# The development and application of an *in vitro* model of *Campylobacter jejuni* interaction with host cell receptors

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This thesis is being submitted in partial fulfilment of the requirements of Kingston University for the award of Doctor of Philosophy.

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### Declaration

I declare that the work reported in this thesis is entirely my own and has been carried out at Kingston University, UK.

This thesis has not been submitted, in whole or in part, for any other degree at this or any other University.

Sona Rubinchik

#### Abstract

*Campylobacter jejuni* is the most common cause of acute bacterial gastroenteritis in humans worldwide. Adhesion to the host cells is an important stage in pathogenesis of *C. jejuni* infection. It was hypothesised that some N-linked glycosylated proteins might be involved in bacterial attachment via interaction with lectins located on the surface of host cells. Glycan moieties of such glycoproteins contain terminal *N*acetylgalactoseamine (GalNAc) residues that are specific to soybean agglutinin (SBA) lectins that are analogues of host cell receptors. *C. jejuni* is also known to express capsule, the role of which in adhesion still remains unknown. The main aims of this project were to investigate the putative glycoprotein adhesins of *C. jejuni* and the involvement of capsule in bacterial adhesion.

In this study an *in vitro* assay was developed to assess bacterial adhesion to immobilised analogues of host cell receptors. This assay was used to verify the binding mechanism of *C. jejuni* through competitive inhibition studies, exoglycosidase treatment and site-directed mutagenesis, with the *C. jejuni* strain 11168H and its isogenic mutants. Results obtained in this study demonstrated that PEB3 is one of the cell surface glycoproteins involved in bacterial interaction with an analogue of a host cell receptor and that the presence of capsule reduces bacterial attachment. In addition, it was demonstrated that the presence of the glycoprotein adhesin JlpA is not required for this interaction. It was also shown that the genes involved in capsule and PEB3 adhesin biosynthesis are differentially regulated, suggesting that capsule and adhesins may be expressed at different stages of infection. Based on these results we hypothesise that capsule may be required for preventing the recognition of adhesins by the host immune system at the initial stages of infection. Following this initial evasion of the host immune response, the genes for capsule

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production may be down-regulated, leading to reduction in capsule production and the resulting exposure of cell-surface adhesins and cell surface molecules required for attachment and/or modulation of the host immune response.

Additionally, a recombinant *Escherichia coli* strain expressing lipopolysaccharide (LPS) modified with a *Campylobacter* glycan was shown to inhibit binding of *C. jejuni* cells to SBA lectin. This finding may be used as the basis for the design of novel antibacterials using competitive inhibition as the mechanism of action. Overall, the results of this study will contribute to a better understanding of the pathogenic mechanism of *C. jejuni* infection and will help in the development of inhibitors of bacterial attachment to host cells. This will help to reduce the number of infections caused by *C. jejuni* and therefore reduce healthcare costs worldwide. Prevention of bacterial attachment or competitive inhibition used as a curative measure would therefore be beneficial to those in both developed and developing nations.

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## List of Abbreviations

ABC transporter	ATP-binding cassette transporter
Abs	Antibodies
BLAST	Basic local alignment search tool
BSA	Bovine serum albumin
Вр	Base pairs
СВА	Columbia blood agar
CCV	Campylobacter-containing vacuoles
CDT	Cytolethal distending toxin
c.f.u.	Colony-forming unit
CPS	Capsular polysaccharide
CRDs	Carbohydrate recognition domains
СТ	Cycle threshold
DAB	3,3' Diaminobenzidine
DC	Dendritic cell
dNTPs	Deoxynucleotide triphosphates
DNA	Deoxyribonucleic acid
Fn	Fibronectin
ELISA	Enzyme-linked immunosorbent assay
ERK	Extracellular-regulated kinases
FSBA	Fluorescein-labelled SBA
ETEC	Enterotoxigenic E. coli
GalNAc	N-acetylgalactoseamine
GBS	Guillian-Barre syndrome
GTPases	Guanosine triphosphatases
His-tag	Histidine-tag
HIV	Human immunodeficiency virus
IFN	Interferon
Ig	Immunoglobulin

kDa	KiloDalton
Kb	Kilobase pair
LB	Luria Bertani/Luria broth
LOS	Lipooligosaccharide
LPS	Lipopolysaccharide
MALT	Mucosa-associated lymphoid tissue
MeOPN	6-O-methyl phosphoramidate
МН	Mueller-Hinton
MGL	Macrophage galactose-type lectins
момр	Major outer membrane protein
MUC2	Mucin 2
NF-ĸB	Nuclear factor-kappa B
NOD1	Nucleotide-binding oligomerisation domain-containing protein 1
OD	Optical density
PAMP	Pathogen-associated molecular pattern
PBS	Phosphate-buffered saline
PCR	Polymerase chain reaction
PRR	Pattern-recognition receptor
PVDF	Polyvinylidene fluoride
qPCR	Quantitative polymerase chain reaction
RNA	Ribonucleic acid
SBA	Soybean agglutinin
SD	Standard deviation
SDS PAGE	Sodium dodecyl sulphate polyacrylamide gel electrophoresis
SOC	Super optimal broth with catabolite repress
Spp.	Species
T4SS	Type IV secretion system
TNF	Tumour necrosis factor
TLR	Toll-like receptor
тмв	3,3',5,5' Tetramethylbenzidine

UDP Uridine diphosphate

WT Wild type

#### **CHAPTER 1: Introduction**

A comprehensive background on *Campylobacter jejuni* and a literature review on the topics relevant to this study are presented here.

#### 1.1 An overview of Campylobacter jejuni

C. jejuni is the leading bacterial food-borne pathogen worldwide (Olson et al., 2008; Zilbauer et al., 2008; Young et al., 2007; Allos, 2001). Consumption of contaminated poultry products is considered to be the main source of human infection, which usually manifests as acute gastroenteritis (Young et al., 2007). Even though the majority of cases are self-limited, the infection can be associated with complications such as Guillain-Barre syndrome (GBS) or Miller Fisher syndrome (Allos, 1997; Zilbauer et al., 2007) that may become life-threatening. C. jejuni are slow growing, Gram-negative, microaerophilic, spiral bacilli (1.5-6.0μm by 0.2–0.5 μm) with uni- or bi-polar flagellae and with an optimal growth temperature ranging from 37°C to 42°C, while cell death occurs between 56°C and 57°C (Altekruse et al., 1999; Allos, 2001; Ketley, 1997; Keener et al., 2004). This microorganism is very fastidious and sensitive to unfavourable growth conditions, such as changes in pH, temperature, the level of oxygen (optimal conditions are 5% O<sub>2</sub>, 10% CO<sub>2</sub>, and 85% N<sub>2</sub>) and dehydration (Jackson et al., 2009: He and Chen, 2010; Mihaljevic et al., 2007). Under unfavourable growth conditions (lack of nutrients, suboptimal growth temperature, osmolarity changes and pH). C. jejuni enters a viable, but non-culturable state (Rollins and Colwell, 1986; Jones et al., 1991; Jackson et al. 2009).

#### 1.2 The genus Campylobacter

In 1906, McFadyean and Stockman described new bacteria that were frequently

isolated from the aborted foetuses of ewes (Skirrow, 2006). Smith and Taylor isolated a similar microorganism several years later (Smith and Taylor, 1919). Due to the spiral shape, *Campylobacter* were initially classified as *Vibrio*, however in 1963 the name *Campylobacter* was proposed by Sebald and Veron due to fundamental differences between these and known species of *Vibrio*, such as DNA base composition and fermentative metabolism (On, 2001). *C. jejuni* was first isolated from the stool sample of a patient with diarrhoea in 1968 by Butzler and colleagues (Dekeyser *et al.*, 1972). In the late 1970s selective media for *Campylobacter* were developed that allowed to test stool samples for the presence of the pathogen (Skirrow, 1977). Since that time *Campylobacter* has been recognised as the most common cause of acute bacterial gastroenteritis in both children and adults (Altekruse *et al.*, 1999; Butzler, 2004; Stafford *et al.*, 2007).

At present the genus *Campylobacter* contains 16 species and 6 subspecies, and belongs to the epsilon class of proteobacteria in the order *Campylobacteriales*. This order also includes the genera *Helicobacter* and *Wolinella* (On, 2001; Young *et al.*, 2007).

#### 1.3 C. jejuni genetics and diversity

The genome of *C. jejuni* NCTC11168 was sequenced in 2000 by Parkhill *et al.*, 2000). It has one circular chromosome of 1,641,481 base pairs (bp) with 30.6% G + C content, encoding 1,643 proteins. The genome of *Campylobacter* is also known to have 29 homopolymeric G tracts, which are multiple repetitions of consecutive G residues (Parkhill *et al.*, 2000; Gundoglu *et al.*, 2007). The presence of homopolymeric tracts has the potential to cause phase variation, which may be responsible for the ability of the bacterium to evade immune

response and persist in the host (Young et al., 2007; Karlyshev et al., 2005; Guerry et al., 2002). Genome-wide analysis has revealed that the C. jejuni genome has hypervariable regions, most of which encode proteins required for the synthesis or modification of cell surface structures such as lipooligosaccharides (LOS), capsule and flagellum (Parkhill et al., 2000). The genome-based analysis of different C. jejuni isolates suggests that there is a considerable genetic diversity between strains (Pearson et al., 2003; Poly et al., 2005, Hofreuter et al., 2006). C. jejuni is naturally competent. It is able to uptake naked DNA from the environment and incorporate it into its genome by recombination (Wang and Taylor, 1990). This mechanism allows for the generation of genetic diversity in Campylobacter (Young et al., 2007). Natural transformation is one of the mechanisms of horizontal gene transfer in C. jejuni. It plays an important role in the spread of new factors, such as antibiotic resistance (Jeon et al., 2010). Components of the type II secretion system, LOS biosynthesis as well as N-linked glycosylation are required for natural transformation (Avrain et al., 2004; Bacon et al., 2000; Fry et al., 2000; Larsen et al., 2004).

#### 1.4 Epidemiology

Infection caused by *Campylobacter* is a considerable problem worldwide since it is a major cause of acute bacteria-mediated gastroenteritis (Olsen *et al.*, 2008; Zilbauer *et al.*, 2008; Young *et al.*, 2007). Over the last 25 years there has been an increase in the number of cases of campylobacteriosis in England and Wales, with 65,032 laboratory confirmed cases of *Campylobacter* infection in 2012 alone (Public Health England, 2013; Nichols *et al.*, 2012). It is the most common cause of diarrhoea in these regions. A UK study reported that *Campylobacter* species were the most common bacterial pathogens causing intestinal disease, with around

9.3 cases per 1000 people in 2008–2009 (Tam *et al.*, 2011). According to the UK Food Standards Agency, *Campylobacter* infection affects 300,000 people each year in this country. In 2013, the estimated costs of campylobacteriosis were approximately £900 million (Wearne, 2013).

The number of *Campylobacter* infection cases is increasing in the European Unioin (EU) as well, with 9 million cases a year costing approximately  $\epsilon$ 2.4 billion (EFSA, 2011). In the United States, incidence of *C. jejuni* infection in 2013 was substantially higher than in 2008, increasing from 5,825 to 6,621 laboratory-confirmed cases per 100,000 people (CDC, 2009; CDC, 2014). Incidence of campylobacteriosis has increased over the last few years in the USA, UK and EU, which adds urgency to the need to better understand the pathogenesis of *C. jejuni* infection.

*Campylobacter* is found in a wide range of domestic animals; in particular it colonises the gastrointestinal tract of chickens. Infected poultry is thus considered to be the greatest source of human infection (Friedman *et al.*, 2004; Sheppard *et al.*, 2009; Altekruse *et al.*, 2009; Young *et al.*, 2007). Consumption of undercooked meat (especially poultry), unpasteurised milk, untreated water or cross-contaminated food products are usually the key risk factors associated with campylobacteriosis (Silva *et al.*, 2011).

