linearized plasmid was transformed to the chromosome of C311 by homologous recombination as described [3]. *N. gonorrhoeae* MS11pgL::kan strain was constructed as described [12].

**Immunological Assays**

Western blotting was performed essentially as previously described [9]. Primary antibodies used were rabbit α-trisaccharide sera [9] and mouse α-FLAG mAb (Sigma-Aldrich), α-ComP (A. baylyi), and α-CooP, α-MetQ, α-Sco, α-Mip, and α-Laz (N. meningitidis) antibodies were produced by inoculating mice with the peptide-conjugated Keyhole Limpet Hemocyanin (synthesized by Mimotopes, Australia). The conjugated peptide sequences corresponding to the target proteins are shown in Table S1. Secondary antibodies used were anti-rabbit IgG and anti-mouse IgG (Sigma-Aldrich and Rockland). Cell lysates of wild-type and mutant strains of *A. baylyi* were prepared from cells in late stationary growth phase, when ComP expression is maximal [20].

**Protein Immunoprecipitation and Purification**

*N. meningitidis* C311 cells were harvested and resuspended in TBSt (Tris buffered saline with 0.05% Tween-20) supplemented with protease inhibitor cocktail (Roche). Cells were heat killed by incubation at 56°C for 1 h, lysed by French press and debris removed by centrifugation at 18,000 rcf for 10 min and filtration through 0.22 µm filters. α-Glycan dynabeads for immunoprecipitation were prepared by rabbit polyclonal sera against the *N. meningitidis* C311 O-glycan [9] or isotype negative control antiserum, and ProtA dynabeads (Invitrogen) according to the manufacturers instructions. Clarified cell lysate was applied to the α-glycan dynabeads and incubated with shaking at 25°C for 1 h. The α-glycan dynabeads were washed thrice with 1 mL TBSt and eluted with 200 µL (Glycine HCl pH 3 with 0.1% Tween-20). FLAG-tagged AniA proteins were purified as described [3].

**Mass Spectrometry**

Purified AniA-FLAG protein was precipitated by addition of 4 volumes of 1:1 acetone:methanol, incubation at −20°C for 16 h and centrifugation at 18,000 rcf for 10 min. The pellet was washed with acetone:methanol, dried, resuspended in 50 µL 50 mM NH4HCO3 with 1 µg trypsin (proteomics grade, Sigma) and digested at 37°C for 3 h. Peptides and glycopeptides were analysed by LC-ESI-MS/MS with an API QSTAR Pulsar i LC/MS/MS system, and MS data was analysed as described [3]. Differences in glycosylation occupancy between AniA variant proteins were compared using a 2-sided Mann-Whitney test. Immunoprecipitated eluted proteins were reduced/alkylated and digested as above. Peptides were desalted with C18 ZipTips (Millipore) and analysed by LC-ESI-MS/MS using a nanoLC (Shimadzu) and TripleToF 5600 mass spectrometer (ABSciex) as described [21]. Peptides were separated on a C18 column (Vydac), with a gradient from buffer A (0.1% formic acid) to buffer B (80% acetonitrile with 0.1% formic acid). Data was exported from.wiff format to.mgf format, and searched with Mascot V2.3 at the Australian Proteomics Computational
Facility (http://www.apc.fsu.edu/). Search parameters were: enzyme, trypsin with up to 1 missed cleavage; fixed modifications, cysteine propionamide; variable modifications, methionine oxidation and asparagine deamidation; peptide tolerance, 0.05 Da; MS/MS tolerance, 50 mmu; LudwigNR database (as at 2 November 2011; 13,321,971 sequences; 5,925,977,534 residues) limited to N. meningitidis and common contaminants (28,391 sequences).

Circular Dichroism Spectroscopy

CD spectroscopy of synthesized peptide (NGAAPAASAPAA-SAPAASASEKSVY; Auspep) in 50 mM potassium phosphate buffer at pH 6.5 was performed using a Jasco J-710 spectrometer as described [22]. The data were collected in the wavelength range 190–269 nm at room temperature. The scan speed was set to be 100 nm/min and the bandwidth was 0.5 nm. Spectra were also obtained from solutions that contained the peptide in 10%, 20%, 30%, 40% and 50% trifluoroethanol (TFE).

