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Identifying the targets and functions of *N*-linked protein glycosylation in *Campylobacter jejuni*

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Campylobacter jejuni is a major cause of bacterial gastroenteritis in humans that is primarily associated with the consumption of inadequately prepared poultry products, since the organism is generally thought to be asymptomatic in avian species. Unlike many other microorganisms, *C. jejuni* is capable of performing extensive post-translational modification (PTM) of proteins by *N*- and *O*-linked glycosylation, both of which are required for optimal chicken colonization and human virulence. The biosynthesis and attachment of *N*-glycans to *C. jejuni* proteins is encoded by the *pgl* (protein glycosylation) locus, with the PglB oligosaccharyltransferase (OST) enabling *en bloc* transfer of a heptasaccharide *N*-glycan from a lipid carrier in the inner membrane to proteins exposed within the periplasm. Seventy-eight *C. jejuni* glycoproteins (represented by 134 sites of experimentally verified *N*-glycosylation) have now been identified, and include inner and outer membrane proteins, periplasmic proteins and lipoproteins, which are generally of poorly defined or unknown function. Despite our extensive knowledge of the targets of this apparently widespread process, we still do not fully understand the role *N*-glycosylation plays biologically, although several phenotypes, including wild-type stress resistance, biofilm formation, motility and chemotaxis have been related to a functional *pgl* system. Recent work has described enzymatic processes (nitrate reductase NapAB) and antibiotic efflux (CmeABC) as major targets requiring *N*-glycan attachment for optimal function, and experimental evidence also points to roles in cell binding *via* glycan–glycan interactions, protein complex formation and protein stability by conferring protection against host and bacterial proteolytic activity. Here we examine the biochemistry of the *N*-linked glycosylation system, define its currently known protein targets and discuss evidence for the structural and functional roles of this PTM in individual proteins and globally in *C. jejuni* pathogenesis.

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Introduction

Campylobacter jejuni is a Gram negative enteric pathogen with helical cell morphology. *C. jejuni* is also microaerophilic and typically requires oxygen levels to be no greater than 10% for growth.[1] Gastrointestinal infection caused by this organism was first characterized in the late 1970s[2] and *C. jejuni* is now considered the most common causative agent of gastroenteritis in the developed world, with an estimated 400 million people infected worldwide annually.[3] Infection in humans is acquired though consumption of contaminated water or food, particularly under-cooked or inappropriately handled poultry products (with estimates suggesting between 75–90% of supermarket chicken is contaminated with the organism[4]), since *C. jejuni* is generally considered an asymptomatic commensal in avian species.[5] While the differences in human and avian response to *C. jejuni* infection are largely unknown, there is evolving evidence that differences in host mucin *O*-glycan composition, particularly sulfated *O*-glycans, may play a role in colonization.[6] Furthermore, chicken mucins from different regions of the gastrointestinal tract can inhibit human epithelial cell virulence,[7] providing further evidence for glycan recognition in the establishment of host-specific niches.[8]

Human disease is generally self-limiting and symptoms present as fever and abdominal cramping that progress from mild to, in some cases, severe diarrhoea.[2,3] Relapse is possible in the absence of medical intervention, and is likely due to gut persistence for up to 3 weeks.[9] *C. jejuni* infection is also an established antecedent for an increasing number of debilitating conditions including Guillain–Barré Syndrome (GBS),

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Miller–Fisher Syndrome (MFS), immunoproliferative small intestine disease, reactive arthritis and Sweet's syndrome.[10,11] The basis for these post-acute immune-mediated disorders is thought to be largely based on cross-reactivity between antibodies directed against *C. jejuni* surface lipooligosaccharide (LOS) and human cell surface gangliosides, and this relationship has been reviewed extensively.[12–14]

Several *C. jejuni* genomes have been sequenced from laboratory-adapted and clinical strains and several features remain consistent; the organism encodes ~1620–1650 genes, a large proportion of which encode membrane-associated proteins that are poorly functionally annotated.[15–17] Human infection is not completely understood but involves bacterial adherence to gut epithelial cells, followed by invasion and subsequent toxin production. Several factors are critical in *C. jejuni* host colonization, including flagellar-based motility, cell shape, chemosensing and chemotaxis mediated by transducer-like proteins (Tlps), as well as a number of adhesins including the fibronectin-binding proteins *Campylobacter* adherence factor CadF and fibronectin-like protein FlpA, the surface-exposed lipoprotein JlpA and the PEB antigens [reviewed in[18–20]]. The ability to survive in the hostile environment encountered during gut infection, consisting of for example low pH, presence of bile salts and competitive factors from established microflora, is paramount to establishing disease and *C. jejuni* is adapted to utilize nutrients, such as amino and organic acids as primary carbon sources, that are in rich supply in the gut micro-environment (*e.g.* serine and proline from mucins, organic acids produced as a by-product of metabolism by resident microorganisms).[21,22] *C. jejuni* lacks typical virulence-associated type III/IV secretion systems (T3SS/T4SS) employed by many other enteric bacteria to secrete toxins and proteases that directly interact with host cells, although it is now well-established that extracellular virulence factors (*e.g.* the *Campylobacter* invasion

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Ashleigh Dale received a Bachelor of Science with Honours at the University of Sydney at the end of 2018 and commenced her PhD candidature in biochemistry the following year. Her current work involves implementing cross-linking mass spectrometry approaches to define the interactome of C. jejuni and characterize protein–protein interactions in the hope of elucidating mechanisms of pathogenesis in this organism.

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Zeynep Sumer-Bayraktar received a PhD in biochemistry from Macquarie University, Sydney Australia in 2016. Her research focuses on protein post-translational modifications, specifically the glycan-components of N- and O-linked glycosylation using liquid chromatography and mass spectrometry-based approaches. In her current work, Zeynep investigates the role of protein glycosylation in Campylobacter jejuni human gut colonization and the glyco/proteomic responses of the human host against C. jejuni infection.

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antigens [Cia] and cytolethal distending toxin [CDT]) are secreted *via* the flagellar export apparatus that acts as a pseudo-T3SS.[20,23] Another mechanism by which *C. jejuni* virulence determinants can interact with host cells is *via* their packaging into outer membrane vesicles (OMVs;[24–26]). Finally, despite the somewhat small size of the genome, *C. jejuni* devotes considerable resources to post-translational modification (PTM) of proteins by *N*- and *O*-linked glycosylation, both of which are considered established virulence determinants.

Protein glycosylation in *C. jejuni*

Despite their ability to synthesize large polysaccharides, bacteria were long thought to be enzymatically incapable of modifying proteins with glycans. In the past two decades however, this opinion has largely been overturned with the identification of conserved bacterial *N*- and *O*-linked glycosylation systems in many microorganisms.[27–30] Such systems are almost universally biologically important and associated with pathogenic processes including cell–cell recognition and binding,[31] however their ultimate purpose and functions remain to be determined. *C. jejuni* was the first bacterium to be recognized as containing a 'general glycosylation system' that could widely modify proteins.[32–34] Since then, our understanding of the biochemistry, targets and putative functions of these PTMs has increased rapidly. While our knowledge remains incomplete, recent advances in glycoproteomics-focused mass spectrometry (MS) have generated large-scale site identifications in *C. jejuni*[35] and other organisms, which have enabled directed functional studies to elucidate the roles of these modifications in bacterial phenotypes associated with pathogenicity.

O-Glycosylation in *C. jejuni*

C. jejuni modifies its flagella by *O*-glycosylation of the flagellin structural protein with derivatives of the bacterial-specific sialic acid-like monosaccharides, pseudaminic acid or the closely related legionaminic acid.[36–41] At least 19–23 serine/threonine sites are modified on the FlaA flagellin depending on the strain employed,[42–46] and *O*-glycan attachment is essential for both chicken and human infection phenotypes, including motility, autoagglutination, chicken colonization, and human epithelial cell adherence and invasion.[47–49] Unlike *N*-glycosylation (see below), there is considerably more structural heterogeneity with respect to the attached glycan in individual strains, including both chemical and steriometric differences. Synthesis of pseudaminic and legionaminic acid occur independently of one another, beginning with nucleotide-linked precursors; pseudaminic acid as a uridine diphosphate (UDP)-linked and legionaminic acid as a guanosine diphosphate (GDP)-linked precursor. Enzymatic affinities for specific nucleotide precursors are critical for differentiation of the two pathways and this prevents competition for intermediates.[38] Synthesis of pseudaminic acid from UDP-*N*-acetylglucosamine (UDP-Glc*N*Ac) is performed by the actions of PseB, PseC and PseH, which act sequentially to form UDP-2,4-di*N*Ac-6-deoxy-altropyranose.[50–52] Following release of UDP by PseG, this sugar serves as the substrate of PseI to form pseudaminic acid.[50,52–54] Synthesis of legionaminic acid and derivatives mirrors pseudaminic acid in many respects; from a GDP-Glc*N*Ac precursor, formation of UDP-2,4-di*N*Ac-6-deoxy-glucose is catalyzed by the sequential activities of LegB, LegC and LegH.[38] In principal, the lack of initial LegB epimerase activity creates the structural distinction between pseudaminic and legionaminic acids – instead this activity is performed by the hydrolysing 2-epimerase LegG alongside nucleotide release to form 2,4-di*N*Ac-6-deoxy-mannose, which is then used by the legionaminic acid synthase LegI to form legionaminic acid.[38,47] Both pseudaminic and legionaminic acid are subsequently conjugated onto cytodine monophosphate (CMP) nucleotides by the CMP-sugar synthetases PseF and LegF, respectively, prior to attachment onto FlaA by an undefined glycosyltransfersase.[38,50] Unlike other Gram negative bacteria,[55–57] in *C. jejuni* there appears to be no other substrates of *O*-glycosylation (at least those modified with the flagellar glycan; see below) beyond FlaA. There is conjecture that given the role of the flagellar apparatus as a T3SS-like export apparatus that proteins secreted *via* this pathway may also be *O*-glycosylated in a similar manner to the FlaA flagellin. No studies however, have been able to globally identify extracellular proteins from this organism, mostly due to the very specific requirements (presence of confounding serum or host cells) needed to induce secretion in *C. jejuni*.