Although *Campylobacter* species are the most common causes of diarrhoea worldwide, there is a difference in the epidemiology of *Campylobacter* infections in developed and developing countries. In developed countries there are sporadic cases as well as outbreaks of *Campylobacter*, with the majority of cases occurring in summer. Young adults (15–24 years) are found to be more susceptible (Olson *et al.*, 2008; Altekruse *et al.*, 1999; Coker *et al.*, 2002; Nichols *et al.*, 2012; Friedman *et al.*, 2000). In developing countries, infection is more common in

young children due to poor sanitation and close human contact with animals, and tends to be asymptomatic (Ketley, 1997).

#### 1.5 Clinical features and complications of campylobacteriosis

The majority of campylobacteriosis cases are caused by *C. jejuni* and *C. coli* (Lastovica and Skirrow, 2000; Ellis-Iversen *et al.*, 2009). Humans become infected through consumption of contaminated food or drink with symptoms starting after 24–72 hours of exposure to the pathogen. The common manifestation of the disease is acute gastroenteritis with non-specific symptoms such as diarrhoea, fever and abdominal cramps (Blaser, 1997; Allos, 2001). The symptoms last from three to seven days. The outcome of the disease depends on virulence of the strain and host immunity (Zilbauer *et al.*, 2007). Infection caused by the antibiotic-resistant strains leads to more severe clinical outcomes compared with antibiotic-sensitive strains of *C. jejuni* (Helms *et al.*, 2005). Even though in the majority of cases the disease is self-limiting, post-infection complications can be severe, especially in immunocompromised patients (Butzler, 2004).

The *C. jejuni* pathogen is also implicated in the development of musculoskeletal disorders such as reactive arthritis, in which knees and ankles are most affected, and GBS, which is associated with paralysis of cranial and peripheral nerves (Hannu *et al.*, 2004; Hannu *et al.*, 2002; Allos, 1997).

Several weeks after *Campylobacter* gastroenteritis the symptoms of GBS can develop with some cases requiring hospitalisation (Butzler, 2004). However, only approximately one in 1000 infected people is affected by GBS (Guerry and Szymanski *et al.*, 2008). The structural similarity (molecular mimicry) between sialylated surface carbohydrate structures (LOS) of certain *C. jejuni* strains and human ganglioside structures present on the peripheral nerves plays an important role in the development of GBS (Yuki *et al.*, 2004). Molecular mimicry leads to the production of autoreactive antibodies followed by inflammation, tissue damage and temporary infection-associated paralysis (Godschalk *et al.*, 2004; Komagamine and Yuki, 2006; van Doorn *et al.*, 2008). Around 50 to 60% of *C. jejuni* isolates can express sialic acid-containing LOS and these isolates are more invasive compared to strains that express nonsialylated LOS (Godschalk *et al.*, 2004; Louwen *et al.*, 2008). Genes responsible for the synthesis, modification and transfer of sialic acid are found in several LOS classes (A, B, C, M and R), however development of GBS is associated only with LOS class A (Parker *et al.*, 2008). Molecular mimicry can also lead to Miller Fisher Syndrome, which is a milder form of GBS (Ang *et al.*, 2002; Mori *et al.*, 2001) and is associated with LOS class B (Godschalk *et al.*, 2004).

Other complications of campylobacteriosis include intestinal haemorrhages (Chamovitz *et al.*, 1983), toxic megacolon (McKinley *et al.*, 1980) and peritonitis (Lang *et al.*, 2009), although these complications are rare. In some cases irritable bowel syndrome has been reported as a consequence of *C. jejuni* infection (Gradel *et al.*, 2009). Chronic *C. jejuni* infection was also linked to the development of small bowel mucosa-associated lymphoid tissue (MALT) lymphomas, also known as marginal zone lymphomas (Lecuit *et al.*, 2004; Suarez *et al.*, 2006).

#### **1.6 Pathogenesis**

Despite being the most common cause of acute bacterial gastroenteritis, the pathogenic mechanism of *C. jejuni* infection is still not completely understood. The bacteria colonise the distal small intestine and colon and induce local acute inflammatory changes (Ketley, 1997). Similar to other intestinal pathogens, *C. jejuni* adherence and invasion of the gastrointestinal epithelium are considered to

be important events in establishment of the disease (Janssen *et al.*, 2008; Zilbauer *et al.*, 2008). There are several defences that the host uses, including saliva, a mucus layer and peristalsis that intestinal pathogens need to avoid. Thus, to establish the disease, *C. jejuni* resists the peristaltic forces of the small intestine and penetrates the mucus layer in order to reach the underlying epithelium (Figure 1.1).



Figure 1.1. Schematic representation of human intestinal lumen. Campylobacter is able to actively swim through the mucus layer that covers the intestinal epithelium and survive in intestinal crypt. (Diagram adapted from Heikema, 2013)

In order to cross the mucus layer, *C. jejuni* is able to avoid entrapment in the lumenal mucins and the bactericidal effect of antimicrobial peptides (Hansson, 2012; Lievin-Le and Servin, 2006). Mucins are net-like polymers, the major functions of which are to limit bacterial contact with the intestinal epithelium via

entrapment of bacteria and to transport them out of the intestinal tract (Hansson, 2012). However, *Campylobacter* is not trapped in the mucin since it freely moves along the mucus strands, which might be due to its small size, spiral shape and flagella-mediated motility (Lee *et al.*, 1986: McSweegan *et al.*, 1987). Moreover, it was shown that mucin is a strong chemoattractant for *Campylobacter*, and the viscosity of mucin affects the speed and swimming pattern of this bacterium (Hugdahl *et al.*, 1988; Shigematsu *et al.*, 1998). The higher the viscosity of mucin, the faster *C. jejuni* swims in it, and a high viscosity of mucin tends to increase adhesion to and invasion of the epithelial cells *in vitro* (Ferrero and Lee 1988; McSweegan *et al.*, 1987).

#### **1.6.1 Invasion**

As soon as *Campylobacter* penetrates the intestinal mucus, it can multiply and interact with host epithelial cells provoking an inflammatory response that leads to invasion of the cellular barrier (Figure 1.2) (van Putten *et al.*, 2009). Analysis of intestinal biopsies of patients with campylobacteriosis and *in vitro* studies of *C. jejuni* indicate that bacteria are internalised by epithelial cells (van Spreeuwel *et al.*, 1985; Oelschlaeger *et al.*, 1993; Ketley, 1997). Despite research into the process of internalisation of pathogen by host cells, the mechanism remains unclear (Ó Croinin and Backert, 2012).

The majority of studies report that *C. jejuni* enters epithelial cells via local depolymerisation of cortical actin filaments and it forms microtubuli-based projections (Oelschlaeger *et al.*, 1993; Hu and Kopecko, 1999; Kopecko *et al.*, 2001; Monteville *et al.*, 2003; Russell *et al.*, 1994). During contact with the epithelial cell, *C. jejuni* triggers membrane ruffling and invaginations. This process requires involvement of cellular factors such as caveolin-1 and small Rho

guanosine triphosphatases (GTPases) Rac1 and Cdc42, which leads to cytoskeletal rearrangements (Eucker and Konkel, 2012; Krause-Gruszxzynska *et al.*, 2007; Hu *et al.*, 2008). In addition to the actin- and/or microtubule-dependent uptake process, which is very energy consuming, an invasion pathway called subinvasion has been identified (van Alphen *et al.*, 2008). It involves active migration of cells towards the subcellular spaces followed by bacterial entry at the basal cell side. *C. jejuni* is able to disrupt tight junctions between polarised cells and can be actively translocated across the epithelial monolayer, gaining access to the subepithelial tissue (Konkel *et al.*, 1992c; Bras and Ketley, 1999; Grant *et al.*, 1993). In later studies it was identified that *C. jejuni* invades the polarised intestinal cells via the subcellular invasion pathway, thus *C. jejuni* uses an actinand microtubule-independent mechanism in order to invade polarised intestinal epithelial cells and remain alive intracellularly for up to 48 hours (Bouwman *et al.*, 2013). This process is controlled by nutrients and requires functional flagella (van Putten *et al.*, 2009).

In order to penetrate the intestinal barrier via the basolateral membrane, *C. jejuni* may use mucosal M cells (van Alphen *et al.*, 2008), which are specialised epithelial cells that deliver the pathogen to the underlying immune cells (Walker *et al.*, 1988; Sansonetti and Phalipon, 1999). From infected M cells, *C. jejuni* spreads and penetrates the subepithelial layer, and after loss of tight junction integrity go on to invade villus epithelial cells (Kalischuk *et al.*, 2010; Chen *et al.*, 2006).

Following internalisation by epithelial cells, *C. jejuni* remains within a membrane-bound intracellular compartment and rolls along microtubules (Russel *et al.*, 1994; Hu and Kopecko, 1999; Konkel *et al.*, 1992c). *C. jejuni* are encapsulated within endosomal-like compartments called Campylobacter-

containing vacuoles (CCVs) that are able to avoid delivery to lysosomes (Watson and Galain, 2008). Once formed, CCV are transported along microtubules to the Golgi apparatus in the perinuclear region. Invasion from the basolateral surface results in the presence of *C. jejuni* in endolysosomal compartments (Bouwman *et al.*, 2013). Replication of internalised bacterial cells results in premature death of host epithelial cells due to the cytotoxic effects of *C. jejuni* (Konkel *et al.*, 1999; Russell *et al.*, 1993).



**Figure 1.2. Current model of** *C. jejuni* invasion strategies. Followed by initial adhesion, *C. jejuni* enters epithelial cells (1) at the apical side (actin- and/or microtubule-dependent uptake process), where it is survives inside of CCV. (2) Disruption of tight junction between epithelial cells enables migration (3) into subcellular space. (4) Sub-invasion, which is internalisation of the pathogen by epithelial cells at the cell basolateral side. (5) Transcytosis, which is uptake and transport of the pathogen across M cells. CheVAW: chemotaxis proteins CheA, CheV and CheW (van Alphen *et al.*, 2008). (Figure adapted from Jagusztyn-Krynicka *et al.*, 2009).

#### 1.6.2 Host response to infection

Interaction of Campylobacter with host epithelial lining of the gut initiates

appropriate innate immune responses such as the induction of cytokines,

chemokines and antimicrobial peptides (β-defensins) (Eckmann, 2005; Zilbauer et

al., 2005; Hickey et al., 2000).

Pattern recognition receptors (PRRs) on the surface of epithelial cells recognise pathogen-associated molecular patterns (PAMPs) on the surface of the pathogen. This interaction leads to initiation of the innate immune response, which is crucial for subsequent adaptive immune activation and the outcome of the infection (Akira et al., 2006; Sanderson and Walker, 2007; Eckmann, 2005; Boyd et al., 2007). The first PRRs that C. jejuni comes into contact with are Toll-like receptors (TLRs) that play a role in pathogen recognition and detection (Takeda et al., 2003; Young et al., 2007). TLR-5 is involved in flagella recognition and upon initiation of signalling responses within the host cell; gene expression of proinflammatory molecules involved in early host immunity against infection is stimulated (O'Hara and Shanahan, 2006; Gewirtz et al., 2001; Hayashi et al., 2001). LOS and lipoproteins are also implicated in the inflammatory response via activation of TLR2 and TLR4/MD2 (Hu et al., 2006a, 2006b; Zheng et al., 2008). Intracellular PRR nucleotide-binding oligomerisation domain-containing protein 1 (NOD1) is involved in maximal induction of the innate response with C. jejuni (Zilbauer et al., 2007). Infection of epithelial cells by C. jejuni and the presence of cytolethal-distending toxin (CDT) activates the transcription factors nuclear factor-kappa B (NFkB) and activator protein 1 (AP-1), which results in phosphorylation of extracellular signal-regulated kinases (ERK) and p38 mitogenactivated protein (MAP) kinases, which in turn induce interleukin 8 (IL-8) production (MacCallum et al., 2005a; Watson & Galan, 2005; Whitehouse et al., 1998; Lara-Tajero and Galan, 2001, Hickey et al., 2000; Zheng et al., 2008). C. jejuni activation of the innate immune response leads to production of proinflammatory cytokines and chemokines such as IL-1a, IL-1B, IL-2, IL-6 and tumour necrosis factor (TNF)  $\alpha$ , interferon (IFN)  $\gamma$  and neutrophil chemoattractant IL-8 (Hickey et al., 1999; Hickey et al., 2000; Johanesen and Dwinell, 2006; Hu

and Hickey, 2005; Bakheit *et al.*, 2004; Jones, M. *et al.*, 2003). These factors are crucial in promoting tissue damage through recruitment of monocytes and neutrophils, the end result of which is the development of diarrhoea (Al-Banna *et al.*, 2008; MacCallum *et al.*, 2005b; Zilbauer *et al.*, 2008).