Molecular Modelling

Modelling of the amino acid sequence corresponding to the glycosylated region (+3)WPGGNTTS (Galβ1–4Galα1–3,2–4-diacetamido-2,4,6-trideoxyhexose) AGVASSSTIK (73) of C311#3 pilin was calculated and modelled by Chemdraw and DYANA. The two ends of the peptide (W57 and K73) were constrained 19.7 Å apart as in the corresponding region of N. gonorrhoeae pilin according to its published pili crystal structure [23].

Results

Creation of Hidden Markov Models to Distinguish between PgL and WaaL Candidates

To identify PgL homologs in bacterial genomes we developed a hidden Markov model (HMM) that would resolve the subset of PgL protein O-OTases from the wider PFAM PF04932, which contains both WaaL O-antigen ligases and PgL proteins. This family of enzymes has low overall amino acid similarity but contains a small region of conservation that is the basis for PFAM PF04932. To identify sequence features which accounted for the protein acceptor substrate specificity of PgL, we performed multi-sequence alignments of protein sequences of close homologues of PgL and used conserved features not present in WaaL to create two HMMs, pglL_A and pglL_B (Fig. 1). HMM pglL_A has been submitted to the Pfam database with accession number PF15864. These HMMs did not identify well-characterized WaaL proteins from enteric organisms, suggesting that they may be useful for the identification of PgL homologs in bacterial genomes.

Identification of PgL Homologs in Bacterial Genomes

The pglL-A HMM was used to search the NCBI non-redundant protein database to identify candidate PgL O-OTases (Table 1). Similar results were obtained with the pglL_B search. This analysis identified PgL homologs in 31 distinct Gram-negative bacterial species. These included pathogens such as Burkholderia, Vibrio, Yersinia, Aeromonas and Acinetobacter, and several non-pathogenic environmental species including Polavimonas, Rhodopseudomonas and Methylibbam.

Examination of the genome localization of these PgL homologs revealed that in the majority of cases (21/31) they were immediately adjacent to or closely associated with a gene(s) encoding type IV pilin homologs (Table 1, Fig. 2). The close association of the pglL O-OTase with an obvious target glycoprotein in so many cases suggests that the HMM analysis identified both the glycosylation pathway and target acceptor protein. A further indication that the genes identified are PgL rather than WaaL homologs is that they are not located within LPS biosynthetic loci [24]. The pglL_A and pglL_B motifs are located on either side of the Wzy_C motif common to both PgL and WaaL, and represent conserved regions in predicted periplasmic loops of PgL and adjacent transmembrane regions. This suggests they have an important structural or functional role in PgL activity. Three residues important for the function of E. coli WaaL [25] located in the Wzy_C motif are also conserved amongst PgLs (E. coli WaaL R288, H338 and R215; N. meningitidis PgL R298, H349, R224). We also identified additional residues conserved in PgLs but not in WaaL (N. meningitidis PgL Q178, N180, G316, G318, H400, E404, P406) and residues conserved in both PgLs and WaaL (N. meningitidis: PgL P313).

Experimental Confirmation of O-OTase Activity in a PgL Homolog from Acinetobacter Baylyi

We tested the hypothesis that the pilin homologs closely associated with the PgL O-OTase candidates were the cognate targets for glycoproteins. In A. baylyi strain ADP1, the pglL gene (accession number ACIAD3337) is adjacent to the comP gene (ACIAD3338) which encodes a pilin-like protein which is essential for natural transformation and has previously been shown to be glycosylated [20]. However, the mechanism of glycosylation of ComP has not previously been investigated. We created a knockout mutant in the pglL gene of A. baylyi strain ADP1, and complemented this mutant strain with expression of plasmid-borne native pglL. Western blot analysis of extracts from the wild-type ADP1 and ADP1[pglL::kan] mutant strains using an α-ComP antibody indicated the presence of the 20 kDa glycosylated ComP protein in the wild-type strain and a shift in MW to the 18 kDa non-glycosylated form of ComP in the mutant strain (Fig. 3), consistent with the loss of glycosylation of this protein. This glycosylation could be partially rescued by complementation with native pglL, but not with empty vector. This validated the role of the PgL homolog in glycosylation of the ComP pilin-like protein in strain ADP1.