It has been suggested that the major outer membrane protein (MOMP), which accounts for ~40–50% of the total membrane protein in *C. jejuni*,[17] can also be *O*-glycosylated[58] with a glycan unrelated to the flagellin modification described above. MOMP may be modified at Thr-268 with the tetrasaccharide Gal-β1,3-Gal*N*Ac-β1,4-Gal*N*Ac-β1,4-Gal*N*Ac-α1, although intact glycan-peptide MS validation is yet to be generated. MOMP modification was further indicated by Whitworth and colleagues in *C. jejuni* strain 81–176 by galactose oxidase (GalO)-mediated selective biotinylation and subsequent enrichment of Gal*N*Ac containing cell surface glycoconjugates.[59] Site-directed mutagenesis of Thr-268 indicated that this residue is

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important for autoagglutination, biofilm formation and colonization of both human Caco-2 cells and chickens,[58] a phenotype also consistent with observations on the roles of FlaA glycosylation. It remains to be seen whether additional *O*-glycoproteins are present in *C. jejuni* and whether this PTM occurs as a widespread presence on proteins secreted by the organism during infection.

The *pgl*-encoded *N*-glycosylation system in *C. jejuni*

C. jejuni was the first bacterium demonstrated to possess the ability to *N*-glycosylate proteins. Proteins are modified by the *N*-linked addition of a heptasaccharide glycan (Gal*N*Ac-α1,4-Gal*N*Ac-α1,4-[Glcβ1,3]-Gal*N*Ac-α1,4-Gal*N*Ac-α1,4-Gal*N*Ac-α1,3-di*N*AcBac-β1; where di*N*AcBac is *N*′,*N*′-diacetylbacillosamine [2,4-diacetamido-2,4,6 trideoxyglucopyranose])[33] at the consensus sequon Asp (D)/Glu (E)-X1-Asn (N)-X2-Ser (S)/Thr (T) (where X1,2 ≠ Pro), with Asn (N) being the attachment site.[60,61] The synthesis of the *N*-glycan and attachment to proteins are encoded by the 16 kb *pgl* (protein glycosylation) gene cluster;[32,34,62] the *pgl* cluster is highly conserved among members of the order *Campylobacteriales*,[63,64] although *N*-glycan composition and structure, as well as the genomic location of the *pgl* locus (including being split into multiple loci), can differ between species.[63] Gene transfer of the complete *pgl* cluster into otherwise *N*-glycosylation incompetent bacterial species (*e.g.* most commonly *E. coli*) is sufficient to confer the ability to *N*-glycosylate co-expressed acceptor proteins.[62] Therefore, the *pgl* system has become a model for the production of glycoconjugate vaccines in recombinant expression procedures [reviewed in[65–67]].

Biosynthesis and transfer of the *N*-glycan to proteins (Fig. 1) involves the actions of 10 Pgl proteins (an eleventh member of the locus, *pglG*, does not appear to contribute to the process and remains functionally undefined[68]) and begins with the cytoplasmic synthesis of nucleotide-activated (uridine diphosphate; UDP) UDP-di*N*AcBac from UDP-Glc*N*Ac, which is catalyzed by the activities of (in order) the PglF dehydratase (conferring the rate-limiting step in the Pgl pathway), PglE aminotransferase and PglD acetyltransferase.[69–74] Synthesis of di*N*AcBac has been reviewed extensively elsewhere.[75,76] The potential for cross-talk between the *N*- and *O*-linked pathways is evidenced by shared nucleotide-activated precursors and by the activity of PglD, which can form intermediates from within the legionaminic acid biosynthetic pathway, albeit at substantially reduced catalysis compared with LegH.[38] Di*N*AcBac is attached to the cytoplasmic side of an inner membrane spanning lipid carrier (undecaprenyl-pyrophosphate [Und-P]) by the PglC glycosyl-1-phosphate transferase, and Und-P then serves as the carrier for the nascent *N*-glycan.[77,78] Continued synthesis of the glycan on Und-P-di*N*AcBac involves the sequential addition of 5 *N*-acetylgalactosamine (Gal*N*Ac) residues by three *pgl*-encoded glycosyltransferases (the first by PglA, the second by PglJ and the final three by PglH).[79] Glycan length is controlled by increased competitive inhibition of the PglH active site relative to the number of Gal*N*Ac residues, and is considered limited by the final Gal*N*Ac(x5) product.[80] The PglH tertiary structure also contains a novel 'ruler helix' that binds the pyrophosphate of Und-P and limits PglH catalysis to 3 Gal*N*Ac.[81] Glycan synthesis is completed by the PglI glucosyltransferase, which adds a single glucose (Glc) branch to the third Gal*N*Ac in the *N*-glycan.[68] This last Glc residue is not a strict requirement for *N*-glycosylation as, unlike all previous steps, addition of the complete *N*-glycan (without the Glc branch) to proteins still occurs in the absence of *pglI*,[77,82] albeit at lower catalytic efficiency. Deletion of other *pgl* genes results in either complete loss of the *N*-glycan or the presence of significantly truncated *N*-glycans (*e.g.* *pglD*[82]), as well as compromised protein transfer efficiency.[77] Once the heptasaccharide has been completed, the PglK flippase translocates the Und-P-linked glycan from the cytoplasm into the periplasmic space utilizing a mechanism dependent on the hydrolysis of two molecules of ATP.[83,84] The mature glycan is then transferred *en bloc* from Und-P onto target proteins by the PglB oligosaccharyltransferase (OST),[68,85] which recognizes both the Und-P-*N*-glycan complex and peptide acceptor as substrates.[86]

The PglB OST is also capable of releasing the *N*-glycan from Und-P into the periplasm as a 'free oligosaccharide' (fOS),[82,87,88] although the exact proportion of *N*-glycan as Asn-bound:fOS remains a point of contention. Nothaft *et al.* reported a ratio favouring high fOS at ~1 : 10, while Scott *et al.* reported a distribution of 4.5 : 1 in favour of protein-bound *N*-glycan.[82,89] While there are a number of technical considerations that may help explain this discrepancy,[89,90] there may also be dynamic control of fOS production based on environmental conditions and the kinetics of PglB. The fOS itself has been shown to provide protection against osmotic stress, further supporting the notion that the cellular fate of the *N*-glycan may be determined to some degree by environmental sensing.[82] Unlike protein *N*-glycosylation, the free *N*-glycan is highly dependent on the synthesis of the complete heptasaccharide, as *pglI* deficient strains produce ~55% less fOS.[90] The *N*-glycan itself can also be further modified with a phosphoethanolamine (pEtN) group, which is added to the terminal Gal*N*Ac of the heptasaccharide at a small number of glycosites by the sole *C. jejuni* pEtN transferase, EptC.[91] An inability to detect pEtN-modified fOS suggests that variation of the glycan by EptC occurs post-attachment to protein targets.[91]

Attachment of the *N*-glycan to proteins in *C. jejuni*

Modification of protein substrates by PglB at the *C. jejuni* *N*-glycosylation consensus motif is driven by a tryptophan–tryptophan–aspartic acid (WWD) motif, which is common to eukaryotic OST STT3 homologs.[85,92] The OST WWD (WWDYG in *C. jejuni* PglB) motif interacts by hydrogen bonding with residues at the +2 position (Ser/Thr) in the *N*-glycosylation sequon, while isoleucine 572 (Ile-572) of PglB also contacts