#### 1.6.3 Interaction of C. jejuni with professional phagocytes

IL-8 production attracts immune cells such as lymphocytes and neutrophils to the site of inflammation. Interaction of C. jejuni with neutrophils results in the release of reactive oxygen species and, depending on the strain, may lead to bacterial killing (Wooldridge and Ketley, 1997). It is still not clear if C. jejuni is able to survive within professional phagocytes, with some studies reporting internalisation and killing of C. jejuni by monocytes and macrophages (Al-Banna et al., 2008; Iovine et al., 2008; Wassenaar et al., 1997; Wooldridge and Ketley, 1997), whereas other studies report survival and replication of C. jejuni inside monocytes and macrophages, even though CDT-dependent apoptosis can occur (Hickey et al., 2005; Siegesmund et al., 2004). The differences between these results might be attributed to the use of different human macrophages or monocyte-derived macrophages. Another reason for survival of the pathogen inside the monocyte-derived macrophages might be the origin of the cells as monocytes derived from around 10% of donors were not able to kill C. jejuni (Wassenaar et al., 1997). Survival of C. jejuni in murine macrophages for several days was attributed to the production of catalase by the bacterium (Day et al., 2000). Human dendritic cells (DCs) internalise C. jejuni, which induces maturation and cytokine production in these cells as well as a specific cellmediated immune response (Johanesen and Dwinell, 2006; Rathinam et al., 2008; Hu et al., 2006a). DCs are the major antigen-presenting cells in intestinal mucosa

that are involved in both the innate and adaptive immune response, and, being the source of proinflammatory cytokines, they assist in the activation of macrophages and T cells (Medzhitov and Janeway, 1997). It was shown that CD103+ DCs migrate to the intestinal draining lymph nodes where they present antigens to naïve T cells, inducing the primary immune response and differentiation (Schulz *et al.*, 2009).

#### **1.7 Virulence determinants**

Each step in the pathogenesis of *C. jejuni* infection appears to depend upon the expression of a combination of several virulence determinants. Bacterial virulence factors involved in epithelial cell invasion include flagella motility and chemotaxis, surface proteins, protein glycosylation, the presence of capsule and LOS (van Vliet and Ketley, 2001; Young *et al.*, 2007; van Putten *et al.*, 2009).

#### 1.7.1 Flagella and motility

*C. jejuni* has a single flagellum at one or both poles, which plays an important role in virulence of this microorganism. Flagella-mediated motility is very important for colonisation as it helps to overcome peristalsis and enter the mucous layer of intestinal cells (Black *et al.*, 1988; Szymanski *et al.*, 1995; Wassenaar *et al.*, 1993b). The flagella of *C. jejuni* are composed of two flagellin subunits, FlaA and FlaB, which are approximately 59 kDa each and are highly homologous (Guerry *et al.*, 1991; Nuijten, *et al.*, 1990). Different promoters, sigma<sup>28</sup> and sigma<sup>54</sup> regulate the *flaA* and *flaB* expression, though the advantage of differential regulation of expression of these genes is unknown (Hendrixson and DiRita, 2003). Phase variation is observed in the expression of *Campylobacter* flagella, resulting in unstable motility phenotype *in vitro* and *in vivo* (Caldwell *et al.*, 1985;

Hendrixon, 2006; Park et al., 2000). Phase variation occurs through slipped-strand mismatch in homopolymeric tracts, which leads to mutations in the genes involved in regulation and biosynthesis of flagella (flhA, flgS, flgR and mat) (Park et al., 2000; Karlyshev et al., 2002; Hendrixon, 2008). The flaA and flaB genes are both involved in proper flagella function; mutation of the *flaA* gene affects motility more than mutations in *flaB* (Guerry et al., 1991; Wassenaar et al., 1993b). In addition, the *flaA* mutant is not able to invade epithelial cells in vitro due to a truncated flagellum (Wassenaar et al., 1991b; Yao et al., 1994). Both flhA and *flhB* are involved in biofilm formation, whereas mutation of only *flhA* affects auto-agglutination (Golden and Acheson, 2002; Kalmakoff et al., 2006). Glycosylation of the flagellum is required for flagellum formation (Linton et al., 2000: Karlyshev et al., 2002), and glycans of flagella affect flagella-mediated auto-agglutination and micro-colony formation (Guerry et al., 2006). Flagella are also involved in secretion of virulence-associated proteins, such as FlaC, FspA and several invasion antigens. Secreted via the flagella apparatus, FlaC binds to HEp-2 cells and mutation of the *flaC* gene reduces invasion (Song et al., 2004). FspA 2 (which is the variant of FspA) was shown to be able to bind to eukarvotic cells and cause apoptosis of INT 407 cells (Poly et al., 2007). In addition, the synthesis of a set of proteins termed Campylobacter invasive proteins (Cia proteins) might be crucial for internalisation (Konkel et al., 1992a; Konkel et al., 1999). Cia proteins are associated with C. jejuni invasion of INT 407 cells (Konkel, et al., 1999) and are secreted only during the contact of bacterial cells with host cells or in the presence of serum or mucin (Rivera-Amill et al, 2001). Cia proteins were shown to cause host cell membrane ruffling, with subsequent intracellular signal events that promote bacterial uptake (Euker and Konkel, 2012). The involvement of flagella in adhesion is discussed in section

1.8.1.

Motility and chemotaxis have been recognised to play a role in pathogenesis of C. *jejuni* infection. Chemotaxis is the movement of an organism towards or away from a chemical stimulus and it has been shown that non-chemotactic mutants are unable to cause an infection (Takata et al., 1992; Yao et al., 1997), thus chemotaxis is required for the intestinal colonisation of animals. In the study by Hugdahl et al. (1988) it was shown that the major chemoattractants for C. jejuni are mucin and the amino acids serine, proline, aspartate and glutamate. Genome analysis of C. jejuni identified several orthologues of the chemotaxis genes, including cheA, cheW, cheV, cheY, cheR, and cheB (Dasti et al., 2010). A mutant of cheY was shown to be hyperinvasive in cultured cells and CheY was required for directional motility in soft agar (Golden and Acheson, 2002; Yao et al., 1997). The C. *jejuni cheY* mutant was found to be non-chemotactic but with a motile phenotype, and was unable to colonise mice or cause symptoms in infected ferrets (Yao et al., 1997). Additionally, C. jejuni motility was found to be dependent on two energy-taxis proteins CetA and CetB (Hendrixon et al., 2001) that provided energy for motility. However, it was established that only CetA rather than CetB was involved in invasion of human epithelial cells (Elliott and DiRita, 2008).

#### 1.7.2 Cytolethal-distending toxin (CDT)

Similar to other bacterial enteropathogens such as *E. coli*, *Shigella* spp. and *Helicobacter* spp. (Johnson and Lior, 1987; Ocuda *et al.*, 1995; Young *et al.*, 2000), *C. jejuni* secretes CDT, a major virulence factor (Smith and Bayles, 2006). It has three subunits (CdtA, CdtB and CdtC), all of which are required for toxin activity (Lara-Tejero and Galan, 2001). CdtA and CdtC are necessary for binding to host cells (Lee *et al.*, 2003), whereas CdtB affects the nucleus of the cell and
induces arrest in G2 phase causing cell death through DNase activity (Whitehouse *et al.*, 1998; Jain *et al.*, 2008). It was shown that CDT subunits are secreted through outer membrane vesicles into the surrounding environment (Lindmark *et al.*, 2009). Being a membrane-associated protein, CDT stimulates production of IL-8 and activates the pro-inflammatory pathway, which can contribute to inflammatory diarrhoea (Hickey *et al.*, 2000; Zheng *et al.*, 2008). Several studies reported the importance of CDT for intestinal pathogenesis, as CDT affects the invasiveness of *Campylobacter* (Purdy *et al.*, 2000; Jain *et al.*, 2008).

# 1.7.3 Capsule

*C. jejuni* expresses surface-located glycolipids, including capsular polysaccharide (CPS) and lipooligosaccharide (LOS) (Linton *et al.*, 2001), both of which are considered to play a role in epithelial invasion (Bacon *et al.*, 2001; Kanipes *et al.*, 2004). The structures of CPS and LOS are highly variable in different strains as the genes associated with the biosynthesis of both are located in the most variable regions of the genome of *C. jejuni* (Parkhill *et al.*, 2000; Penner and Aspinall, 1997; Parker *et al.*, 2008).

Capsule plays an important role in the pathogenesis of the disease, and the presence of capsule is known to be important for persistence of the organism in the environment (Roberts, 1996). The existence of a capsule in *C. jejuni* was predicted following genome analysis performed by Parkhill and colleagues in 2000 and was confirmed by Karlyshev and colleagues in 2001 using the electron microscope (Parkhill *et al.*, 2000; Karlyshev *et al.*, 2001).

The structure of the capsule of *C. jejuni* 11168 strain contains variable 6-Omethyl phosphoramidate (MeOPN), methyl, ethanolamine and N-glycerol groups (Figure 1.3) (Michael *et al.*, 2002; McNally *et al.*, 2007).

# 6-O-Me-D-*glycero*-α-L-*glc*Hepp 1 ↓ 3 →2)-β-D-Ribf-(1-5)-β-D-GalfNAc-(1-4)-α-GlcpA6(NGro)-(1→

**Figure 1.3.** *C. jejuni* **CPS structure of NCTC 11168.** CPS structure is composed of  $\beta$  -D-Ribose,  $\beta$  -D-Gal/NAc, $\alpha$ -D-GlcpA6(NGro), a glucuronic acid modified with 2-amino-2-deoxyglycerol at C-6, and 6-O-methyl-D-glycero- $\alpha$ -L-gluco-heptopyranose as a side-branch. P, phosphate; Gal, galactose; Gro, glycerol; Me, methyl; Hep, heptose; Rib, ribose; GalNAc, *N*-acetylgalactoseamine; GlcA6, glucuronic acid; NGro, aminoglycerol (Figure adapted from Michael *et al.*, 2002).

Capsule is the major serodeterminant in the Penner serotyping and structural variations of CPSs are attributed to phase variation of expression of capsule and structural genes due to slip strand mispairing and MeOPN modification (Linton et al., 2000; Karlyshev et al., 2000, Karlyshev et al., 2005; Maue et al., 2013). Phase variation results in a mixed population of bacterial cells, some of which do not express capsule at all (Bacon et al., 2001). This has a biological role, as the pathogen can regulate expression of capsule (on or off) during its life cycle. The role of C. jejuni capsule was suggested to enable resistance to hyperosmotic stress, in a study showing that absence of capsule may decrease colonisation under hyperosmotic stress (Cameron et al., 2012). Studies using acapsulated mutants demonstrated the importance of capsule in serum resistance, adhesion and invasion as well as chicken colonisation, and virulence in vivo using a ferret model (Bacon et al, 2001; Jones et al., 2004; Bachtiar et al., 2007). It has been suggested that one of the functions of capsule in other pathogens is resistance to the non-specific and specific host immune response (Finlay and McFadden, 2006; Merino and Tomas, 2001). It was shown that C. jejuni capsule modulates the

immune response, including complement resistance and cytokine induction via NFκB signalling (Keo *et al.*, 2011; Maue *et al.*, 2013).

Capsule may also provide some resistance against ß defensins and lysozyme (Zilbauer *et al.*, 2008). These findings would help to explain how *C. jejuni* is able to colonise the intestinal tracts of animals and humans by evading the host immune response. Overall, capsule plays an important role ensuring *C. jejuni* survival in the environment outside its natural host (Zilbauer *et al.*, 2007; Young *et al.*, 2007). The role of capsule in bacterial adhesion is discussed in section 1.8.3.