General PgL Glycosylation Systems

The genomic localization of pglL close to substrate glycoproteins in most bacteria suggested that these substrates were the key targets for glycosylation (Table 1, Fig. 2). However, several pglL homologs were detected not genomically associated with an obvious glycoprotein substrate, including in the pathogenic Neisseria known to possess general glycosylation systems. Since genes that are not genomically linked cannot be co-transcribed, we anticipated that additional mechanisms based on enzyme-substrate recognition would also enhance glycosylation efficiency in these bacteria. We therefore used N. meningitidis as a model system to investigate the substrate requirements for modification in this genomically unrelated system.

Several PgL substrate glycoproteins in addition to PilE and AniA have been reported in N. gonorrhoeae [4]. However, Western blotting using our α-glycan antisera failed to detect bands in addition to AniA and PilE in N. meningitidis C311 whole cell extracts [3]. To investigate if other glycoproteins were also present in N. meningitidis C311, we performed IP of whole cell extracts using α-glycan antisera, and identified eluted proteins with mass spectrometry. α-Glycan co-IP identified three proteins: PilE, azurin and MesQ (Fig. S1, S2 and S3; Tables S2, S3, S4 and S5). These proteins were not identified by negative control IP with unrelated rabbit antisera, suggesting that they are glycoproteins. To validate the glycosylation status in N. meningitidis of azurin and
MetQ, as well as selected other reported \textit{N. gonorrhoeae} glycoproteins [4], we performed western blotting with protein-specific antisera for each candidate glycoprotein. This showed that AniA, Sco, CcoP and Mip were glycosylated in \textit{N. meningitidis} C311 and \textit{N. gonorrhoeae} MS11, as they displayed clear MW shifts upon genomic deletion of the PglL O-OTase (Fig. 4A,D,E,F). However, MetQ and Laz failed to show clear changes in MW in the presence and absence of glycosylation (Fig. 4B,C). This phenotype was also observed in \textit{N. meningitidis} MC58, and in \textit{N. gonorrhoeae} 1291 and O1G1370. Homologs of all of these proteins had been identified as glycoproteins in \textit{N. gonorrhoeae} [4]. Together with our α-glycan IP results, this suggests that although glycosylated forms of MetQ and Laz can be detected by MS [4], the major fraction of these proteins in the cell under the conditions tested is not in fact glycosylated.

Characteristics of Efficiently Glycosylated PglL Protein Accepter Substrates

The protein substrates of \textit{N. meningitidis} PglL were either predominantly glycosylated or predominantly non-glycosylated. PilE, AniA, Sco, CcoP and Mip were completely glycosylated, as their non-glycosylated forms were not detectable by western blot in wild type \textit{Neisseria}. Laz and MetQ were minimally glycosylated, as their glycosylated forms were not detectable by western blot, but rather only by MS analysis after glycan-specific enrichment. To determine the details of this substrate specificity, we examined the \textit{N. meningitidis} glycoprotein AniA, which has been shown to be glycosylated with up to two glycans in its C-terminal flexible domain within the glycopeptide L\textsubscript{358}SDTAYANGA\textsubscript{387} [3]. No additional sites of glycosylation were detected by this MS analysis [3]. We first tested if AniA had additional glycosylation sites by analysing a FLAG-tagged AniA variant with this 36 amino acid C-terminal flexible domain deleted after Met354. Western blot analysis of FLAG-tagged full-length and C-terminally truncated variant AniA using α-FLAG sera detected both variants, but α-glycan sera only detected full length AniA (Fig. S4). This indicated that no additional glycosylation sites were present in the core nitrite reductase or flexible N-terminal domains of AniA.