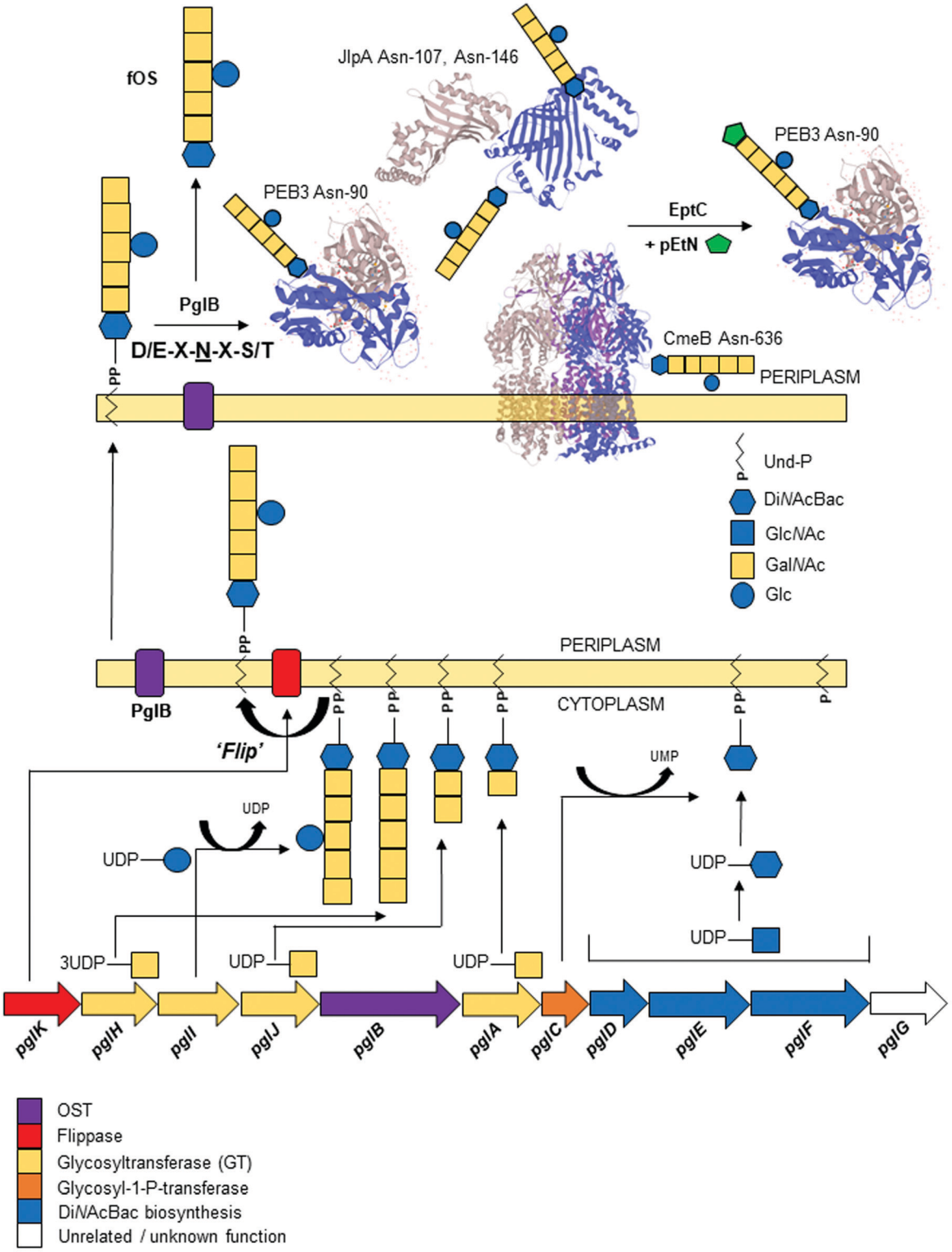

Fig. 1 Schematic of the biosynthesis and attachment of the heptasaccharide *N*-glycan to *C. jejuni* proteins. (lower) The *pgl* gene cluster colour coded by functional class; (middle) glycan biosynthesis begins with the ordered actions of PglFED that convert UDP-Glc*N*Ac to di*N*AcBac. The PglC glycosyl-1-phosphate transferase adds di*N*AcBac-P to the membrane-bound lipid carrier undecaprenylphosphate (Und-P). Glycan assembly continues in the cytoplasm with the sequential addition of 5 Gal*N*Ac (1 by PglA, a second by PglJ and the final 3 by PglH). PglI adds a glucose (Glc) to the third Gal*N*Ac. Following assembly, the PglK flippase flips the *N*-glycan into the periplasm; (upper) the PglB OST transfers the *N*-glycan to proteins predominantly at the consensus sequon D/E-X1-N-X2-S/T (where X1,2 cannot be proline); structures of known glycoproteins PEB3, JlpA and CmeB are shown with the glycan positioned at known glycosites; the pEtN transferase EptC can further modify some glycoproteins with pEtN at the terminal Gal*N*Ac of the heptasaccharide. PglB can also liberate a free glycan (fOS).

the Thr methyl group in target sequons and Ile-572 point mutants have reduced activity.[92] The additional specificity of the *C. jejuni* sequon (requiring D/E at the −2 position compared to N-X-S/T in eukaryotic *N*-glycosylation[61]) is conferred at least partly by PglB Arg-331, which interacts with these acidic residues.[85] In yeast OST STT3, this residue is an Asp, which explains the shorter eukaryotic-like N-X-S/T glycosylation motif based on charge repulsion. The distorted conformation of the peptide in the PglB OST active site is not capable of accommodating Pro at either the −1 or +1 positions,[85] and this conformational constraint may also contribute to the preference of PglB for targeting unstructured regions of its protein substrates.[93] Mechanistically, it is thought that the carboxamide group of the modified Asn is twisted through hydrogen bond interactions with PglB residues Asp-56 and Glu-319, which prime it for nucleophilic attack of the lipid-linked heptasaccharide.[94] A large, partially disordered periplasmic external loop region (known as 'EL5') was also identified that contains a *C*-terminal portion (including Glu-319) involved in sequon binding, and disengagement of EL5 allows release of the glycosylated substrate from PglB.[85] A conserved Tyr residue (Tyr-293) in the *N*-terminal region of EL5 was found to be essential for PglB catalysis but did not influence sequon binding, yet rather was associated with the interaction with the lipid-linked *N*-glycan donor.[95] Additional studies have suggested a further conserved motif (^{475}DGGK^{478}) in PglB may contribute to Und-P binding, and that this region could be essential for function, as PglB orthologs that do not contain this motif are unable to glycosylate proteins or produce fOS.[96]

Despite our knowledge of the structure and function of PglB and other OSTs, a number of elements still remain poorly understood. Firstly, observations of *N*-glycosylation at non-canonical sequons[89,97] are not consistent with the above model, particularly considering that it has previously been demonstrated that such substitutions are catalytically unfavourable.[92] It has been suggested that these atypical or non-canonical occupied sequons may reflect observations that peptide binding is not necessarily the rate-limiting step in the PglB reaction.[95] Evidence for this can be seen in similar turnover rates between sequons containing Thr or Ser at the +2 position despite an apparent 4-fold reduced affinity of PglB for Ser,[92] and this is further supported by similar propensities for the two amino acids at this position *in vivo*.[89] Additionally, while PglB can modify glutamine (Gln) at very low rates in *in vitro* peptide-based assays,[94] no glycosite at Gln has been demonstrated in any *C. jejuni* glycopeptide identified thus far, with the very small number of non-canonical sequons limited to differences at the −2 and +2 positions.[89] Additionally, the exquisite sensitivity of MS-based approaches for glycopeptide identification may mean that even experimentally verified non-canonical sequons could occur at extremely low occupancy and have potentially little biological value. Finally, the current model does not address how PglB is able to perform fOS release given the catalytic importance of also binding a peptide substrate. In yeast, purified STT3 can generate fOS by hydrolyzing the lipid (dolichol rather than Und-P) linked oligosaccharide irrespective of peptide binding,[98] however an observation that the WWD motif is required for PglB-mediated fOS release[82] suggests a peptide substrate is necessary in *Campylobacter*.

Addition of the *N*-glycan does not appear to be coupled to any particular membrane translocation pathway as CmeA was modified when shuttled into the periplasm *via* either the secretory (Sec) or twin-arginine translocation (Tat) bacterial translocation systems.[93] Kowarik *et al.* however, did demonstrate differences in *N*-glycosylation site occupancy when proteins were transported *via* these different systems in *E. coli*,[93] and consistent with their findings that showed lower *N*-glycosylation efficiency with Tat-translocated proteins, only 1 identified *C. jejuni N*-glycoprotein is predicted (by SignalP[99]) to be translocated using this system.[100]

Identification of proteins modified by *N*-glycosylation in *C. jejuni*

In early studies, lectin affinity approaches employing soybean agglutinin (SBA) specific for the Gal*N*Ac residues of the *C. jejuni N*-linked glycan were undertaken in combination with gel electrophoresis for separation of SBA-bound proteins. Gel-separated proteins could also be highlighted by Western blotting using glycan-specific antisera.[33,34] In each case, significant problems were encountered, including the lack of separation of very hydrophobic membrane-associated proteins on gels, the difficulty in performing post-separation analysis and confirmation of glycosylation sites for blotted proteins; and finally, even for those proteins that could be gel separated, the incompatibility of the Asn-*N*-glycan bond (most likely due to the structure of di*N*AcBac) with protein-*N*-glycosidase F (PNGase F) digestion and chemical β-elimination that meant intact glycopeptide analysis was needed for site verification.[35]

Site-specific glycopeptide analysis firstly relied on collision-induced dissociation (CID) MS-based fragmentation, however the highly labile nature of the glycosidic bonds resulted in very poor peptide backbone sequence coverage and therefore an inability to identify the modified sites. The advent of higher energy collisional dissociation (HCD) fragmentation enabled switching between CID (for glycan confirmation) and HCD for peptide fragmentation and sequencing,[35] while concurrent advances in hydrophilic interaction liquid chromatography (HILIC) facilitated better enrichment and separation of glycosylated *C. jejuni* peptides compared to previous studies employing SBA affinity and gel electrophoresis. An optimized workflow employing HCD tandem MS (MS/MS) provides glycan-derived diagnostic oxonium ions from the *C. jejuni N*-glycan (*e.g.* Gal*N*Ac, 204.08 mass:charge [*m*/*z*]) and peptide sequence.[89,91] In addition to improvements in MS-based glycan site identification, glycoprotein analysis can also be coupled to a multi-protease digestion strategy (*e.g.* employing alternatives to trypsin, including pepsin and chymotrypsin) that improve *N*-glycosite coverage and provide independent site verification in many cases.[35]