# 1.7.4 LOS

As a part of the outer membrane of Gram-negative bacteria, LOS is an important factor in the survival of microorganisms and pathogenesis of the infection (Preston et al., 1996). LOS from C. jejuni consists of covalently bound lipid A and surface-exposed oligosaccharides (Moran, 1997). The structure of LOS is highly variable and capable of mimicking human neuronal gangliosides. Sialylation of C. jejuni LOS is associated with ganglioside mimicry (Heikema et al., 2010; Gilbert et al., 2002). This can induce the production of autoantibodies that cross-react with host ganglioside structures present on human peripheral nerves causing autoimmune diseases (Hughes et al., 1999; Godschalk et al., 2007). This may elicit pathogenic disorders such as GBS, which is characterised by acute neuromuscular paralysis (Ang et al., 2002; Yuki et al., 2004). The phase variation in LOS genes due to presence of homopolymeric tracts was linked to changes in LOS ganglioside mimicry (Guerry et al., 2002; Linton et al., 2000). Genes involved in ganglioside mimicry are highly diverse and interchangeable between strains (Gilbert et al., 2004; Gilbert et al., 2002). Recently, it was identified that C. jejuni with sialylated LOS binds a sialoadhesin, which results in

production of autoantibodies (Louwen *et al.*, 2008; Mortensen *et al.*, 2009; Heikema *et al.*, 2010).

Mutation of genes that are involved in the biosynthesis of LOS results in the decreased ability of cells to adhere and invade INT 407 cells (Fry *et al.*, 2000; Guerry *et al.*, 2002). It was also shown that LOS protects *C. jejuni* from mucosal antimicrobial peptides (Keo *et al.*, 2011).

# 1.7.5 Protein glycosylation

Glycosylation is the most common post-translational modification of proteins, responsible for ensuring the amino acids fold into the correct tertiary structure, resulting in proper function of proteins (Drickamer and Taylor, 1998). There are two types of glycosylation, O-linked and N-linked, both of which are present in C. jejuni. Campylobacter O-linked glycans are highly diverse and characterised by attachment of glycans to the hydroxyl group of serine or threonine residues (Thibault et al., 2001; Logan et al., 2009; Szymanski et al., 2002). In contrast, N-linked glycans are highly conserved and glycans are covalently linked to the amino acid group of asparagine. It was shown that Oglycosylation modifies flagella with pseudaminic acid or legionaminic acid derivatives, rather than sialic acid as it was previously thought (Thibault et al., 2001; Logan et al., 2009; Nothaft et al., 2010). The O-glycosylation locus is highly variable between different strains and consists of around 50 genes in strain NCTC 11168 (Karlyshev et al., 2005). Glycosylation of C. jejuni flagella is an important virulence factor, as mutation of the genes responsible for Oglycosylation leads to reduced adherence to and invasion of epithelial cells and decreased auto-agglutination (Guerry et al., 2006). Recently it was shown that in addition to flagella, major outer membrane protein (MOMP) is also an O-

glycosylated protein, which is considered to be involved in biofilm formation and plays a role in the colonisation of chickens (Mahdavi *et al.*, 2014). These findings confirm the importance of O-linked glycosylation in the pathogenesis of *Campylobacter* infection.

There are around 38 identified N-linked glycoproteins in *C. jejuni* (Young *et al.*, 2002). The N-linked protein glycosylation system is encoded by the *pgl* locus consisting of 11 genes (*pglA-F*, *pglH-K* and *gne*), which is conserved among different *C. jejuni* strains and all N-linked glycoproteins contain the same terminal GalNAc residues (Figure 1.4) (Szymanski *et al.*, 1999; Young *et al.*, 2002).

# $\alpha_{1-4}$ $\alpha_{1-4}$ $\alpha_{1-4}$ $\alpha_{1-3}$ $\beta_{1-1}$ GalNAc $\rightarrow$ GalNAc $\rightarrow$ GalNAc $\rightarrow$ GalNAc $\rightarrow$ Bac $\rightarrow$ Asn $\beta_{1-3}$ Glu

Figure 1.4. C. jejuni N-linked glycan structure. N-linked glycoproteins contain the same terminal GalNAc residues. Bac: bacillosamine, 2,4-diacetamido-2,4,6-trideoxyglucose linked to the asparagine residue in the acceptor sequon. GalNAc, N-acetylgalactoseamine; Glu, glucose; Asn, asparagine.

The assembly of heptasaccharide takes place at the cytoplasmic side of the membrane where UDP-bacillosamine is synthesised from UDP-*N*-acetylglucosamine (GlcNAc) by the modifying enzymes PglD, PglE and PglF (Figure 1.5). This is followed by a sequential addition of GalNAc residues by a series of biochemical reactions catalysed by the glycosyltransferases, PglC, PglA, PglJ, PglH and PglI (Glover *et al.*, 2005; Linton *et al.*, 2005). The ABC transporter PglK translocates the entire heptasaccharide across the membrane to the periplasm (Alaimo *et al.*, 2006; Kelly *et al.*, 2006). At the final stage,

oligosaccharyltransferase PglB catalyses the transfer of the heptasaccharide from the lipid to Asn residues of the D/E-X1- N-X2-S/T, where X1 and X2 are any amino acid except proline (Kowarik *et al.*, 2006).





N-linked glycosylation is confined to a small number of species, among them some *Helicobacter* and *Wolinella* spp (Nothaft and Szymanski, 2010). The function of the N-linked glycosylation system is not completely understood. It plays a role in pathogenesis, as mutations in the *pgl* locus lead to a reduced ability of bacterial cells to bind and invade host epithelial cells, as well as impairment of the successful colonisation of the intestines of chicks (Hendrixson and DiRita, 2004; Karlyshev *et al.*, 2004; Szymanski *et al.*, 2002). Furthermore, loss of N-glycosylation affects transport of iron (Palyada *et al.*, 2004) and DNA uptake by the type IV secretion system (T4SS) (Scott *et al.*, 2011). It was shown that a component of a putative T4SS is modified by N-linked glycosylation and plays a role in protein stability, as unglycosylated proteins are not able to produce stable structures (Larsen *et al.*, 2004).

In addition, the loss of a carbohydrate moiety from glycoproteins due to mutation of the *pgl* genes changes the immunoreactivity (no interaction with antisera or antibodies from human volunteers infected with wild type *C. jejuni*) (Szymanski *et al.*, 1999). This may suggest that heptasaccharide is the main target for antibodies and a primary immunogen. It was also shown that the *pglA* mutant of *C. jejuni* stimulates the production of IL-6 from DC compare to the wild type strain (van Sorge *et al.*, 2009), suggesting that N-linked glycosylation might be involved in modulation of the immune response. In a more recent study, it was indicated that N-glycosylation plays a role in survival and protection of *C. jejuni* against gut proteases (Alemka *et al.*, 2013).

#### 1.8 Factors involved in Campylobacter host cell adhesion

Bacterial adhesion to the surface of host cells is an important step in the pathogenesis of many bacterial infections, which affects bacterial uptake (invasion) and innate immune responses (Kline *et al.*, 2009; Klemm and Schembri, 2000; Pizzaro-Cerda and Cossart, 2006). Adhesion is mediated by specialised surface proteins (adhesins), which recognise and bind to receptors on the host cell surfaces (Niemann *et al.*, 2004). There is a wide range of host cell receptors that adhesins recognise, including membrane-associated proteins and extracellular matrix proteins (such as fibronectin and collagen), surface immunoglobulins, glycoproteins and glycolipids (Wilson *et al.*, 2002). Many bacteria express more than one adhesin on their surface, helping pathogens to adapt to changes in environmental conditions, such as different hosts and host tissues (Gerlach and Hensel, 2007). Following adhesion of the microorganism to

the surface of the host cell, it usually starts multiplying, producing toxins and invading the host cells. This leads to initiation of specific biochemical processes such as activation of host cell signalling cascades (Wilson et al., 2002). In pathogenic bacteria the various types of adhesins have different structures, ranging from simple monomeric proteins to structured polymeric macromolecules (Gerlach and Hensel, 2007). Microbial adhesins can be separated into fimbrial and non-fimbrial. Fimbrial adhesins are hair-like structures protruding from the surface of the bacteria, whereas non-fimbrial adhesins remain close to the surface. forming structures that do not protrude (Wilson et al., 2002; Gerlach and Hensel, 2007). The best-studied fimbria are P pili, type I pili and Afa/Dr adhesins, which are exported by the chaperone/usher pathway, in which a periplasmic chaperone and OM assembly platform (usher) are strictly required for pilus assembly (Sauer et al., 2000). Fimbrial adhesins, in which the fimbrial tip binds to the host cell receptors, are present in E. coli, Vibrio cholerae, Pseudomonas aeruginosa and Neisseria species (Donnenberg, 2000; Merz and So, 2000; Hahn, 1997). Nonfimbrial adhesins usually generate closer contact with the host cell and are present in both Gram-positive and Gram-negative pathogens such as *Staphylococcus* spp., Streptococcus spp., Yersinia spp., enteropathogenic E. coli, Neisseria spp. and mycobacterial pathogens (Joh et al., 1999; Novak and Tuomanen, 1999; Cleary and Cue, 2000; Bermudez and Sangari, 2000; Donnenberg, 2000; Merz and So, 2000). Among non-fimbrial adhesins are autotransporters and outer membrane associated proteins (OMPs). Autotransporter proteins are short monomeric or oligomeric proteins that are exported on the surface of Gram-negative bacteria via a Type V secretion system (Hori and Matsumoto, 2010). An example of monomeric autotransporters is ShdA of Salmonella, which has ability to bind to fibronectin in vitro (Kingsley et al., 2002). Several OMPs have ß-barrel-

containing structures that function as adhesins (Neiman *et al.*, 2004). For example, *E.coli* OmpA is involved in adhesion to the Ecgp receptor on the surface of the human brain microvascular endothelial cells causing meningitides in newborn babies (Prasadarao, 2002; Kim, 2000). Both fimbrial and non-fimbrial adhesins may recognise and bind to proteins such as fibronectin, collagen, elastin, laminin, proteoglyans and fibrinogen on the surface of the host cell (Pizarro-Cerda and Cossart, 2006).

As mentioned previously, the host organism has a number of defence mechanisms such as the presence of saliva, mucous flow and peristalsis that can interfere with adhesion of pathogenic bacteria to host cells. The human intestinal mucous layer is the first barrier that *C. jejuni* must successfully penetrate before adhesion and invasion of host cells. Adhesion of *Campylobacter* is not mediated by fimbria or pili, like in other Gram-negative bacteria such as *E. coli* and *Salmonella* (van der Velden *et al.*, 1998; Nougayrede *et al.*, 2003), and instead there are a number of proteins that serve as adhesion factors.

Identification of the bacterial factors involved in *Campylobacter* interaction with host cells is the subject of much research (Flanagan *et al.*, 2009; Novik *et al.*, 2010; Dasti *et al.*, 2010). Currently, there are several *in vitro* methods available to study adhesion of *C. jejuni* to host cells. Cell association methods are based on the interaction of *C. jejuni* with eukaryotic cell lines *in vitro*. These experiments include the c.f.u.-based adherence assay and experiments using radioactivelylabelled *C. jejuni* cells to infect cultured cells (Backert *et al.*, 2013). However, these methods do not allow direct quantification of extracellular-attached bacteria only, as all cell-associated bacteria including intracellular bacteria are recovered after lysis of cultured cells. The determination of extracellular-attached bacteria is only possible in combination with a gentamicin protection assay (which

determines the amount of intracellular bacteria) (Friis *et al.*, 2005). Another way to identify the number of bacterial cells on the surface of cultured epithelial cells is the use of immunofluorescence microscopy (IFM) (Backert et al, 2013). A review of the literature has shown that use of c.f.u.-based adherence assay combined with an invasion assay is a useful method that characterises adhesiondefective mutants. For example, adhesins such as CadF, FlpA and JlpA were identified or confirmed using this approach (Monteiville *et al.*, 2003; Flanagan *et al.*, 2009; Jin *et al.*, 2001). In addition, the involvement of surface glycoconjugates such as CPS, LOS and N-linked glycoproteins in adhesion was identified using adhesion-defective mutants (using *kpsE* and *kpsM* mutants, *galE* mutant and *pglB* and *pglE* mutants) (Bacon *et al.*, 2007; Fry *et al.*, 2000; Szymanski *et al.*, 2002).