We identified the precise sites of glycosylation in the Leu358-Lys387 glycopeptide by site-directed mutagenesis and LC-ESI-MS/MS analysis of peptides and glycopeptides from purified variant glycoproteins. The extent of glycosylation is likely underestimated by this MS analysis due to reduced ionisation efficiency of the glycosylated peptides relative to their unglycosylated forms. Nonetheless, relative quantification of glycosylation occupancy is possible with this analysis [26,27]. Up to two sites of glycosylation were detected in wild type AniA (Fig. 5A, Fig. S4 and [3]). As this

Figure 1. \textit{N. meningitidis} PglL topology and conservation. (A) Transmembrane profile of \textit{N. meningitidis} PglL with the regions identified by the PglL\_A, PglL\_B and Wzy\_C hidden Markov models indicated by red, green and blue lines and highly conserved amino acids coloured in red and orange. (B) The PglL protein Phobius transmembrane helix prediction with predicted transmembrane regions represented by dashed-lines. (C) CLUSTALX plot of sequence conservation of CLUSTALW alignment of the putative PglL proteins. (D) Regions identified by the PglL\_A, PglL\_B and Wzy\_C hidden Markov models indicated by red, green and blue boxes respectively.

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Bacterial O-Glycosylation Enzymes and Substrates
sequence included two identical repeats of the local sequence Ala-Ala-Ser-Ala-Pro, encompassing Ser373 and Ser378, we created AniA variants with each of these Ser residues individually mutated to Ala (Table S6). LC-ESI-MS/MS analysis of both of these variants showed loss of a single efficiently modified glycosylation site, as these variants showed very low levels of di-glycosylated peptide (Fig. 5B,C,F). Further, a variant with both Ser373Ala and Ser378Ala mutations showed loss of both efficiently used glycosylation sites, as essentially only un-glycosylated peptide was identified (Fig. 5D,F). This confirmed that the two Ser residues present in the local sequence Ala-Ala-Ser-Ala-Pro (Ser373 and Ser378) were efficiently glycosylated by PglL. Several other Ser residues are present in the Leu358-Lys387 glycopeptide, and of particular note were the residues present in an imperfect repeat reminiscent of the efficiently glycosylated sites, Ala-Ala-Ser-Ala-Pro-Ser373. The local sequence context of Ser373 differed from the efficiently glycosylated Ser373 and Ser378 only by having the sequence Ser373 Ala-Ser rather than Ser373/8-Ala-Pro. We tested if this local sequence influenced glycosylation by creating a Ser385Pro AniA variant in a Ser373Ala, Ser378Ala background. Indeed, this AniA-Ser373Ala, Ser378Ala, Ser385Pro variant showed significantly increased glycosylation compared with the Ser373Ala, Ser378Ala control, with substantial mono-glycosylated peptide detected (2-sided Mann-Whitney test, P = 0.01, Fig. 5E,F).

To investigate the structure of the AniA glycosylation acceptor sites, we performed circular dichroism (CD) spectroscopy to characterize the secondary structure of a synthesized peptide corresponding to the unglycosylated AniA glycopeptide. The CD spectrum of AniA in phosphate buffer showed substantial negative ellipticity centred at 198 nm (Fig. 6A), indicative of an unstructured conformation. The glycosylation site in PilE (NTS63(glycan)AG) is part of a short α-helix located in the so called ‘ab loop’