This approach has now yielded the identification of 134 sites of *C. jejuni* *N*-glycosylation from 78 membrane-associated proteins that have been experimentally confirmed (predominantly by MS), including periplasmic proteins, lipoproteins, inner membrane proteins and at least one protein that is thought to be surface-exposed (the lipoprotein JlpA[101]) across 5 *C. jejuni* strains,[33,35,61,63,89] meaning that *C. jejuni* is likely to be the most complete glycoproteome yet described in the literature (Table 1). Some glycoproteins are modified at multiple sites; for example, the Cj0152c putative membrane protein (which shares significant sequence similarity with the *Helicobacter pylori* neuraminidase/sialidase) contains 6 occupied canonical sites, as well as a single atypical site (Fig. 2A). Cj0152c also contains an additional pseudo-sequon (^{70}ENNPT^{74}) that is not occupied, and that is predicted to be located in the cytoplasmic region of the protein. Cj0610c (encoding the peptidoglycan *O*-acetyltransferase PatB) is potentially the most 'modified' protein in *C. jejuni* since it contains 5 confirmed *N*-glycosites and 10 *N*-sequons in total, all of which are predicted to be located within the periplasm; structural elucidation of this protein could be particularly useful in determining the three-dimensional constraints involved in *N*-glycan site occupancy (see below). A further 5 proteins (Cj0114, Cj0592c, Cj0843c, Cj1013c and Cj1670c) each contain 4 verified *N*-glycosites (Table 1). Additionally, eight proteins have been identified with the pEtN-modified *N*-glycan attached.[91] Although the function of the pEtN-glycan remains completely unknown, the proteins displaying this modification are amongst the most immunogenic in *C. jejuni*, including the major antigen PEB3 (Cj0289c), and the previously identified immunogens CjaC (Cj0734c), CjaA (Cj0982c) and JlpA (Cj0983c).[17,34,101–103] Despite this, deletion of the *eptC* pEtN transferase responsible for pEtN modification of the *N*-glycan did not influence the reactivity of these proteins with human serum.[91] Further work is required to better understand the occupancy levels of non- to pEtN-modified *N*-glycan on these glycosites and thus to assist in determining the biological role of the pEtN group in this context. It is also important to note that a second *Campylobacter* species, *C. gracilis*, exclusively modifies proteins with an *N*-glycan displaying a terminal pEtN group,[63] however again, the role of this modification remains to be elucidated.

As discussed above, despite PglB showing a preference for Thr at the +2 position,[92] there is no obvious bias towards Thr in the identified *N*-glycosites; in fact only 60 of 134 identified sites contain sequons with a Thr in this position (44.8%), with 73 containing Ser (54.5%) and the final sequon displaying alanine (Ala) in a non-canonical sequon (Table 1).[89] Conversely, there is clear preference for Asp at the −2 position with 84 sequons displaying this amino acid (62.7%) compared with only 47 displaying Glu (35.1%). The final 3 sequons were non-canonical (Table 1). These data align with previous studies that have tested various sequon compositions and their glycosylation efficiency by the PglB OST and found DQNAT to be the optimal sequon, as well as an ~5-fold preference for Asp, rather than Glu, at the −2 position.[104]

Structural constraints of *N*-glycosylation

C. jejuni contains ~500 *N*-glycosylation sequons within the translated genome sequence, depending on the strain examined (for example, 510 sequons are found in strain HB93-13[35]), and ~370 of these are found in >260 predicted membrane-associated proteins (or proteins of unknown localization) suggesting that there are evolutionary constraints associated with maintenance of the sequon in proteins connected with this sub-cellular localization; similar sequon bias (albeit against the presence of the sequon) has been observed for the HMW system in *Haemophilus influenzae*.[105] Realistically, the modifiable *N*-glycoproteome is likely to be considerably smaller, given that both topological and structural constraints likely play a crucial role in the ability of the PglB OST to modify a given sequon. While tools such as PSORTb[106] provide predicted sub-cellular localization for a given protein sequence, it is absolutely critical to understand that the topology of the protein defines PglB sequon accessibility. This is particularly important for proteins associated with the cytoplasmic/inner membrane in Gram negative organisms, since regions within these proteins can be cytoplasmic, and thus any sequons contained within those regions will not be amenable to the catalytic activity of PglB. For the 134 *N*-glycosites shown in Table 1, we employed a variety of localization and topology tools that show 133 (99.2%) are predicted to localize to the periplasm (Fig. 2A and Table 1). Only a single site, ^{3}EINKT^{7} from DsbI (Cj0017c), is predicted to localize to the cytoplasm. This site is challenging to accurately predict given its proximity to the *N*-terminus and the difficulty in orienting termini into the inner membrane (inside or outside). Furthermore, the site was identified only in a single study[35] and was based on a low scoring, manually validated and very short glycopeptide sequence; an approach no longer valid due to many improvements in computational intact glycopeptide analysis (another site identified in a similar manner is the non-canonical ^{50}AMNVS^{54} from Cj0864). Despite the overwhelming association of experimentally verified *N*-glycosites with periplasmic localization, many sequons in membrane-associated proteins that have not been experimentally identified are predicted to localize to the cytoplasm (or be located within cleaved signal peptides) and therefore cannot be glycosylated (for examples, see Fig. 2B and C). Fundamentally, this means that the theoretical *N*-glycoproteome of *C. jejuni* may only comprise between 200–250 possible sites.

Beyond localization and topology, the next major influence on sequon occupancy is the tertiary conformation of the protein, with the three-dimensional structure of both the target protein and PglB itself dictating site accessibility.[85,93,107] Unlike in eukaryotes, where *N*-glycosylation occurs in the endoplasmic reticulum (with further processing in the Golgi apparatus) prior to or during folding (and hence partially dictates the final conformation), the prevailing viewpoint is that the *C. jejuni* *N*-glycan is added to already, or at least partially, folded substrates,[93,100] meaning that existing tertiary structural

Table 1 Experimentally validated *C. jejuni* proteins modified by *N*-glycosylation. Cj, gene identifier from *C. jejuni* NCTC11168 genome sequence; 81–176, gene identifier from *C. jejuni* 81–176 genome sequence; gene, gene name if known; identification, protein identification taken from NCTC11168 UniProt entry (additional information added by BLAST and literature search); sequence/site, sequence is shown for NCTC11168

Cj	81–176	Gene	Identification	Sequence/site[#]	Location	Topology
Cj0011c	**0037**	*cj0011c*	Putative non-specific DNA-binding protein (competence ComEA-like; natural transformation protein)	49EA**N**FT53	IM (1)	PP
Cj0017c	**0044**	*dsbI*	Disulfide bond formation protein DsbI	3EI**N**KT7	IM (5)	Cyto[a]
Cj0081	**0118**	*cydA*	Cytochrome bd oxidase subunit I	283DN**N**ES287	IM (9)	PP
				351EN(S)**N**DT355		PP
Cj0089	**0124**	*cj0089*	Putative lipoprotein (TPR tetricopeptide repeat-like helical domain protein)	73DF**N**KS77	LP/IM (SP)	PP
Cj0114	**0149**	*cj0114*	Putative periplasmic protein (TPR tetricopeptide repeat-like helical domain protein; putative Tol-Pal system protein YbgF/ putative cell division coordinator CpoB)	99EN**N**FT103	OM	PP
				153DA(V)**N**LS157		PP
				171DS**N**ST175		PP
				177EN**N**NT181		PP
Cj0131	**0166**	*cj0131*	Putative peptidase M23 family protein/putative zinc metallo-peptidase (putative Gly–Gly endopeptidase)	73DD***N***TS75	Unk (1)	PP
Cj0143c	**0179**	*znuA*	Putative periplasmic ABC transport solute-binding protein (zinc-binding ABC transporter ZnuA)	26E(D)Q**N**TS30	PP	PP
Cj0152c	**0188**	*cj0152c*	Putative membrane protein (45.3% similarity to *H. pylori* sialidase A/neuraminidase)	126EQ**N**NT130	Unk (1)	PP
				157DN**N**KA161[+]		PP
				163ET**N**RT167		PP
				182DK**N**IS186		PP
				188EN**N**IS192		PP
				193EN**N**TT197		PP
				250DF**N**IS254		PP
Cj0158c	**0194**	*cj0158c*	Putative haem-binding lipoprotein (cytochrome *c* oxidase Cbb3-like protein)	119DK**N**HS123	LP/OM (SP)	PP
Cj0168c	**0204**	*cj0168c*	Putative periplasmic protein	26DV***N***QT30	PP (SP)	PP
Cj0176c	**0212**	*cj0176c*	Putative lipoprotein	29DL**N**KT33	LP/OM (SP)	PP
Cj0177	**ND**	*ctuA/chaN*	Putative iron transport protein (putative iron-regulated lipoprotein)	83EG**N**LS87^	IM (1)	PP
Cj0182	**0213**	*cj0182*	Putative transmembrane transport protein (ABC transporter transmembrane family; long chain fatty acid ABC transport protein; peptide antibiotic transport protein SbmA)	58DS**N**ST62	IM	PP
				70EN**N**AT74		PP
Cj0199c	**0230**		Putative periplasmic protein	126DI**N**LS130	Unk (1)	PP
Cj0200c	**0231**	*cj0200c*	Putative periplasmic protein	33DN**N**KT37	Unk (SP)	PP
Cj0235c	**0260**	*secG*	Uncharacterized protein (preprotein translocase subunit SecG)	87EN**N**NT91	IM (2)	PP
				118DV**N**SS122		PP
Cj0238	**0263**	*cj0238*	Putative mechanosensitive ion channel family protein (MscS family membrane integrity protein)	24DA**N**IS28	IM (5)	PP
				56DE**N**SS60		PP
Cj0256	**0283**	*eptC*	Putative sulfatase family protein (phosphoethanolamine transferase EptC; lipid A/lipooligosaccharide pEtN transferase EptC)	213EN**N**HT217	IM (5)	PP
Cj0268c	**0295**	*cj0268c*	Putative transmembrane protein (SPFH domain/band 7 family protein; FtsH protease regulator HflC)	274EA**N**AT278	Unk (1)	PP
Cj0277	**0304**	*mreC*	Homolog of *E. coli* rod-shape determining protein MreC	91DQ**N**ST95	Unk (1)	PP
Cj0289c	**0315**	*peb3*	Major antigenic peptide PEB3 (thiosulfate/sulfate-binding protein)	88DF***N***VS92	Unk (SP)	PP
Cj0313	**0335**	*cj0313*	Putative integral membrane protein (putative lipooligo-saccharide export ABC transporter permease LptG)	173DL**N**LS177	IM (6)	PP
				196DG**N**IT200		PP
Cj0365c	**0388**	*cmeC*	Outer membrane channel protein CmeC (multi-drug antibiotic efflux system CmeABC protein)	30EA**N**YS34	OM (SP)	PP
				47EN**N**SS51		PP
Cj0366c	**0389**	*cmeB*	Efflux pump membrane transporter CmeB (Multi-drug antibiotic efflux system CmeABC protein)	634DR**N**VS638	IM (12)	PP
Cj0367c	**0390**	*cmeA*	Periplasmic fusion protein CmeA (multi-drug antibiotic efflux system CmeABC protein)	121DF**N**RS125	IM (1)	PP
				271DN**N**NS275		PP
Cj0371	**0395**	*cj0371*	UPF0323 lipoprotein Cj0371 (putative secreted protein involved in flagellar motility)	75DL**N**GT79	LP/OM (SP)	PP/SE[b]
Cj0376	**0400**	*cj0376*	Putative periplasmic protein	50DK**N**QT54	Cyto	PP
Cj0397c	**0420**	*cj0397c*	Uncharacterized protein	105DF**N**NT109	Unk (1)	PP
Cj0399	**0422**	*cvpA*	Colicin V production protein homolog CvpA	179DL***N***NT183	IM (4)	PP
Cj0404	**0428**	*dedD*	Putative transmembrane protein (SPOR sporulation domain-containing protein; putative cell division protein DedD)	101EQ**N**NT105	Unk (1)	PP
Cj0454c	**0479**	*cj0454c*	Putative membrane protein	91EN**N**KS95	IM (1)	PP
Cj0455c	**0480**	*cj0455c*	Putative membrane protein	60LQ**N**QT64[+]	IM (1)	PP
Cj0494	**0515**	*cj0494*	Putative exporting protein	26DN**N**IT30	Unk	PP/SE
Cj0508	**0536**	*pbpA*	Penicillin-binding protein PbpA (penicillin-binding protein 1A; peptidoglycan transpeptidase PBP1A)	312DA**N**LS316	IM (1)	PP
Cj0511	**0539**	*ctpA*	Putative secreted protease (protease family S41; carboxy-terminal protease CtpA)	67DQ**N**IS71	IM (1)	PP
Cj0515	**0543**	*cj0515*	Putative periplasmic protein	207EL**N**AT211	IM (3)	PP
				234DF**N**AS238		PP