#### 1.8.1 Confirmed protein adhesins

At present several confirmed adhesins in *C. jejuni* such as CadF, FlpA, JlpA, MOMP and FlaA have been described, the data of which are summarised in Table 1.1.

CadF is a 37 kDa outer membrane protein that binds to fibronectin and belongs to the OmpA-like protein family (Konkel *et al.*, 1997; Konkel *et al.*, 2005). In a study by Montewille *et al.* (2003), it was shown that the presence of anti-CadF antibodies inhibits the binding of *C. jejuni* mutant cells to human INT 407 cells by around 50% compared to wild type. Additionally, using a competitive inhibition binding assay with a *C. jejuni* F38011 wild type and F38011cadF mutant, only the F38011 wild type was able to inhibit binding of other wild type strain 81-176 to INT 407 cells (Montewille *et al.*, 2003).

 Table 1.1. Campylobacter protein adhesins with identified host cell receptors<sup>1</sup> (modified from Rubinchik et al., 2012).

Gene name	Product Name	Summary of experimental data	Host cell receptors	Conclusion
cj1478	CadF	Adhesion of F38011/cadF mutant INT 407 cells was reduced (Monteville et al., 2003) Purified CadF from strain F38011adhered to INT 407 cells (Monteville et al., 2003)	Fn	Both mutation and adhesion studies confirm specific interaction of CadF with host cell recentors
cj1279	FlpA	Reduced adhesion of F38011/ <i>flpA</i> mutant to LMH cell line (Flanagan <i>et al.</i> , 2009) Reduced adhesion of of F38011/ <i>flpA</i> mutant to INT 407 cells (Flanagan <i>et al.</i> , 2009) Phenotypic changes were confirmed by complementation studies (Konkel <i>et al.</i> , 2010)	Fn	Specific interaction with host cell receptors present on cells of human and chicken origin
cj0983	JĪpA	Reduced adhesion of TGH9011/ <i>jlpA</i> mutant in strain to HEp-2 cells (Jin <i>et al.</i> , 2001) Adhesion of TGH9011 to HEp-2 cells was reduced in the presence of purified <i>JlpA</i> in a dose-dependent manner (Jin <i>et al.</i> , 2001) No effect of <i>jlpA</i> mutation on adhesion of strain F38011 chicken LMH cells (Flanagan <i>et al.</i> , 2009) No difference in adhesion in strain 81-176 <i>jlpA</i> mutant to T84 cells (Novik <i>et al.</i> , 2010)	Hsp90a	Confirmed adhesin with TGH9011 cells but not with other cells
Cj1339	FlaA	<ul> <li>Purified flagella from strain 81116 adhered to INT 407 cells (McSweegan et al., 1986)</li> <li>Purified flagella did not prevent binding of strain 81116 to INT 407 cells (Wassenaar et al., 1991b)</li> <li>No difference in adhesion of 81116 mutant to INT 407 cells (Grant et al., 1993)</li> <li>Reduced adhesion of mutant in strain 81-176/flaA mutant to INT 407 cells (Yao et al., 1994)</li> <li>Deletion of <i>flaA</i> in strain NCTC 11168 led to significant reduction in binding to BgAg (Mahdavi et al., 2014)</li> </ul>	BgAg	Confirmed interaction of FlaA with BgAg
cj1259	МОМР	Free MOMP inhibited <i>C. jejuni</i> adhesion to INT 407 cells (Moser <i>et al.</i> , 1997) Purified MOMP inhibited binding of NCTC 11168 to H-II glycoconjugate (Mahdavi <i>et al.</i> , 2014) Substitution of MOMP lead to significant reduction in binding to BgAg as well as inhibited binding of <i>C. jejuni</i> cells to Caco-2 cells (Mahdavi <i>et al.</i> , 2014)	BgAg	Confirmed interaction of MOMP with BgAg. Specific interaction with host cell receptors present on cells of human origin and chicken colonisation

'This table lists the genes and products involved in direct interaction with host cells receptors

Fibronectin is a component of the extracellular matrix and has a molecular mass of 250 kDa (Pankov and Yamada, 2002). It has been shown that adhesion of *Campylobacter* to fibronectin is required for maximal adherence and invasion of intestinal epithelial cells (Ziprin *et al.*, 1999; Monteville *et al.*, 2003; Konkel *et al.*, 2005). Fibronectin is also a receptor for another confirmed adhesin, FlpA. Since it is a fibronectin-binding protein, it contains Fn type III domains (Flanagan *et al.*, 2009; Konkel *et al.*, 2010). Mutation of the *flpA* gene affects bacterial ability to colonise chicken intestine and reduces bacterial binding to chicken LMH hepatocellular carcinoma epithelial cells and to human INT 407 cells (Flanagan *et al.*, 2009). In addition, it has been shown that the presence of anti-FlpA specific antibodies inhibits binding of *C. jejuni* cells to host cells in a dose-dependent manner (Konkel *et al.*, 2010). Supported by complementation, these findings confirmed the role of FlpA in adhesion to fibronectin (Flanagan *et al.*, 2009; Konkel *et al.*, 2010).

Another confirmed adhesin is JlpA, which is associated with the outer membrane lipoprotein and has a molecular mass of 42 kDa (Jin et al., 2001). The crystal structure of JlpA reveals protruding flexible surface loops with a wide hydrophobic concave face that is orientated toward the extracellular space (Kawai et al., 2012). Mutation of *jlpA* gene resulted in reduced adherence of Campvlobacter to HEp-2 epithelial cells (Jin et al., 2001). Preincubation of HEp-2 epithelial cells with purified JlpA protein has been shown to inhibit the adhesion of bacterial cells to HEp-2 epithelial cells, and in addition, the presence of JlpAspecific antibodies was demonstrated to inhibit the binding in a dose-dependent manner (Jin et al., 2001). Later it was shown that JlpA binds to heat shock protein 90a (Hsp90a) on the surface of HEp-2 epithelial cells and this binding is inhibited by the presence of geldamicin and/or anti-human Hsp90a antibody (Jin et al., 2003). Interaction of JlpA and Hsp90a triggers the intracellular activation of NFkB and p38 MAP kinase, which suggests JlpA is involved not only in adhesion, but also in the pro-inflammatory immune response of the host (Jin et

al., 2003). However, these results contradict other studies, which have shown that a mutation of the *jlpA* gene did not result in diminished adherence to T84 cells (colonic adenocarcinoma cell line) and the *jlpA* mutant was still able to bind to chicken LMH cells (chicken hepatoma cell line) and subsequently colonise the intestinal tract of chickens (Novik *et al.*, 2010; Flanagan *et al.*, 2009). These conflicting results may suggest that the choice of host cell line is very important in adhesion studies, since only certain host cells are able to produce receptors for this adhesin.

As previously mentioned, several studies have suggested that the flagellum plays a role in the attachment of C. jejuni to host cells (McSweegan and Walker, 1986; Newell et al., 1985; Song et al., 2004). In particular, it was shown that purified flagella specifically bind to INT 407 cells and the presence of intact flagella is important for binding (McSweegan and Walker, 1986). Non-motile flagella adhere better to human epithelial cells in vitro, suggesting that motility might interfere with adhesion (McSweegan and Walker, 1986; Newell et al., 1985). Conversely, incubation of INT 407 cells with purified flagella prior to infection with C. jejuni did not inhibit binding of bacterial cells to human epithelial cells, suggesting that flagella may not have specific adhesive properties (Wassenaar et al., 1991b). In addition, it was also shown that both flagellated and aflagellated C. jejuni 81116 adhere to INT 407 cells (Grant et al., 1993). These data contradict subsequent studies demonstrating that inactivation of a flagellin-encoding gene flaA resulted in a reduction of C. jejuni adhesion to the INT 407 cells (Yao et al., 1994, Yanagawa et al., 1994). Further to this, in a more recent study, it was suggested that flagella are required for adhesion and biofilm formation, as aflagellated mutants could not adhere to coverslips with the same efficiency as wild type cells (Svensson et al., 2014). Flagella may be involved in the initial

steps of adhesion of bacteria to epithelial cells. However, further studies are required to confirm the validity of this finding.

Recently it has been shown that both FlaA and MOMP are BgAg-binding adhesins (Mahdavi *et al.*, 2014). BgAgs are common ABO histo-blood group antigens that are made up of a complex of fucosylated carbohydrates expressed on the surfaces of erythrocytes and gastrointestinal epithelium. BgAgs have also shown to be present in milk, saliva and tears (Hakomori, 1984; Lloyd, 1987). MOMP encoded by the *porA* gene consists of nine antigenically variable external loops and 16–18 membrane strands connected by short periplasmic turns (Zhang *et al.*, 2000). The MOMP is produced in large quantities and is involved in transport of ions across the bacterial cell wall (Goulhen *et al.*, 2004). It was shown that in the presence of free MOMP the adhesion of *C. jejuni* cells to INT 407 cells was partly inhibited, suggesting that MOMP plays a role in adhesion (Moser *et al.*, 1997).

As it was not possible to generate a *porA* mutant previously, the role of MOMP in interaction with host cells could not be confirmed (Flanagan *et al.*, 2009). However, in a very recent study by Mahdavi *et al.* (2014) it was confirmed that MOMP plays a role in adhesion. Furthermore, it was shown that MOMP is an O-linked glycoprotein. Glycosylation of MOMP affects conformation of the protein as well as its ability to bind to BgAg. The involvement of MOMP in adhesion to Caco-2 cells and in chicken intestinal colonisation was demonstrated in addition to its role in the formation of a biofilm and auto-aggregation (Mahdavi *et al.*, 2014).

#### 1.8.2 Putative adhesins

It was suggested that other C. jejuni proteins could be involved in adhesion

(Flanagan *et al.*, 2009; Novik et al., 2010). However the limited number of studies and their contradictory results do not allow final conclusions to be drawn regarding the function of these proteins. They are therefore referred to as 'putative' and are listed in Table 1.2.

Gene	Product Name	Summary of experimental data	Pfam domains	Conclusion
cj1349	Cj1349	Reduced adhesion of F38011/cj1349 mutant to LMH cells (Flanagan <i>et al.</i> , 2009)	Fn-binding domain (FbpA)	Studies with purified protein were not performed. Fibronectin predicted as a
		(Flanagan <i>et al.</i> , 2009)		not confirmed)
cj0628/ cj0629	СарА	Reduced adhesion of NCTC11168H/ <i>capA</i> mutant to Caco-2 cells (Ashgar, <i>et al.</i> , 2007) Reduced adhesion of capA mutant in	None	No complementation studies to confirm the results. Studies with purified protein were not performed
		(Flanagan et al., 2009)		
cj0091	Cj0091	Reduced adhesion of NCTC 11168/cj0091 mutant to INT 407 cells (Oakland et al., 2011)	None	Studies with purified protein were not performed
cj0268c	Cj0268c	Reduced adhesion of cj0268c mutant to Caco-2 cells (Tareen <i>et al.</i> , 2013) Phenotypic changes were confirmed by complementation studies (Tareen	None	Studies with purified protein were not performed and no information regarding receptors
		et al., 2013)		
<i>cj0588</i>	ПуА	keduced adhesion of 20086 mutant in strains 81-176 and 81116 to Caco-2 cells (Salamaszynska-Guz <i>et al.</i> , 2008)	rtsj-like methyltransferase	studies to confirm the results
		Purified TlyA protein from 81-176 confirmed interaction of it with Caco- 2 cells (Salamaszynska-Guz <i>et al.</i> , 2008)		
cj0921	PEB1	Purified PEB1 from strain 85H binds to HeLa cells (Kervella <i>et al.</i> , 1993) Reduced adhesion of <i>peb1A</i> mutant in strain 81-176 using HeLa cells (Pei <i>et al.</i> , 1998)	Bacterial extra- cellular solute- binding proteins, family 3	Contradictory data
		No difference in adhesion of peb1A mutant of strain F38011 mutant to LMH line (Flanagan <i>et al.</i> , 2009)		
		No difference in adhesion in strain 81- 176 peb1A mutant to T84 line (Novik et al., 2010)		
cj0289	PEB3	Major antigenic protein (Pei et al, 1991) Transporter protein (Min et al. 2009)	Bacterial extra- cellular solute- binding protein	Original data on its role as an adhesin not confirmed
		Cell surface located glycoprotein (Linton <i>et al.</i> , 2002)		

**Table 1.2.** Campylobacter adhesion-related proteins<sup>1</sup> (modified from Rubinchik et al., 2012).

cj0596	PEB4	Purified PEB4 from strain 85H did not bind to HeLa cells (Kervella <i>et al.</i> , 1993) Reduced adhesion of <i>peb4</i> mutant of strain NCTC11168 to INT 407 cells (Asakura <i>et al.</i> , 2007) Pleiotropic effect of mutation (severe changes in outer membrane profile – possible affect on adhesins) (Rathbun <i>et al.</i> , 2009)	Peptidyl prolyl isomerase	Contradictory data/ Complementation studies did not confirm changes in phenotype. Possible periplasmic chaperone
cj1677/ cj1678	СарВ	Expression not detected (Ashgar et al., 2007)	None	No experimental data available (no cell binding assays were performed). Putative adhesin (high level of similarity to CapA is expressed as a single polypeptide)
cj0737	P95	After incubation of <i>C. jejuni</i> 85H with Caco-2 cells, significant fluorescent signal was obtained, indicating that this strain is able to efficiently bind cultured cells (Kelle <i>et al.</i> , 1998)	Haemagglutination activity domain	No mutagenesis or adhesion studies were performed to confirm a proposed function of P95 as an adhesin

<sup>1</sup> This table lists proteins either involved in interaction with host cell receptors indirectly or those whose function as adhesins is not conclusive (e.g. insufficient experimental evidence or contradictory data). Host cell receptors for these proteins are not known.