| PID: | Score | E value | Species | Genetic context* |
|------|-------|---------|---------|------------------|
| 91790502 | 51.6 | 1.60E-09 | Polaromonas sp. JS666 | pilin, 2 |
| 89900058 | 49.3 | 7.90E-09 | Rhodobacter ferrireducens T118 | pilin |
| 126643191 | 48.6 | 1.30E-08 | Acinetobacter baumannii ATCC 17978 | pilin |
| 120613309 | 47.7 | 2.40E-08 | Acidovorax avenae subsp. citrulli AAC00-1 | pilin |
| 121611683 | 47.3 | 3.20E-08 | Verminephrobacter eiseniae EF01-2 | pilin |
| 84394373 | 47 | 3.90E-08 | Vibrio splendidus 12801 | EA |
| 148977877 | 47 | 3.90E-08 | Vibrionales bacterium SWAT-3 | EA |
| 50083393 | 46.7 | 4.90E-08 | Acinetobacter sp. ADP1 | GalE, Pmm |
| 59806333 | 46.3 | 6.40E-08 | Neisseria ghaniae FA 1090 | hypothetical membrane protein |
| 15793774 | 46.3 | 6.40E-08 | Neisseria meningitidis | hypothetical membrane protein |
| 124265256 | 45.9 | 8.30E-08 | Methylbacterium petroleumihum PI1 | pilin |
| 119944149 | 45.8 | 9.20E-08 | Psychromonas ingrahamii 37 | E, transglycosylase SLT domain protein |
| 126656137 | 44.9 | 1.70E-07 | Marinobacter sp. EL817 | pilin |
| 86147861 | 44.6 | 2.10E-07 | Vibrio | EA |
| 121609153 | 43.6 | 4.30E-07 | Verminephrobacter eiseniae EF01-2 | acyltransferase 3, ribonuclease II |
| 21672281 | 42.7 | 7.90E-07 | Aeromonas hydrophila | wzz |
| 121532578 | 42.3 | 1.00E-06 | Raistonia picketii 12J | pilin |
| 90412963 | 40.2 | 4.30E-06 | Photobacterium profundum 3TCK | EA |
| 17545278 | 39.6 | 6.80E-06 | Raistonia solanacearum | pilin |
| 51245303 | 39.5 | 7.20E-06 | Desulfitalea psychrophila LS54 | pilin |
| 7797651 | 39.2 | 8.60E-06 | Yersinia intermedia ATCC 29909 | pilin |
| 134279817 | 38.3 | 1.60E-05 | Burkholderia pseudomallei 305 | pilin |
| 53274275 | 38.3 | 1.60E-05 | Burkholderia mallei ATCC 23344 | pilin |
| 76809217 | 38.3 | 1.60E-05 | Burkholderia thailandensis E264 | pilin |
| 153886317 | 38.2 | 1.80E-05 | Raistonia picketti 12D | pilin, 2 |
| 344969682 | 38 | 1.90E-05 | Chromobacterium violaceum ATCC 12472 | pilin, 2 |
| 149911011 | 37.8 | 2.30E-05 | Mortella sp. PE36 | EA |
| 123441130 | 36.6 | 5.30E-05 | Yersinia enterocolitica 8081 | pilin |
| 77958742 | 36.6 | 5.30E-05 | Yersinia bercovieri ATCC 43970 | pilin |
| 91790501 | 36.2 | 6.80E-05 | Polaromonas sp. JS666 | pilin, 2 |
| 121595941 | 35.9 | 8.40E-05 | Acidovorax sp. JS42 | cytochrome c |
| 90407310 | 35.9 | 8.80E-05 | Psychromonas sp. CNPT3 | EA |
| 121606830 | 35.8 | 9.50E-05 | Polaromonas naphthalenivorans CI2 | pilin |

*Genetic context: EA, pgL between homologues of a exonuclease ABC subunit A and an aminotransferase class V; pilin, a type IV pilin homologue, pilin 2, two closely associated pilin homologues; E, exonuclease ABC subunit A; other genes are described by their homology or commonly known gene names.

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[23], so to investigate if the AniA peptide in solution samples an energy landscape that contains transiently structured conformations we obtained CD spectra in the presence of increasing concentrations of TFE, which allows peptide intramolecular hydrogen bonds to form by limiting competing bond formation with solvent water. The CD spectra showed that increasing TFE caused loss of negative ellipticity at 198 nm with a corresponding increase in negative ellipticity around 225 nm (Fig. 6). Subtraction of the spectrum of the AniA peptide in 0% TFE from that in 50% TFE resulted in a spectrum with positive ellipticity at 195 nm and a broad negative peak centred on 220 nm (Fig. 6B). These features are suggestive of a helical conformation, but we note that even in 50% TFE the AniA peptide was still predominantly unstructured. NMR analysis (Fig. S5) of the AniA peptide in the absence of TFE showed that most amide protons had chemical shifts clustered between 8.1 ppm and 8.3 ppm; Val24 and Tyr25 were shifted upfield due to Tyr ring current effects. In agreement with the CD results, the NMR result was indicative of an unstructured conformation. The presence of increasing concentrations of TFE showed a corresponding increase in the dispersion of amide chemical shifts (both upfield and downfield shifts were observed) suggesting that some residues adopted a structured conformation.