Table 1 (*continued*)

Cj	81–176	Gene	Identification	Sequence/site[#]	Location	Topology
Cj0530	**0555**	*cj0530*	Putative periplasmic protein (AsmA family protein DUF3971 domain)	519DF**N**AS523 617DS**N**KT621	OM (1)	PP/SE PP/SE
Cj0540	**0565**	*cj0540*	Putative exporting protein	173EN**N**NS177	Unk (0)	PP/SE
Cj0587	**0615**	*cj0587*	Putative integral membrane protein	282DN**N**LS286	IM (8)	PP
Cj0592c	**0620**	*cj0592c*	Putative periplasmic protein (putative lipoprotein; Cj0591 paralog)	96DI**N**QS100 103EN**N**ES107 127EN**N**QS131 137DV**N**MT141	Unk (SP)[c]	PP PP PP PP
Cj0599	**0627**	*cj0599*	Putative OmpA family membrane protein (putative chemotaxis protein MotB; Putative flagellar motor motility protein MotB; Cj0336c MotB paralog)	97EA**N**IT101 109DL**N**ST113 168DN**N**IT172	Unk (1)	PP/SE[d] PP/SE PP/SE
Cj0608	**0637**	*cj0608*	Putative outer membrane efflux protein (putative TolC-like outer membrane protein; putative antibiotic efflux CmeC paralog)	35DL**N**LT39	OM (2)	PP
Cj0610c	**0639**	*cj0610c*	Putative periplasmic protein (SNGH family hydrolase; putative lipase/esterase; peptidoglycan *O*-acetyltransferase PatB)	82DE**N**LS86 98DE**N**TS102 113DA**N**IS117 296EN**N**RS300 331EE**N**AS335	Unk (1)	PP PP PP PP PP
Cj0633	**0661**	*cj0633*	Putative periplasmic protein (putative polysaccharide deacetylase; putative glycoside hydrolase/deacetylase)	73DN**N**KS77 123DT**N**LT127 129DQ**N**LT133	Cyto (1)	PP PP PP
Cj0648	**0676**	*cj0648*	Putative membrane protein (putative lipooligosaccharide transport system substrate-binding protein LptC)	49ES**N**TS53 103EG**N**VT107	IM (1)	PP PP
Cj0652	**0680**	*pbpC*	Penicillin-binding protein PbpC (pencillin-binding protein PBP2; peptidoglycan transpeptidase PBP2)	99DL**N**AS103 467EN**N**NT471	IM (1)	PP PP
Cj0694	**0717**	*ppiD*	Putative periplasmic protein (SurA domain-containing outer membrane protein folding protein; peptidyl-prolyl cis/trans isomerase PpiD)	132DF**N**KT136 306DQ**N**IS310 426DQ**N**SS430	IM (1)	PP PP PP
Cj0734c	**0757**	*hisJ*	Probable histidine-binding protein (periplasmic lipoprotein CjaC; solute transport protein HisJ)	26EN(S)***N***AS30	IM (PP)	PP
Cj0776c	**0797**	*cj0776c*	Putative periplasmic protein	87DE**N**QS91 103EN**N**QS107 111DT**N**TS115	Cyto (1)[e]	PP PP PP
Cj0780	**0801**	*napA*	Periplasmic nitrate reductase NapA (catalytic subunit of the NapAB complex)	385DD**N**ES389	IM (PP)	PP
Cj0783	**0804**	*napB*	Periplasmic nitrate reductase NapB (electron transfer subunit of the NapAB complex)	48EA**N**FT52	IM (PP)	PP
Cj0843c	**0859**	*slt*	Putative secreted transglycosylase (soluble lytic murein peptidoglycan transglycosylase)	97DA**N**LT101 173DL**N**TG(S)177 327DA**N**AS331 374DY**N**KT378	IM (PP)	PP PP PP PP
Cj0846	**0862**	*cj0846*	Uncharacterized metallophosphoesterase (Ser/Thr phosphatase family protein)	280DL**N**TS284	IM (3)	PP
Cj0864	**0880**	*cj0864*	Putative periplasmic protein (putative thiol: disulfide interchange protein DsbA homolog)	50A**M**N**N**VS54[+f]	IM (PP)	PP
Cj0906c	**0915**	*pgp2*	Putative periplasmic protein (peptidoglycan L-D-carboxypeptidase Pgp2)	53DK**N**IS57	IM (SP)	PP
Cj0944c	**0968**	*cj0944c*	Putative periplasmic protein (putative flagellar protein FliL; chemotaxis-associated protein)	219EN**N**AS223 238DE**N**ST242	Cyto (0)[g]	PP
Cj0958c	**0981**	*yidC*	Membrane protein insertase YidC (integral membrane protein assembly/folding protein YidC)	40EQ**N**IT44 48QQ**N**TS52[+] 154DE**N**GS158	IM (5)	PP PP PP
Cj0982c	**1001**	*cjaA*	Putative amino acid transporter periplasmic solute-binding protein CjaA	137DS***N***IT141	IM (PP/LP)[h]	PP
Cj0983	**1002**	*jlpA*	Uncharacterized lipoprotein Cj0983 (surface-exposed lipoprotein JlpA)	105E(K)A***N***AS109 144DI**N**AS148	OM (SE)	SE SE
Cj1007c	**1025**	*cj1007c*	Putative mechanosensitive ion channel family protein (MscS family osmotic stress resistance protein)	17DV**N**RT21	IM (4)	PP
Cj1013c	**1032**	*cj1013c*	Putative cytochrome *c* biogenesis protein CcmF/CycK/CcsA family protein CcsB	178EN**N**NS182 230DE**N**LT234 530DL***N***ST534 731DG**N**WT(I)735	IM (14)	PP PP PP PP
Cj1032	**1051**	*cmeE*	Membrane fusion component of antibiotic efflux system CmeDEF	199DQ**N**GT203	IM (1)	PP
Cj1053c	**1073**	*cj1053c*	Putative integral membrane protein (amino acid/carbohydrate/antibiotic transport permease motifs protein; lipooligosaccharide ligase-like motif protein)	75DI**N**VS79 96DN**N**QS100	IM (2)	PP PP
Cj1055c	**1075**	*cj1055c*	Putative sulfatase family protein (putative arylsulfatase; putative phosphoglycerol transferase lipooligosaccharide synthesis protein homolog)	616ES**N**DT620	IM (5)	PP

Table 1 (*continued*)