Among identified putative adhesins is Cj1349, which is a potential Fn/fibrinogenbinding protein. Mutation of *cj1349c* resulted in reduced adhesion of bacterial cells to chicken LMH cells by 14%, however this mutation did not affect chicken colonisation by *C. jejuni* (Flanagan *et al.*, 2009). Due to the absence of complementation studies and studies with purified protein this protein is considered to be putative adhesin.

CapA is a cell surface lipoprotein autotransporter reported to be involved in *C. jejuni* adherence. A mutation of the *capA* gene resulted in a reduced ability to adhere to and invade human Caco-2 and chicken intestinal cells, and also caused low colonisation efficiency in a chick model (Ashgar *et al.*, 2007). In another study, mutation of *capA* did not reduce the capacity of mutant to colonise chicks, but showed decreased adherence to chicken epithelial cells *in vitro* (Flanagan *et al.*, 2009).

In addition to *capA*, another gene (*capB*) coding for a putative autotransporter was identified in the genome of *C. jejuni*. CapB protein might also be considered a putative adhesin as it has high amino acid sequence similarity to CapA and also contains two pairs of open reading frames (ORFs). However, while CapA was shown to interact with host cells, expression of CapB was not detected (Ashgar *et al.*, 2007).

Another protein found to be involved in *Campylobacter* adhesion is lipoprotein Cj0091, which mediates binding of *C. jejuni* to INT 407 cells and plays a role in chicken colonisation (Oakland *et al.*, 2011). As *cj0091* mutation affects colonisation in the early stages of the infection, there is a possibility that Cj0091 may only be involved in initial adherence.

Cj0268c is annotated as a putative transmembrane protein and shown to be involved in adhesion to and invasion of host cell (Novik *et al.*, 2010; Tareen *et al.*, 2013). *Cj0268c* mutants had a reduced ability to adhere to Caco-2 cells by 40%, and complementation of this gene restored binding ability to wild type adhesion levels (Tareen *et al.*, 2013). Since detailed characterisation of the protein was not performed and there is no information available regarding receptors on host cells, this protein is regarded as a putative adhesin.

Another protein that may be involved in *C. jejuni* adhesion is homologous to bacterial haemolysin TlyA (Salamaszynska-Guz and Klimuszko, 2008). In *H. pylori*, TlyA is a bifunctional protein; mutation of *tlyA* results in low haemolytic activity and decreased adhesion to gastric epithelial cells (Martino *et al.*, 2001). Recombinant TlyA expressed in *C. jejuni* 81-176, was found to be responsible for the interaction with Caco-2 cells. In addition, the ability of the *tlyA* mutant to adhere to Caco-2 cells was two-fold lower when compared to wild type (Salamaszynska-Guz and Klimuszko, 2008).

In 1989 Fauchere et al. characterised two proteins that bind to HeLa cells, which were later identified as major antigenic proteins of C. jejuni; PEB1 and PEB4 (Fauchere et al., 1989; Pei et al., 1991; Kervella et al., 1993). Using acidic glycine extracts of whole C. jejuni cells and gel filtration chromatography, Pei et al. identified four cell-binding major antigenic proteins (PEB1 to PEB4) that might be suitable for vaccine development and serological detection (Pei et al., 1991), PEB1, also known as PEB1a, is encoded by the *peb1A* gene and plays an important role in adherence and host colonisation (Pei et al., 1993; Pei et al., 1998). PEB1 is a surface exposed and periplasmic (partially exposed and partially periplamic) component of an aspartate/glutamate ABC transporter (Leon-Kempis et al., 2006). PEB1 is a major periplasmic protein required for the uptake of important in vivo carbon sources such as aspartate and glutamate (Leon-Kempis et al., 2006). Mutation of peb1A resulted in 50- to 100-fold reduction of C. jejuni adhesion to HeLa cells and also showed a reduction in the ability of bacterial cells to colonise intestinal cells of rats (Pei et al., 1998). However, peb1A mutation showed no effect on the ability of C. jejuni to adhere to cultured epithelial cells and to chicken LMH cells, as was reported in more recent studies by Novik et al. (2010) and Flanagan et al. (2009). Although the results on the role of PEB1 in adhesion were contradictory, it was found that it is involved in binding and transport of L-aspartate and L-glutamate (Leon-Kempis et al., 2006). Further studies are required to verify if this protein has a dual function.

The role of PEB4 (another major antigenic protein of *C. jejuni*) in adhesion was studied using a *peb4* mutant, which demonstrated reduced binding of bacterial cells to INT 407 cells, as well as a reduction in biofilm formation and colonisation of mice (Asakura *et al.*, 2007). It was also shown that *peb4* expression is induced at 37°C, demonstrating that it would be possible for it to be expressed in humans

(Rathbun *et al.*, 2009). However, no complementation studies were conducted to confirm the adhesin function of PEB4, thus it is still unclear whether this protein is an adhesin.

Another putative adhesin that was identified at the same time as PEB1 and PEB4 is PEB3 protein (Pei *et al.*, 1991). PEB3 is highly immunogenic and reactive with convalescent sera from people suffering with *C. jejuni* infection (Pei *et al.*, 1991). In a study designed to identify putative glycoproteins of *C. jejuni*, Linton *et al.* identified that soybean agglutinin (SBA) binds multiple *C. jejuni* proteins on Western blot using whole cell lysates (Linton *et al.*, 2002). In the same study, SBA was used to selectively purify putative glycoproteins that were identified as PEB3 and CgpA. Proteins were purified using a lectin-based affinity purification method and identified by mass spectrometry (Linton *et al.*, 2002). Later, Young *et al.*, using mass spectrometry and nuclear magnetic resonance spectroscopy, identified more than 30 proteins that are also N-linked glycosylated (Young *et al.*, 2002).

PEB3 is considered to be one of the most abundant glycoproteins that is glycosylated at Asn 90, and interacts with soybean agglutinin (SBA) *in vitro* due to the presence of  $\alpha$ -linked GalNAc residues (Linton *et al.*, 2002; Rangarajan *et al.*, 2007). Rangarajan *et al.* (2007) reported that PEB3 is an adhesin based on personal communication, however there is no published data available supporting this suggestion. The crystal structure of PEB3 was described as a class II periplasmic binding protein with two domains and a citrate ligand-binding site between them (Figure 1. 6). Additionally, the findings of Min *et al.* (2009) indicate that one of the biological roles of PEB3 is to transport 3phosphoglycerate, suggesting a possible dual function of this protein. The amino acid sequence of PEB3 protein revealed 54% identity with AcfC (99%

coverage), an accessory colonisation factor of *V. cholera* (Peterson and Mekalanos, 1988) and 56% sequence identity with the Paa protein (97% coverage) of *E. coli* (Batisson *et al.*, 2003). Although the function of AcfC protein still remains unknown, it was shown it is necessary for efficient colonisation by *V. cholera* (Peterson and Mekalanos, 1988). Paa protein was suggested to play the role of an adhesin based on its cell surface location and the presence of a sulphitebinding domain (Batisson *et al.*, 2003). However, this hypothesis has not been supported by any experimental data. The *paa* mutant of *E. coli* was shown to be unable to bind to microvilli of intestinal epithelial cells (Batisson *et al.*, 2003).



Figure 1.6. Crystal structure of *Campylobacter jejuni* PEB3 protein. The PEB3 monomer (A) and PEB3 dimer (B) with citrate ligands and the sequents to which Nlinked glycans can be attached shown with arrows. (Adapted from Rangarajan *et al.*, 2007).

# 1.8.3 The role of capsule in Campylobacter adhesion

The role of the capsule in bacterial adhesion depends on the nature of the bacterial

pathogen, as well as structural features of adhesins. For example, the F1 capsule

of Yersinia pestis prevents fimbrial adhesins from interaction with host cell

receptors (Runco *et al.*, 2008). Additionally, it was shown that capsule of *E. coli* and *Klebsiella pneumonia* shields the function of short bacterial adhesins, such as Ag43 and AIDA-I (Schembri *et al.*, 2004). While the production of a capsule by *Neisseria meningitides* does not have any effect on bacterial attachment mediated by PilC1 adhesin (Deghmane *et al.*, 2002), the Opc adhesin was reported to be active only in acapsulated strains (Virji *et al.*, 1995).

CPS of C. jejuni is a known virulence factor that may be involved in attachment, since the adhesion of capsule-deficient mutants to host cells in vitro was reduced (Bacon et al., 2001; Bachtiar et al., 2007). Inactivation of kpsM gene in strains 81-176 led to a two-fold decrease in adhesion to INT 407 cells and 10-fold less invasive ability when compared to the wild type strain. Complementation studies have shown only partial restoration of adhesive properties (Bacon et al., 2001). Similar results were obtained with kpsE mutants of strain 81116, demonstrating a significant decrease in adhesion and two-fold decrease in invasion of INT 407 cells (Bachtiar et al., 2007). Although this data may suggest the involvement of capsule in adhesion, these findings have not been confirmed by complementation. In contrast to these findings, other studies identified that a kpsM mutant in strain 11168H showed a higher level of adhesion to Caco-2 cells (Karlyshev et al., 2008), suggesting a masking effect of capsule. The difference between the bacterial strains and tissue cell lines, as well as a discrepancy in assay conditions may explain contradictory results.

#### 1.8.4 Campylobacter adhesion involving lectin-glycan interaction

As noted earlier, in the process of adhesion, specific structures on the bacterial cell surface interact with host cell receptors. Evidence shows that glycans of different pathogens such as viruses, bacteria, parasites and fungi can bind host

lectins and initiate the stimulation of an immune response (van Kooyk and Rabinovich, 2008; Vasta *et al.*, 2009). Glycans expressed on the surface of pathogens can be either similar to host glycans or can be completely unique and not expressed in the host (Garcia-Vallejo and van Kooyk, 2009).

C. *jejuni* has the ability to recognise and interact with multiple carbohydrate structures, such as mannose, N-acetylneuramic acid, galactose and fucose (Day et al., 2009). Until recently, it was believed that C. jejuni could not metabolise carbohydrates, and only uses amino acids as a source of energy (Guccione et al., 2008). However, several strains of C. jejuni use L-fucose for growth due to the presence of a gene operon that is upregulated in the presence of fucose or mucin (Muraoka and Zhang, 2011; Stahl et al., 2011). However, due to the lack of 6phosphofructokinase, which is a key enzyme in energy metabolism, the ability of Campylobacter to use carbohydrates as a source of energy for growth is limited (Velayudhan and Kelly, 2002). Observed interaction of Campylobacter with host carbohydrates may be important in adhesion as well as in host defence mechanisms. For example, the presence of fucosylated glycans in human milk is considered to prevent infection in infants (Newburg et al., 2005). Additionally, binding of C. jejuni to mucin and Lewis antigen present in human breast milk was previously reported (McAuley et al., 2007; Morrow et al., 2004; Morrow et al., 2005).