Discussion

Post-translational modifications of bacterial proteins are difficult to identify and a bioinformatic means of identifying potential glycosylation systems and their targets would enable the characterisation of many more systems. PglL proteins in particular have been difficult to identify due to the relatively low levels of homology between members of this family and the overlap in similarity to WaaL O-antigen ligases. Previously, PglL O-OTases have been identified by homology with known WaaL/O-OTases and the presence of the Wzy_C motif common to these distinct functions [12], and then O-OTase function distinguished from WaaL O-antigen ligase function by experimentation using mutagenesis of the putative gene or cloning and expression in a recombinant system [28]. In the current study we identified two conserved motifs (PglL_A and PglL_B) that are found in PglL homologs but not in WaaL O-antigen ligases (Fig. 1). In silico analysis using these motifs identified pglL genes in diverse Gram-negative bacteria, showing that bacterial protein glycosylation systems are much more common than previously appreciated. The PglL homolog we identified from Y. enterocolitica (Table 1) (Ye777; waaLXS; protein accession 123441130) has been studied in Y.
enterocolitica and in E. coli for a role in LPS biosynthesis. Y. enterocolitica encodes three WaaL homologs, and while all three could complement LPS biosynthesis with deletion of E. coli waaL, Ye777/waaLXS was not involved in LPS biosynthesis in the native organism Y. enterocolitica [29]. This is consistent with Ye777/waaLXS being a protein O-OTase, as previously speculated [29] and as predicted by our HMM analysis. During the preparation of this manuscript, PglL-like O-OTase BTH_I0650 of B. thailandensis [30], VC0393 of V. cholerae [30] and A1S_3176 of A. baumannii [31] were identified by homology with Neisseria PglL and the presence of the Wzy_C motif followed by experimentation to rule out a WaaL function. Our HMM analysis predicted that these genes were PglL homologs (Table 1), providing further support for our analysis. The bioinformatic approach described herein efficiently predicts many other such protein O-glycosylation systems.

In P. aeruginosa, the PilO system glycosylates pilin via the addition of a single unit of the LPS O-antigen repeat [32]. The pilO gene is adjacent to the pilin gene and in the same orientation, however, the PilO O-OTase, despite sharing similarity with PglL of Neisseria and O-antigen ligases, does not contain the PglL motifs we describe here. Indeed, examination of protein databases does not reveal homologs with a high degree of similarity to PilO outside of the P. aeruginosa species suggesting that PilO might have a slightly different mode of action to the PglL family.

The pglL gene and the gene encoding its presumptive target protein are often found in the same orientation and in close proximity, which suggests they are co-transcribed. This may increase protein co-localisation and thereby increase the efficiency of the glycosylation reaction. However, the requirement of genomic co-localisation is not absolutely required. PglL of Neisseria is not located adjacent to the pilin structural gene, pilE, and N. meningitidis and N. gonorrhoeae have general O-glycosylation systems capable of modifying serine and threonine residues in many