Cj	81–176	Gene	Identification	Sequence/site[#]	Location	Topology
Cj1126c	**1143**	*pglB*	Undecaprenyl-diphosphooligosaccharide-protein glycosyltransferase (PglB oligosaccharyltransferase)	532DY**N**QS536	IM (12)	PP
Cj1219c	**1232**	*cj1219c*	Putative periplasmic protein (uncharacterized protein involved in outer membrane biogenesis assembly)	47DV**N**IT51	OM (1)	PP
Cj1345c	**1344**	*pgp1*	Putative periplasmic protein (peptidoglycan D-L-carboxypeptidase Pbp1)	59DY**N**IT63 159EI**N**AS163 348DG**N**ET352	Cyto (1)	PP PP PP
Cj1373	**1376**	*cj1373*	Putative integral membrane protein (antibiotic resistance sterol-sensing domain protein; RND superfamily export protein MmpL family)	134DI**N**RT138 497DQ**N**TS501	IM (12)	PP PP
Cj1444c	**1438**	*kpsD*	Capsule polysaccharide export system periplasmic protein KpsD	37DQ**N**LS41 50EN**N**LT54	IM (PP)	PP PP
Cj1496c	**1488**	*cj1496c*	Putative periplasmic protein (putative magnesium transporter MgtE-like protein; putative motility chaperone MotE; putative flagellar protein FliG)	71EV**N**AT75 167DN**N**AS171	Cyto (PP)	PP PP
Cj1565c	**1550**	*pflA*	Paralysed flagellar motility protein A PflA	456DN**N**AS460 495EG**N**FS499	Cyto (PP)	PP PP
Cj1621	**1608**	*cj1621*	Putative periplasmic protein	197DL**N**KT201	E (1)	PP
Cj1661	**1652**	*cj1661*	Putative ABC transport system permease (putative antibiotic macrolide export protein MacB; putative cell division protein FtsX)	188EN**N**QS192	IM (4)	PP
Cj1670c	**1666**	*cgpA*	Putative periplasmic protein (campylobacter glycoprotein A; AMIN-domain containing protein, membrane protein assembly protein)	26DQ**N**IT30 71DV**N**KS75 104EK**N**SS108 111ES**N**ST115	Unk (0)	PP PP PP PP
ND	**0063**	*sirA*	Dissimilatory sulfite reductase SirA/MccA	213DG**N**LS217	IM (1)	PP
ND	**0701**	*kdpC*	Potassium-transporting ATPase KdpC subunit	83DT**N**ES87	IM (1)	PP
ND	**1263**	*1263*	Uncharacterized protein[i]	26EQ**N**GS30	Unk (SP)	PP
VirB10	**pVir0003**	*virB10*	Type IV secretion system protein VirB10	30EE**N**VS34 95DN**N**IT99	OM (SP)	PP PP

[#]Where glycosylation site was identified only in another strain this sequence is shown in (brackets), [+]non-canonical sequon denoted by underlining of atypical amino acid at −2 or +2 position, Asn (N) highlighted in bold and shaded in italicized bold is also modified by pEtN-modified N-glycan; location, predicted subcellular localization as determined by PSORTb (vers. 3.0.2.)[106] and Lipo P 1.0,[139] (*x*) number of predicted transmembrane regions (TMR), or presence of signal peptide (SP), unless experimentally proven all lipoproteins were considered anchored to OM or IM (dependent on Lipo P use of the '+2 rule', Asp at +2 from lipo-Cys predicts IM anchoring, all other amino acids predict OM anchoring) with protein facing into the periplasm; topology, predicted location of the N-glycosylation site as determined by TmPred (https://embnet.vital-it.ch/software/TMPRED) and TOPCONS.[140] Cyto, cytoplasm; E, extracellular; IM, inner membrane; LP, lipoprotein; OM, outer membrane; PP, periplasm; SE, surface exposed; Unk, unknown. ^Site identified by expression in *E. coli* containing the *pgl* cluster and over-expression in *C. jejuni* [H. M. Frost, PhD Thesis, University of Manchester, 2015], not seen in any wild-type *C. jejuni* glycoproteome studies. [a] Cj0017c localization depends on correct prediction of orientation for *N*- and *C*-terminus of protein. [b] Cj0371 co-localises to the poles of *C. jejuni* cells and thus co-localises with flagella.[134] Thus, the protein is potentially surface-exposed (SE). [c] Cj0592c PSORT b predicts unknown localization; Lipo P predicts a lipoprotein signal peptide with OM anchor (Asp at +2 position to SpII cleavage site); protein is described as 'putative periplasmic protein'. [d] Cj0599 PSORT b predicts unknown localization; protein contains C-terminal OmpA domain suggesting OM localization and therefore topology could be PP or SE. [e] Cj0776c PSORT b predicts cytoplasmic localization; 1 predicted TMR; TOPCONS predicts 1 TMR with the majority of the protein localized to the periplasm. [f] Cj0864 Ding *et al.*[141] reported this sequence as DM[ox]NVS (where the methionine is methionine sulfoxide), however the NCTC11168 sequence indicates the −2 position is an alanine. This sequence was also low scoring as discussed in the text. [g] Cj0944c PSORT b predicts cytoplasmic localization; Lipo P and TOPCONS predict 1 SP and periplasmic location. [h] Cj0982c PSORT b predicts periplasmic localization; TOPCONS and Lipo P predict lipoprotein with IM anchoring. Experimental evidence in ref. 103. [i] Cjj81176_1263 was originally described in ref. 89 and 91 as CJE1384.

constraints are a major factor in the final attachment and kinetics of the modification. Sequons buried within the tertiary structure are therefore inaccessible to PglB and cannot be modified, irrespective of their sub-cellular location. The earliest structural consideration of *C. jejuni N*-glycosylation was based on the crystal structure of the major antigen PEB3 (Cj0289c),[108] which showed the *N*-glycosite at ^{88}DF**N**VS^{92} occurs in a flexible exposed loop region readily accessible to the PglB OST. Therefore, without determining structures of glycoproteins it remains difficult to predict which sequons will be occupied and the likely level of site occupancy, and there are only very few *N*-glycoproteins for which three-dimensional structures are currently available. In addition to PEB3, and PglB itself,[85] structures of components of the tripartite antibiotic efflux system CmeABC (Cj0365c–Cj0367c) have also been elucidated,[109,110] and all 3 are *N*-glycoproteins (Table 1). CmeA is the periplasmic membrane fusion family protein, with 2 *N*-glycosites both predicted to be located within the periplasm (Table 1). CmeC is the outer membrane channel and examination of the crystal structure[109] shows that both experimentally verified glycosylated sequons (^{30}EA**N**YS^{34} and ^{47}EN**N**SS^{51}) are located in a periplasmic disordered exposed loop region that leads from the membrane-embedded *N*-terminal lipidated cysteine (following removal of the signal peptide) to the first structured part of the protein. Therefore both sequons are consistent with the known structural requirements for *N*-glycosylation.[93,99,108]

CmeB, which is the inner membrane efflux pump, contains one well characterized *N*-glycosite (^{634}DR**N**VS^{638}). A second sequon (^{653}DRNAS^{657}) is located proximal to this confirmed site, but no experimental evidence exists for this site being