Mannose derived from the cell wall of *Candida albicans* inhibited the *in vitro* binding of *Salmonella typhimurium* to intestinal cells of day-old chickens (Oyofo *et al.*, 1989). Inhibition of binding of *C. jejuni* to Caco-2 cells in the presence of free mannose was later reported (Russell and Blake, 1994). Direct binding of *C. jejuni* to mannose was confirmed in a study by Day *et al.* (2009). This interaction was specific, as binding of *C. jejuni* to Caco-2 cells was inhibited in the presence

of the Man-specific lectin ConA. Being a component of N-glycan structures of host cells, mannose is used by many bacteria for adherence (Parry *et al.*, 2006). For example, uropathogenic *E. coli* binds to host tissues using Man-specific lectin FimH (Thomas *et al.*, 2004; Thomas *et al.*, 2002).

C. jejuni was shown to be attracted to mucin in the mucous layer of the intestine (Hugdahl et al., 1988; McAuley et al., 2007; Tu et al., 2008). One of the mannosylated and sialylated structures that C. jejuni initially interacts with in the intestinal tissue is the cell surface-bound mucin receptor MUC1 (McAuley et al., 2007; Linden et al., 2008). In vivo studies have demonstrated that C. jejuni gastric colonisation was partially decreased by MUC1. Furthermore, membrane-bound MUC1 was shown to protect epithelial cells from CDT in vitro (Linden et al., 2008a,b).

Another glycan that is recognised by *C. jejuni* is Le antigen, which is a fucosylated glycan present on mucins of the human intestine (Hanisch, 2001). *C. jejuni* binding to intestinal cells was inhibited in the presence of free fucose, indicating the interaction of this oligosaccharide with the bacterium is specific (Cinco *et al.*, 1984). Different pathogens bind to fucosylated glycans of the host cells. For example, *P. aeruginosa* Fuc-specific lectin binds to the fucosylated mucosal layer of airways, facilitating colonisation (Rhim *et al.*, 2001). Fucose, a prominent component of mucin, was shown to act as a chemoattractant for *C. jejuni* (Hugdahl *et al.*, 1988; Tu *et al.*, 2008).

Human milk was reported to prevent infection of HEp-2 cells, due to the presence of fucosylated oligosaccharide fractions (Ruiz-Palacios *et al.*, 2003). In the same study, fucosylated oligosaccharide inhibited colonisation of mice by *Campylobacter*. This interaction was due to the binding of *C. jejuni* to difucosylated terminal Le<sup>b</sup> structures and 2' fucosyllactose that is present in

human milk glycoproteins (Morrow et al., 2004). It was shown that human breast milk fucosylated glycoproteins inhibit colonisation by C. *jejuni*, indicating that C. *ieiuni* interacts with the fucosylated glycoporoteins of host tissues (Morrow *et al.*, 2005). C. jejuni may recognise fucosylated and terminal galactose structures of another mucin MUC2, which is the most abundant gel-forming mucin (Day et al., 2012). Day et al. (2009) confirmed the specificity of binding to fucose and galactose by inhibition of attachment of C. jejuni to Caco-2 cells using Fucspecific lectin ulex europaeus agglutinin 1 (UEA-1; terminal alfa 1-2 Fuc binding lectin) and galactose-recognising lectin erythrina cristagalli agglutinin (ECA). Additionally, the interaction of C. jejuni with BgAgs, which are fucosylated carbohydrates expressed on the surfaces of erythrocytes and gastrointestinal epithelium, was recently reported (Mahdavi et al., 2014). Day et al. (2009) hypothesised that interaction of Campylobacter with mannose and/or Nacetylneuraminic acid may be important in initial contact with host cells, followed by interaction with fucose and terminal galactose resulting in persistent infection. These findings highlight the importance of C. jejuni interaction with glycans of the host cells. However, the nature of recognition of the host glycans by C. jejuni is still not completely understood.

In contrast, as noted earlier, *C. jejuni* has its own surface-exposed glycan structures, such as N-linked glycoproteins and LOS, which may be involved in the recognition and interaction of glycan binding to receptors of host cells. The involvement of LOS in adhesion was shown in other pathogens (Abu-Lail and Camesano, 2003). Thus, this interaction may mediate binding of bacterial carbohydrates to host cell protein receptors, such as integrins (Makihira *et al.*, 2002; Isberg and Leong, 1990; Wong and Isberg, 2005).

Carbohydrate recognition is important for the proper function of the innate

immune system of the host. Various classes of glycan-binding receptors (lectins) are expressed on the surface of immune cells (Vasta, 2009; van Kooyk and Rabinovich, 2008). Glycan-binding lectins include C-type lectins, galectins, sialic acid-binding immunoglobulin-like lectins (siglecs), surfactant proteins A and D, nonintegrins (DC-SING and L-SING) and ficolin, and they possess carbohydrate recognition domains (CRDs) specific to oligosaccharide moieties present on CPS, LPS and glycoproteins of microbial pathogens (Mitchell *et al.*, 2001; Holmskov *et al.*, 2003; Alvarez *et al.*, 2002). N-linked glycans found on viruses such as the Nipah virus, which causes severe encephalitis, and HIV-1, interact with galectins (Levroney *et al.*, 2005; Rabinovitch and Toscano, 2009). An interaction of galectins with the surface glycans of *Trypanosoma cruzi* and *Leishmania* parasites has also been reported (Vasta, 2009). Another glycan structure that interacts with galectins is LacdiNAc (GalNac  $\beta$ 1-4 GlcNAc) of *Shistasoma mansoni* (van der Berg *et al.*, 2004).

A human lectin intelectin has been shown to interact with D-galactofuranosyl residues of pathogenic Gram-positive bacterial species *Nocardia rubra* (Tsuji *et al.*, 2001). Interaction of human lectins with surface glycans of pathogenic microorganisms such as *K. pneumoniae*, *Helicobacter pylori*, *Streptococcus pneumoniae*, and *Neisseria gonorrhoeae* was earlier summarised (Vasta, 2009). It is possible that similar lectin-glycan interactions may take place during interaction of *Campylobacter* with host cells, as these bacteria are known to express a diverse range of cell-surface glycans (LOS, LPS, CPS and O- and N-linked glycoproteins) (Guerry and Szymanski, 2008). *C. jejuni* glycan structures are important virulence factors that are involved in adhesion and invasion of host cells, as well as in evasion of the immune system (Guerry *et al.*, 2002; Bacon *et al.*, 2001; Logan *et al.*, 2002, Guerry *et al.*, 2007). O-linked and N-linked

glycosylation of proteins have been identified as important processes affecting *Campylobacter* virulence (Logan *et al.*, 2002, Guerry *et al.*, 2007). Although it remains unknown whether the N-linked glycoproteins are required for adhesion, there is some evidence suggesting that they may modulate the host's immune response (Iovine *et al.*, 2008, van Sorge *et al.*, 2009). The interaction between *Campylobacter* glycans and carbohydrate-binding domains of the host may be important in immune evasion of *C. jejuni* (Jarvis and Vedros, 1987; Khatua *et al.*, 2010). The interaction of *C. jejuni* N-linked glycoproteins with C-type lectins of macrophage galactose-type lectins (MGL) specific to GalNAc-terminated glycans was reported by van Sorge *et al.* (2009).

C-type lectins are calcium-dependent carbohydrate-binding proteins that can be specific either to mannose (Man)-specific or galactose (Gal) (Weis *et al.*, 1998). The majority of C-type lectins have more than one CRD and are membraneassociated receptors that are recognised by different pathogens (Drickamer, 1999). C-type lectins are also involved in antigen uptake, signalling and adhesion (Geijtenbeek *et al.*, 2002).

Many C-type lectins are expressed on macrophages and DC, and it was shown that maturation of DC results in a loss of C-type lectin expression (Figdor *et al.*, 2002). Pathogens that target C-type lectins modulate DC response, which is the mechanism responsible for the evasion of host immune response. For example, interaction of cell-surface glycans of *Mycobacterium tuberculosis* with C-type lectins expressed on DC induces signalling that leads to the production of antiinflammatory cytokines such as IL-10, which in turn inhibits maturation of DC, further assisting bacteria to evade the host immune response (Lugo-Villarino *et al.*, 2011).

Surface-exposed siglecs are a family of type I membrane proteins that are

expressed on immune cells and involved in immune recognition of bacteria and viruses (Crocker et al., 2007; Jones, C. et al., 2003; Rempel et al., 2008; Vanserheijden et al., 2003). More than 20 types of pathogenic microorganism are able to incorporate host sialic acids into their own glycoconjugates, among them Neisseria meningitides, T. cruzi and Streptococcus group B (Dam and Brewer, 2010). It is apparent that sialylation is important in the survival of the pathogen within the host, as it is involved in molecular mimicry, important in evasion of an immune response. Sialic acid-containing LOS of Campylobacter HS-19 strain has been shown to interact specifically with Siglec-7 on monocytes and natural killer cells (Avril et al., 2006). Additionally, specific binding of GBS-related C. jejuni strains to Siglec-1 has been demonstrated (Heikema et al., 2010). Campylobacter may benefit from expression of sialyated LOS as it may modulate the host innate immune response (Bax et al., 2011). Similarly, Gram-negative pathogens such as N. meningitidis and P. aeruginosa demonstrate a greater ability to evade the immune system due to the variability of their surface antigenic structures such as LOS and glycoproteins (Jarvis and Vedros, 1987; Khatua et al., 2010).

# 1.9 Management and control of Campylobacter infection

Control measures are important for the reduction of transmission of *Campylobacter* infection. Since *Campylobacter* is considered to be a food-borne pathogen of animal origin and humans become infected through consumption of contaminated food, it is suggested that strategies should focus on public education, personal hygiene and knowledge of potential cross-contamination in the kitchen and the importance of proper cooking of meat (Allos, 2001; Crushell *et al.*, 2004; Havelaar *et al.*, 2007).

# **1.9.1 Reduction strategies**

As contaminated poultry meat represents the main source of Campylobacter infections in humans, the reduction of this pathogen in broiler chickens should be one of the strategies to reduce incidence. Considerable risk reduction may be obtained by freezing carcasses for 2-3 weeks (Sting et al., 2012). However, the increase in demand for fresh meat enforces implementation of other strategies. The use of *Campylobacter*-specific bacteriophages may potentially decrease bacterial contamination in poultry (Connerton et al., 2011; Carrillo et al., 2005). However, this treatment has shown to be effective only for a short period of time due to the development of resistance to bacteriophages (Loc et al., 2005; Wagenaar et al., 2005). In order to be effective, the use of bacteriophage treatment should commence several days prior to slaughter (Jeon et al., 2010). One of the control strategies to reduce incidences of Campylobacter infection is called scheduled slaughter, which aims to identify colonised flocks before slaughter and keep them separate from non-colonised flocks, thus reducing the risk of contamination during slaughter as well as implementing decontamination treatment of colonised batches (Wagenaar et al., 2005).

Another approach for controlling incidences of *Campylobacter* infection is the competitive expulsion concept, which is based on inhibiting *Campylobacter* colonisation by immediate feeding of freshly hatched chicks with products that contain microbiota from adult chickens (Barrow and Page, 2000; Zhang *et al.*, 2007). *Salmonella* infection has been successfully prevented using this method, however due to the lack of standardisation and safety this method has not been effective in *Campylobacter* (Laisney *et al.*, 2004; Wagner, 2006).

It is known that contamination of meat occurs during the slaughtering process, thus prevention of faecal contamination from the poultry itself should be

considered in reducing the spread of *Campylobacter* to food (Rosenquist *et al.*, 2006). One of the approaches, which have already been implemented, is a short-term feed withdrawal prior to slaughter in order to reduce the content of the intestine (Warris *et al.*, 2004). In general, prevention of faecal contamination during slaughter process should be one of the main strategies to reduce contamination of broiler carcasses by *Campylobacter* (Sting *et al.*, 2012).