Figure 3. Phenotypic analysis of Acinetobacter baylyi strain ADP1 candidate PglL O-OTase mutants. Western blot analysis using α-ComP antibody of wild-type (ADP1), pglL mutant (ADP1pglL::kan), pglL mutant complemented with plasmid-borne pglL (ADP1pglL::kan pWH1266-pglL) and pglL mutant with empty vector (ADP1pglL::kan pWH1266).
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Figure 4. Western blot analysis of putative Neisserial glycoproteins. N. gonorrhoeae MS11pglL::kan, N. gonorrhoeae MS11, N. meningitidis C311pglL::kan and N. meningitidis C311 whole cell extracts were separated by SDS-PAGE, blotted to nitrocellulose membrane and probed with (A) α-AniA, (B) α-Laz, (C) α-MetQ, (D) α-Sco, (E) α-Mip or (F) α-CcoP antisera.
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different protein substrates [3,4]. Apart from PilE, which is the most abundant glycoprotein, the additional substrates are modified in flexible, low-complexity regions [3,4]. However, the factors controlling selection of particular sites for glycosylation in these domains are poorly understood. Our results here show that the local sequence Ala-Ala-Ser-Ala-Pro found in AniA, in particular the Pro, allows efficient glycosylation of Ser residues (Fig. 5). However, in all of the variant proteins examined, extremely low
levels (<1%) of glycosylation at additional sites were repeatedly detected (Fig. 5). This suggested that PglL does not recognize a strictly defined ‘sequon’, but rather glycosylates Ser residues with different efficiencies or rates depending on the local sequence or structural environment. Comparison of the AniA and PilE glycosylation sites reveals that only the primary amino acid sequence Ser(glycan)-Ala is common. This sequence is unlikely to define the PglL substrate, as the same sequence occurs in many other non-glycosylated proteins, and also in other, non-glycosylated regions of AniA and PilE. The pilin target serine is at a surface loop, on a section that contains a short α-helix (Fig. 6C, and [23]). Secondary structure may therefore be a key aspect of PglL substrate specificity. This is supported by our in vitro CD spectroscopy and in vivo mutagenesis analysis of AniA glycosylation acceptor sites. CD spectroscopy of the AniA peptide in solution with TFE suggested that this peptide samples conformations that contain regular helical structures (Fig. 6). Further, the proline residues proximal to glycosylated serines in AniA (Fig. 5) may temporarily introduce the local structure required for efficient glycosylation. This may be similar to peptide substrate binding shown in the X-ray structure of the Campylobacter lari N-OTase [33], where the ‘N-glycosylation sequon’ (D/E-x-N-x-S/T) [5] is not required for catalysis, but rather for protein acceptor recognition. The requirement that N. meningitidis PglL substrates have a turn immediately C-terminal to the serine to be glycosylated may be due to specific interactions resulting in increased acceptor protein binding affinity, or spatial constraints at the O-OTase active site. This is consistent with this polypeptide sequence binding to PglL with an induced fit mechanism, or that the proline adjacent to the target sites key for glycosylation in AniA may give rise to local temporary turns mimicking the constrained loop in PilE.

It has been shown that purified PglL protein can be used in in vitro assays to glycosylate substrate protein in the presence of solubilized glycan-pyrophosphate-undecaprenyl as donor glycan substrate [34]. In these in vitro assays, the N. gonorrhoeae O-OTase could glycosylate purified PilE protein, but could not glycosylate a short peptide containing the glycosylation site and surrounding residues. This is in agreement with our data, consistent with local structural conformation rather than sequence being key to recognition by the PglL O-OTase. Interestingly, an unrelated class of bacterial cytoplasmic O-glycosyltransferases also recognize a structural motif in its protein acceptor substrates [35]. In all Neisserial glycoproteins except for PilE, glycosylation occurs in flexible linker extensions that are N- or C-terminal or linking two domains [4]. Such extensions would be likely to minimally impact protein folding and function, and as such would not have large evolutionary barriers. It is likely that these factors have allowed the Neisserial glycosylation system to evolve from an ancestral targeted system that modified the single abundant PilE substrate, to a general system with substrates that contain flexible N-, internal or C-terminal extensions that are local structural mimics of the PilE glycosylation site. Efficient glycosylation of only folded PilE by PglL [34] implies that glycosylation in vivo in the Neisseria most likely occurs only after protein folding. This is in contrast to the distantly homologous system of N-glycosylation by bacterial N-OTase, which glycosylates asparagines in unfolded polypeptide or flexible regions of folded proteins [36]. N-OTase is generally coupled to polypeptide translocation to access unfolded protein substrate [37], and this contrast suggests that PglL may have a different sub-compartmental localisation which allows efficient post-folding glycosylation of proteins including PilE, AniA, Sco, CcoP and Mip, but which allows only limited modification of other substrates including MetQ and Laz. Sco, CcoP and Mip are periplasmic, and as such may have prolonged access to PglL, allowing efficient glycosylation. In contrast, MetQ, Laz and AniA are outer membrane proteins, and so must be glycosylated by PglL before transport from the periplasm to the outer membrane. Efficient modification of AniA may be due to the C-terminal position of its flexible glycosylated domain, in contrast to the N-terminal flexible domains of MetQ and Laz. Additional factors including protein-specific secretion rate or subcellular targeting may also be important in controlling the efficiency of glycosylation of particular proteins. We note that previous reports characterising the glycosylation system of N. gonorrhoeae [4] relied on MS identification of enriched glycoproteins and an ex vivo E. coli expression system to identify PglL substrate proteins. As such, differences in efficiency of glycosylation were not distinguished. During the preparation of this manuscript seven additional putative glycoproteins were reported from N. gonorrhoeae using a glycan-specific enrichment and MS identification strategy [38]. Subsequent analysis of His-tagged versions of these putative glycoproteins expressed in N. gonorrhoeae revealed that many of these proteins were essentially unmodified, as we also observed in the current study (Fig. 4) for several other candidate glycoproteins reported by the authors in a previous study [4]. These stark differences in the glycosylation efficiency of the various putative Neisserial glycoproteins were not discussed by the authors [38]. However, their data and our current study emphasize the importance of studying the native organism using a range of complementary analytical techniques in determining if a protein is efficiently glycosylated, and thereby appropriately defined as a glycoprotein, rather than being a minor or accidental substrate only identified by very sensitive glycan-specific enrichment and MS detection.