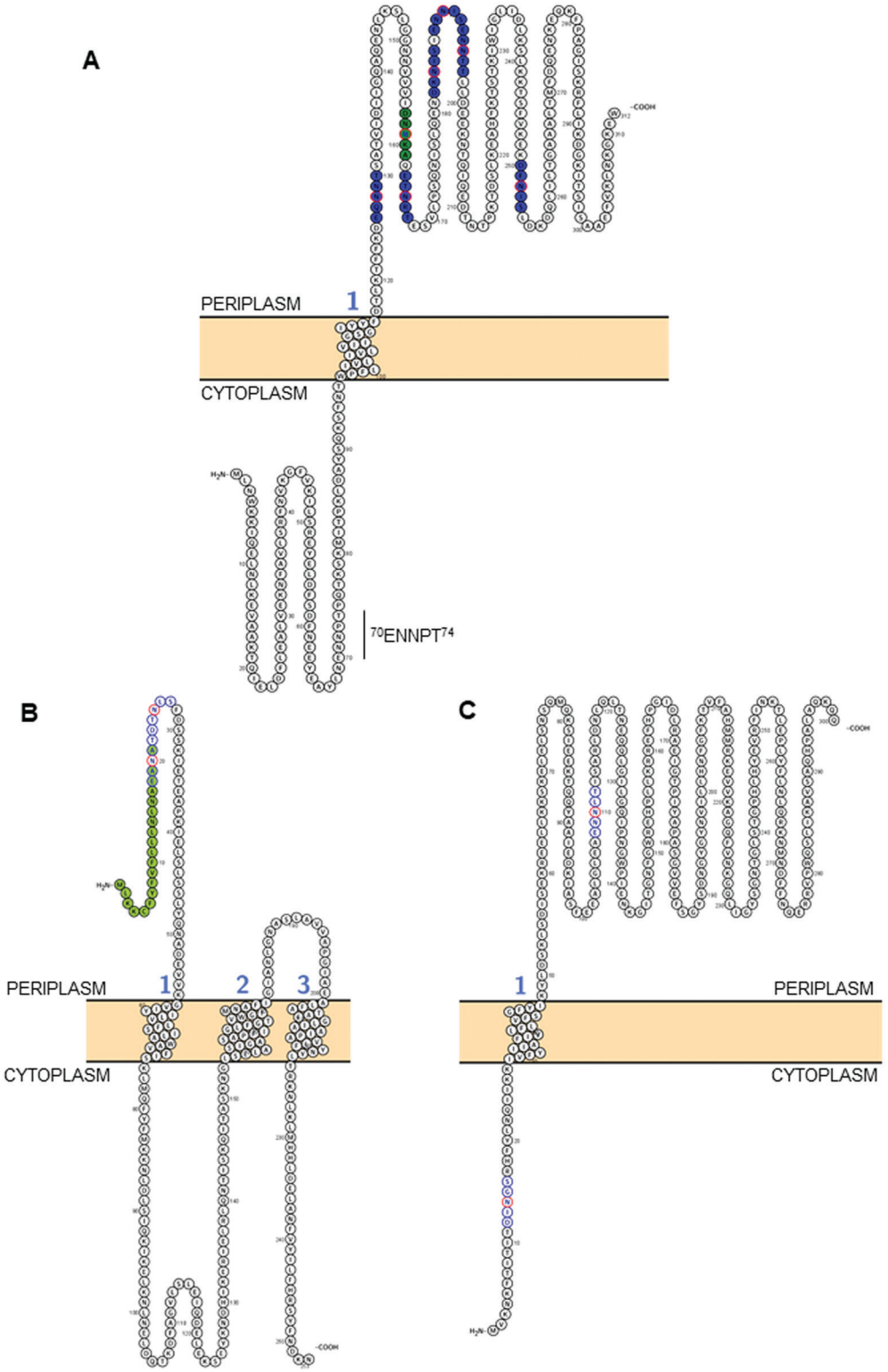

Fig. 2 Modelling of predicted surface topologies of 3 *C. jejuni* *N*-glycoproteins. (A) Cj0152c; positions of experimentally verified *N*-glycosites (Asn; N) are shown in red circles with occupied sequons shown in blue fill, the position of a non-canonical, but occupied sequon is shown in green fill; (B) Cj0179 (ExbB1); positions of two sequons (not experimentally verified) are shown in blue with the Asn residues in red, the *N*-terminal signal peptide that overlaps the first sequon is in green; (C) Cj1087c; positions of two sequons (not experimentally verified) are shown in blue with the Asn residues in red, the sequon at position ^{12}DINGS^{16} is predicted to reside in the cytoplasm and hence cannot be glycosylated. All topologies were visualized using Protter.[142]

occupied in any *C. jejuni* strain, and hence CmeB is the only protein with both an occupied and unoccupied glycosite for which structural information can currently be determined. These two sites are also of interest since their sequons are near identical and hence, any effects of differences at the −2 and +2 positions, as described above, are likely to be negligible (indeed the arginine [Arg] at the −1 position is shared, while the +1 position is a semi-conservative substitution from valine [Val] to alanine [Ala], which are both aliphatic amino acids) and most likely do not influence site occupancy. Interrogation of the CmeB tertiary structure shows that both sequons are located in the large periplasmic section of the protein located between the sixth and seventh transmembrane-spanning regions (TMR; residues 554–867, with CmeB predicted to contain 11 TMR, excluding the *N*-terminal signal peptide) and are found in short disordered exposed loop regions separated by a small alpha-helix (Fig. 3A). Tertiary structure modelling shows that ^{634}DRNVS^{638} is located close to the membrane and the modified Asn is highly solvent accessible, while ^{653}DRNAS^{657} is located further into the periplasm. Although solvent accessible, Asn-655 is partially occluded by Arg-654 (Fig. 3A). The CmeB structure was next modelled in protein complex with the PglB OST, using the model sequon DQNAT[104] to provide the PglB binding conformation. CmeB/PglB docking clearly demonstrated a preference for the Asn-636 site, consistent with the identification of this site in several MS-based studies (Fig. 3B and C), while the Asn-655 site does not appear to readily interact with the PglB model, and hence therefore is likely to either not be glycosylated or glycosylated at only very low site stoichiometry.

Further evidence for structural constraints determining optimal glycosylation have been shown for the doubly glycosylated surface-exposed glycoprotein JlpA.[101] Scott *et al.* showed that JlpA must be glycosylated at one site (^{144}DINAS^{148}) before a second site (^{105}EANAS^{109}) can be glycosylated, inferring that structural modifications to JlpA conferred by Asn-146 glycosylation open the protein conformation and allow PglB to add the *N*-glycan to the second site. These structural constraints have since been confirmed using structural predictions and crystallography.[111] Finally, nuclear magnetic resonance (NMR) analysis of a recombinant *C. jejuni* CmeA domain indicates that the *N*-glycan itself adopts a rigid rod conformation[112] that appears to fold back over the exposed protein (thus suggesting a role in protection from proteolysis), although it remains to be seen how well conserved this is *in vivo*. Although no examples have been shown in the literature, the converse may also be true in that the *N*-glycan itself may hinder accessibility of a second site in a given protein to the PglB OST. Despite this possibility, proteins such as Cj0152c (Fig. 2A) have multiple sites in close sequence space; occupied sequons are found at 7 sites, with 3 (Asn-184, Asn-190 and Asn-195) located within 20 amino acids. To determine if *N*-glycan steric hindrance of PglB occurs, better understanding of individual site occupancy, in the context of tertiary structures, is needed.

A final structural/topological consideration is the role of *N*-glycosylation in OMVs that have been associated with *C. jejuni* virulence.[24–26] OMVs package cytoplasmic, periplasmic, outer membrane-associated and *N*-glycoproteins in a 'bleb'-like structure.[24] PglB is located in the cytoplasmic/inner membrane, which is not typically associated with OMVs. It is possible however, that inner membrane fragments may also be packaged into OMVs, and all *C. jejuni* OMV proteomics studies have demonstrated the identification of integral cytoplasmic membrane proteins (*e.g.* CmeB[24]). Packaging of PglB into OMVs may enable glycosylation of sites not typically found in the membrane; however despite this, we and others have observed no such cytoplasmic *N*-glycosites, even at low levels, which may imply that PglB does not occur in OMVs, or that OMVs are not induced (or collected) under the culture conditions employed in the *N*-glycosite discovery studies conducted thus far. *C. jejuni* OMV composition is however, altered in *pgl*-negative compared with wild-type *C. jejuni*,[113] suggesting *N*-glycosylation does impact protein packaging, although no differences were observed in the ability of OMVs from either *pgl* positive or negative bacteria to induce an immune response.[113]

Putative functions of *C. jejuni* protein *N*-glycosylation

Deletion of genes from the *pgl* cluster (except *pglI*) results in *C. jejuni* that are poorly able to colonize chickens and display reduced adherence to, and invasion of, human epithelial cells.[114,115] Additional recent modelling of *C. jejuni* virulence in a human small intestine-like gut-immune co-culture model also revealed that *pgl*-negative *C. jejuni* (in this case, *pglE* deletion) were vastly deficient (~100 times less) in adherence and invasion.[113] Therefore, *N*-glycosylation is considered a fundamental virulence determinant in this organism. Despite this, until recently[116,117] there have been very few studies that have broadly characterized *pgl*-associated phenotypes, and the function(s) of the *N*-glycosylation system in general, and even more so the role of the *N*-glycan on individual proteins, remains almost completely unknown. Genome-wide and functional screens have shown an association between glycosylation and biofilm formation, amongst other traits, and *pgl*-negative *C. jejuni* are attenuated in some, but not all, models of biofilm growth.[116,118] *C. jejuni pgl* deletion strains incapable of *N*-glycosylating proteins display a number of additional altered traits including a reduced capacity for natural transformation,[119] altered antibiotic resistance,[117] greater susceptibility to host-derived proteases,[120] impaired motility[116] and modified binding to host cell surface lectins.[121] Proteomics-based approaches have been employed in an attempt to globally characterize phenotypes associated with *N*-glycosylation.[116,117] *pgl* negative *C. jejuni* displayed evidence of induction of the stress response and were attenuated for survival at temperature extremes,[82,116] particularly survival at lower temperatures, which has further implications for the *pgl* system acting as an interventional target to limit the presence of the organism on supermarket chicken for human consumption. Loss of glycosylation influenced metabolism and nutrient transport, as well

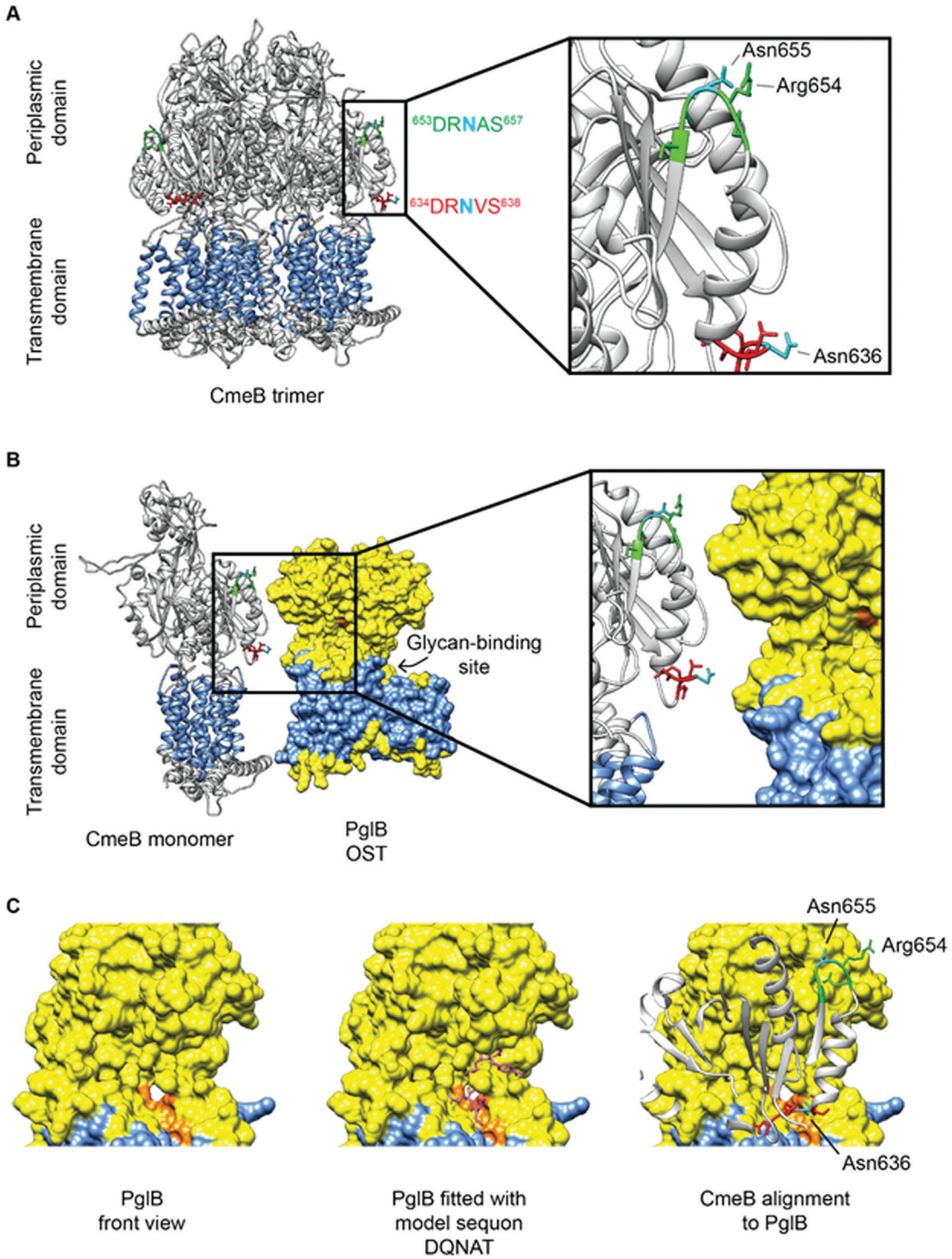

Fig. 3 CmeB modeling with PglB highlighting *N*-glycosylation sequons. (A) CmeB trimer (Protein Data Bank [PDB]: 5LQ3) has a transmembrane domain (highlighted in blue with 11 TMR) and periplasmic domain. The experimentally validated sequon (^{634}DRNVS^{638}) is labelled red and the non-identified sequon (^{653}DRNAS^{657}) is labelled green, with both Asn labelled cyan. Both Asn are located on the periplasmic side on exposed loops and are solvent-accessible with Asn-636 more accessible than Asn-655; (B) The PglB OST (PDB: 3RCE) shown in yellow has a transmembrane spanning domain (highlighted in blue with 12 TMR) and a larger periplasmic region where the catalytic domain is located. The sequon recognition site is highlighted in orange and facing towards CmeB with the glycan-binding site located behind. Sequon ^{634}DRNVS^{638} is in closer proximity and has better accessibility to the PglB catalytic site; (C) (left) PglB viewed from the front (90° counter-clockwise rotation to upper panels) reveals the sequon-binding surface in orange, (Middle) PglB fitted with the model peptide mimic DQNAT, (right) alignment of CmeB to PglB (90° counter-clockwise rotation to panel B) reveals that sequon ^{634}DRNVS^{638} is more spatially likely to fit into the active site of PglB suggesting this sequon is more readily glycosylated than ^{653}DRNAS^{657}. Analysis was performed in UCSF Chimera 1.14 (build 42094).

as chemoattraction towards some of these substrates.[116] Finally, *pgl*-negative *C. jejuni* displayed very strongly reduced abundance of proteins involved in respiration using alternative electron acceptors under low oxygen conditions; a phenotype paramount to *C. jejuni* colonization of all hosts, and potentially associated with a loss of proton motive force.[116] This phenotype could be linked to reduced nitrate reductase (NapA/NapB) activity, which was shown in both PglB OST (Δ*pglB*) and glycan biosynthesis (Δ*pglFED*) negative *C. jejuni*.[116] Since both NapA and NapB are experimentally proven glycoproteins (Table 1), this loss of activity may be associated with a requirement for glycosylation in formation of the NapAB complex, in generating a structural conformation that maximizes Nap catalysis, or in providing stability against protein degradation.

The membrane-associated targets of the *pgl N*-glycosylation system are largely functionally uncharacterized 'putative' proteins. The remaining proteins share some degree of sequence identity with well characterized proteins from other organisms, while only a very small number have been experimentally validated. Examination of the relationships between glycoprotein identifications (Table 1) highlight several clusters of potentially functionally related classes of protein, including those involved in antibiotic resistance (all 3 members of the CmeABC antibiotic efflux system are glycosylated, as is CmeE of the CmeDEF efflux system), and antibiotic resistance has been strongly associated with the *pgl* system.[117] Additionally, proteins with putative functions, or sequence similarity to proteins, involved in peptidoglycan biosynthesis, modification and *C. jejuni* helical cell morphology (Pgp1, Pgp2, MreC, PatB [Cj0610c], Cj0843c and the penicillin-binding proteins PbpA and PbpC), LOS and capsular polysaccharide (CPS) transport and assembly (Cj0313/LptG, Cj0648/LptC, Cj1053c, Cj1055c and KpsD), and membrane protein translocation and assembly (SecG, Cj0238, PpiD, YidC, Cj1219c, CgpA) are also enriched in the 78 identified *N*-glycoproteins, however these phenotypes have not yet been tested in *pgl* negative *C. jejuni* or *N*-glycosite mutants.

While several of the above studies have examined phenotypes from the perspective of *pgl* negative and positive *C. jejuni*, comparatively fewer studies have attempted to exploit site-directed mutagenesis to understand the role of the *N*-glycan in individual proteins. This is mainly due to the difficulty in generating site mutants in *C. jejuni*, which is considered poorly tractable and somewhat recalcitrant to molecular biology approaches considered standard in species such as *E. coli*. Despite this, a limited number of studies have been performed.[122–124] *N*-Glycosite point mutants in *cmeA* (CmeA contains 2 glycosites; Table 1) have increased susceptibility to several antimicrobials including bile salts and ciprofloxacin, and are attenuated for chicken colonization.[125] The PglB OST is also capable of transferring the *N*-glycan to itself,[61] however recombinant PglB expressed in otherwise non-glycosylating *E. coli* remains capable of catalyzing the transfer of *N*-glycans to proteins,[62] suggesting PglB does not strictly require modification with the heptasaccharide to maintain function. Plasmid encoded VirB10 (as well as CmeA, discussed above) was reported to require *N*-glycosylation to perform its function (in natural transformation) at wild-type levels.[123] VirB10 is not universally distributed among strains of *C. jejuni*, however observations of impaired natural transformation in the absence of *N*-glycosylation have also been observed in studies of the Cj0011c *N*-glycoprotein.[126] Several confirmed *N*-glycoproteins (including DsbI, JlpA, PEB3, EptC, Cj0268c, Cj0371, Cj0454c, Cj0511c/CtpA, Cj0587 and Pgp1/Pgp2) have been associated with host colonization;[127–134] however, these focused studies of individual glycoproteins have only rarely attempted to provide evidence of a contribution from the *N*-glycan, rather than testing gene-specific deletion mutants. *In vitro* expression and functional analysis of *C. jejuni N*-glycoproteins in non-*pgl*-containing *E. coli* suggest that *N*-glycosylation is not required for the function of a number of glycoproteins,[128,130,135,136] however, without site mutants or comparative expression in *pgl*-positive expression systems, it is not possible to compare the functional efficiency of these proteins when glycosylated.

While evidence that *C. jejuni* protein *N*-glycosylation occurs on folded substrates indicates that the modification is not a driver of protein folding, there is a mounting body of evidence to suggest that the *N*-glycan may be important for protein stability. Mansell *et al.* demonstrated that the glycoproteins PEB3, CjaA and PatB/Cj0610c displayed differences in protein stability in an *N*-glycosylation competent, *pgl* system-containing *E. coli*.[137] These proteins also showed altered folding when glycosylated, further supporting the JlpA evidence that indicates glycan attachment can alter conformational state.[111] Similarly, Min *et al.* showed an increase in thermostability for recombinant expressed PEB3 engineered to have an additional *N*-glycosylation site in comparison to an unmodified variant.[138] Finally, Alemka *et al.* showed that a *pgl*-negative strain displayed reduced viability when cultured under physiological levels of human- and chicken-derived proteases,[120] which also supports the notion that *N*-glycosylation is involved in conferring protein stability.

Conclusions

N- and *O*-linked glycosylation in *C. jejuni* are fundamental requirements for virulence. Interventions targeting the biosynthesis of unique bacterial sugars may be useful in the future to reduce severity of human infection, and in particular to limit serious immune-mediated complications. Additionally, knowledge of the biochemistry, structural biology and the many peptide targets of these pathways provides a unique opportunity to better understand the functional roles of these PTM in conferring organism-wide phenotypes, and in specific protein functions. The overall lack of data regarding the function of *N*-glycosylation on *C. jejuni* proteins means that the association with virulence remains poorly understood, and could reflect a general requirement for glycosylation in a global, *C. jejuni*-specific process (such as protection against proteolytic degradation) and/or that the effect is protein-specific. For the latter, comprehensive knowledge of glycosylation sites is still required despite our advances in understanding the glycoproteome in

this organism. Therefore, several approaches are needed; (i) a full phenotypic characterization of different *pgl* mutants that are attenuated for virulence, coupled with multi-omics approaches to determine affected pathways; (ii) a comprehensive analysis of occupied and unoccupied *N*-glycosylation sequons, and their occupancy, that can be quantified across many changes in environmental or host-specific conditions to create a knowledge bank of sites suitable for mutational analysis; and (iii) testable hypotheses regarding the role of the *N*-glycan that can be examined by interventional approaches. Ultimately, it remains likely that the *pgl N*-glycosylation system plays a multi-factorial role in *C. jejuni* biology that is imperative in environmental, avian and human niches occupied by the organism.

Conflicts of interest

There are no conflicts to disclose.

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