The ability of the O-glycosylation system of the pathogenic Neisseria to modify many protein substrates may be related to the need to physically unlink the genes encoding PglL and the pilus biogenesis machinery. The pilE gene of Neisseria is highly antigenically variable and the system that promotes antigenic variation in pilE, by high levels of homologous recombination between pilE and non-expressed copies of the gene pilS, is dependent on the context of the pilE gene for efficient recombination between pilE and pilS [39]. There may therefore have been selective pressure for the pglL gene to be located distally from the pilE gene in Neisseria. The close genomic location of pglL and substrate glycoprotein in many bacteria likely confers efficiency to the glycosylation machinery. Non-linked pglL would therefore likely require increased protein acceptor substrate recognition or alternative substrate targeting mechanisms. Such features of efficient protein substrate selection, other than genomic location, could then allow the evolution of efficient glycosylation sites in many proteins. Unlike sequon-based recognition in general N-glycosylation systems [3,36,40], structural features dominate recognition of protein substrates in the general Neisserial O-linked glycosylation system.

Supporting Information

Figure S1 Peptide mapping coverage of Azurin (NMB_1533) after IP with α-glycan antisera. Peptides identified with p<0.05 (ions score >23) are underlined. (TIF)

Figure S2 Peptide mapping coverage of PilE (NMB_0018) after IP with α-glycan antisera. Peptides identified with p<0.05 (ions score >23) are underlined. (TIF)
Figure S3 Peptide mapping coverage of MetQ (NMB_1946) after IP with α-glycan antisera. Peptides identified with p<0.05 (ions score >23) are underlined.

(PDF)

Figure S4 N. meningitidis AniA glycosylation (A) Cartoon of domains of N. meningitidis AniA protein showing: lipid-anchored N-terminal cysteine; N-terminal flexible region; AniA core fold; glycosylated C-terminal flexible region; Δ, truncated variant at Met354. (B) Western blots of FLAG-tagged purified AniA: wild type and C-terminally truncated (at Met334, Δ in (A)), detected with either anti-FLAG or anti-glycan antisera.

(TIF)

Figure S5 750 MHz NMR spectra of the AniA glycosylation peptide in increasing concentrations of TFE-d$_6$ (in 20 mM KPi, pH 6.5). The amide and aromatic region is shown (6.6–8.6 ppm). Increasing TFE-d$_6$ results in upfield and downfield shifts of amide resonances. The shift of V389 and Y390 are shown dashed.

(TIF)

Table S1 Peptide sequences used for conjugate to Keyhole Limpet Hemocyanin to raise protein-specific antisera.

(PDF)

Table S2 Proteins identified from N. meningitidis after IP with α-glycan antisera.

(PDF)

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