# 1.9.2 Chemotherapy

As *Campylobacter* gastroenteritis is usually a self-limiting disease, antibiotics are rarely prescribed, and so maintenance of electrolyte balance and replacement of fluid are the common therapies (Altekruse *et al.*, 1999). However, in immunocompromised patients or in patients with severe enteritis, bacteraemia or extraintestinal complications, the use of antibiotics is necessary (Zilbauer *et al.*, 2008; Blaser and Engberg, 2008).

The first choice of antimicrobials in confirmed cases of *Campylobacter* infection is erythromycin, which is a macrolide antibiotic (Zilbauer *et al.*, 2007). For cases of enteritis of unknown origin or travellers' diarrhoea, fluoroquinolone (e.g. ciprofloxacin) is used (Zilbauer *et al.*, 2007). However, an increase in resistance of *Campylobacter* to both erythromycin and ciprofloxacin has been reported (Engberg *et al.*, 2001; Blaser and Engberg, 2008). Chloramphenicol can be considered when antibiotic resistance arises. In the case of serious systemic infection patients should be treated with aminoglycosides (Blaser and Engberg, 2008). Due to the increase in antibiotic resistance, current research should focus on development of alternative and novel therapeutics for both treatment and prophylaxis, such as development of vaccines and inhibitors of attachment.

#### 1.9.3 Vaccines

The use of vaccines in poultry would prevent or reduce colonisation in chickens and thereby reduce the number of infections in humans (Neal-McKinney et al., 2014). In addition to this, it may be used as a prophylaxis measure for travellers or immunocompromised patients. However there is currently no effective Campylobacter vaccine available due to challenges in vaccine development. One attempt using a viable, non-colonising strain of C. *jejuni* for vaccination of chickens did not provide any protection (Ziprin et al., 2002). Additionally, it was demonstrated that the use of whole-cell vaccines only provided partial protection in chickens (de Zoete et al., 2007; Noor et al., 1995; Rice et al., 1997). The use of an inactivated bacterial preparation on a ferret model produced similar results (Burr et al., 2005). Due to the high level of genetic and antigenic diversity of Campylobacter strains, implementation of such a vaccine for poultry stock is challenging, as poultry becomes colonised with a number of different strains of Campylobacter during their lifetime (Jagusztyn-Krynicka et al., 2009). In humans, the use of inactivated or attenuated Campylobacter vaccines causes the potential risk of complications such as GBS or Miller Fisher syndrome (Moran et al., 2005; Prokhorova et al., 2006). Therefore, only strains of Campvlobacter with LOS that does not undergo phase variation and cannot induce GBS through ganglioside mimicry should be used in the development of whole cell vaccines (van der Woude and Baumler, 2004). The phenomenon of phase variability in humans was demonstrated using inactivated vaccine preparations or by infecting volunteers with the virulent 81-176 strain (Prendergast et al., 2004). Anti-ganglioside antibodies were detected, however they were transient and did not persist. Due to the gaps in the knowledge of GBS the development of a human whole cell vaccine is problematic.

Another approach to vaccine development, which is safer than a whole cell vaccine, is development of subunit vaccines that contain specific antigens from *C. jejuni*. Potential target proteins should be present on the surface of the cell, expressed at high concentrations, be recognised by the immune system and be conserved among different serotypes of the pathogen (Jagusztyn-Krynicka *et al.*, 2009). Flagellin, which is known to be recognised during infection, is one of the vaccine candidates (Martin *et al.*, 1989). Using a FlaA-based subunit vaccine on mice led to partial immune protection, inducing short-term immunity (Lee *et al.*, 1999). However, vaccine development remains challenging due to genetic diversity among strains and glycosylation of flagella (Wang and Taylor, 1990; Scott, 1997; Karlyshev *et al.*, 2005; Logan *et al.*, 2002).

The alternative approach to prevent Campylobacter infection is the use of glycoconjugated vaccine, where immunogenic protein is covalently linked to polysaccharide to induce both humoral and cellular immune responses (Trotter et al., 2008). Among widely used glycoconjugated vaccines are vaccines against Haemophilus influenzae type b (Hib), N. meningitides and S. pneumonia (Trotter et al., 2008). The CPS of Campylobacter can be used for development of a subunit vaccine, as some common structures of CPS (heptosyl and phosphoramid residues) have been already identified (Kanipes et al., 2006; McNally et al., 2005; McNally et al., 2006; Szymanski et al., 2003). Although the Campylobacter polysaccharide alone has low immunogenicity, CPS conjugate vaccine (conjugated to an inactive diphtheria toxin as a carrier protein) induced significant serum response and protection in mice and New World monkeys (Monteiro et al., 2009). In this study diphteria toxin mutant was used as a carrier protein, which was CPS conjugated. Even though the use of CPS as a vaccine candidate looks promising, there may be a number of issues including safety, cross-reactivity,

structural variability of CPS and capsular switching phenomenon that require further development in order to make an effective CPS vaccine (Jagusztyn-Krynicka *et al.*, 2009).

At present, proteomics allows a quick search of potential targets for vaccine development. Prokhorova *et al.* (2006) has identified eight *Campylobacter* surface proteins that were cloned and expressed in *E. coli* and used for the immunisation of mice. Induction of a specific immune response and the partial protective effect in mice was observed and one of the proteins was tested for development of a human vaccine (Jagusztyn-Krynicka *et al.*, 2009). In another study, 200 membrane-associated proteins were identified, which included CadF, FlaA, Omp18, Omp50, Peb1, Peb2 and Peb4 that were recognised by convalescent patient sera (Cordwell *et al.*, 2008).

Using specific vectors, such as attenuated microbial strains, antigens of infectious bacteria can be delivered to the immune system. This approach was used for the development of a Salmonella vaccine expressing *Campylobacter* PEB1. Attenuated *Salmonella enterica* sv. Typhimurium was used as a vector carrying the *peb1* gene. This vaccine was used for oral immunisation of mice. However, despite inducing humoral immunity, IgG antibodies did not show a protective effect (Sizemore *et al.*, 2006).

Another antigen that was used in *Salmonella* vaccine was CjaA, which is the component of the ABC transport system, a solute-binding protein (Muller *et al.*, 2005). It was suggested that CjaA plays a role in *in vivo* colonisation (Holmes *et al.*, 2005). In the work by Wyszynska *et al.* (2004) it was demonstrated that vaccination of chickens by *S. enterica* sv. Typhimurium expressing *Campylobacter* CjaA induced an immune response and resulted in reduced colonisation. However, in a later study with the new generation of *Salmonella* 

vaccines, no reduction in colonisation of the chicken intestine was observed, even though there was a strong immune response present (Laniewski *et al.*, 2014). According to the authors (Laniewski *et al.*, 2014) in order to develop an efficient anti-*Campylobacter* subunit vaccine based on attenuated *Salmonella*, this vaccine should be multicomponent. Another approach to increase the efficacy of subunit vaccines is the use of an adjuvant, such as the modified heat labile toxin (LT) or cholera toxin (Jagusztyn-Krynicka *et al.*, 2009).

#### 1.9.4 Inhibitors of adhesion

The process of adhesion involves a variety of bacterial cell surface structures interacting with host cell receptors (as described above), thus the possibility of interfering with such interactions may provide a new focus in the development of antimicrobial strategies (Shoaf-Sweeney and Hutkins, 2009; Thomas, 2010). Use of anti-adhesive therapy, based on the prevention or reduction of contact between bacteria and the host cell, may be another method to control *Campylobacter* infection (Figure 1.7). This approach may provide a safer alternative to antimicrobial therapy and may also reduce the level of colonisation in poultry. Another advantage of this is its low level of activity on normal intestinal flora, due to targeting of pathogen-specific adhesins/receptors. The method also carries no risk of developing resistance due to the conserved nature of host cell receptors.

Several approaches can be used to prevent pathogen colonisation by targeting specific adhesin-receptor interactions. One approach is the use of anti-adhesion compounds that either block or interferes with adhesion of pathogens to specific host cell receptors (Lane *et al.*, 2010). Another approach is to immunise the host

with bacterial surface epitopes in order to stimulate antibody production within the host (Krachler and Orth, 2013).



**Figure 1.7. Illustration of anti-adhesion therapy strategies.** Inhibition of bacterial attachment by affecting biosynthesis and expression of adhesin (A and B) or host cell receptors (C). Competitive replacement using soluble inhibitors of attachment (D, E and F) or using anti-adhesive antibodies (G). (Adapted from Krachler and Orth, 2013).

In most cases, specific interaction between host cell receptors and bacterial adhesins involves carbohydrates (Odenbreit, 2005). Carbohydrates are present in large quantities on the surface of both host cells and bacterial cells, thus the use of carbohydrate-binding antagonists may be an attractive approach for anti-adhesion therapy. Successful inhibition of attachment using oligosaccharides was shown in *H. pylori, P. aeruginosa* and *Legionella pneumophila* (Simon *et al.*, 1997;

Gustafsson et al., 2006; Ramphal et al., 1991; Plotkowski et al., 2001; Thomas et al., 2004; Ader et al., 2008).

Several studies have focused on the inhibitory effects of 'decoy' carbohydrates on *Campylobacter* attachment (Ruiz-Palacios *et al.*, 2003; Newburg *et al.*, 2005; Wittscher *et al.*, 2007). The majority of anti-adhesion carbohydrates are dietary based, for example human and animal milk oligosaccharides, egg yolk and honey oligosaccharides, as well as oligosaccharides derived from plants (Sharon and Ofek, 2000; Lane *et al.*, 2010; Wittscher *et al.*, 2007). Milk oligosaccharides are proven to effectively inhibit *E.coli* binding to host cells (Martin-Sosa *et al.*, 2002, Cravioto *et al.*, 1991; Nascimento de Araujo and Giugliano, 2000). As noted previously, the role of human milk in protection of infants from *Campylobacter* infection has been previously shown (Newburg *et al.*, 2005). The role of plant-derived carbohydrates in preventing bacterial adhesion was studied by Wittscher *et al.* (2007). It was shown that Okra extracts reduced the attachment of *C. jejuni* to chicken colonic mucosa (Wittscher *et al.*, 2007).

The process of adhesion may involve several adhesins on the surface of a pathogen, thus, in order to be effective, anti-adhesion therapy should target as many different adhesins as possible. Therefore, identification of receptors to each adhesin, and the contribution of each adhesin to the process of adhesion and colonisation should be established. In spite of several adhesins of *Campylobacter* having already been described, a greater understanding of the adhesion process of *Campylobacter* to host cells may help in the further development of anti-adhesins for this pathogen.

#### **1.9.5 Probiotics and bacteriocins**

Probiotics, such as *Bifidobacterium* and *Lactobacillus* may be beneficial for the host as, when appropriately administered, they may prevent invasion of intestinal tissues by enteropathogens (Ventura *et al.*, 2009, Fooks and Gibson, 2002). The mechanism of action of probiotics is complex, and may include competition for host-surface receptors and nutrients, direct probiotic-pathogen interaction, production of specific antibacterials (bacteriocins and hydrogen peroxide) and

increase of host barrier protection due to increased mucin production (Sherman *et al.*, 2009; Mack *et al.*, 1999, Sherman *et al.*, 2005; Gueimonde *et al.*, 2006). Probiotics may work indirectly through utilisation of anti-adhesive carbohydrates as a food source, which, in turn, results in an increase in the number of probiotics (Sela *et al.*, 2008). Thus, the use of anti-adhesive carbohydrates may have a dual action, as they may also work as prebiotics (Lane, 2010).

The use of probiotics shortens the duration of viral-induced diarrhoea and prevents *Clostridium difficile*-associated diarrhoea (Szajewska *et al.*, 2007; Parkes *et al.*, 2009). Additionally, probiotics were shown to inhibit binding of *H. pylori*, *Salmonella cholerasuis* sv. Typhimurium and enterotoxigenic *E. coli* (ETEC) to human epithelial cells (Myllyluoma *et al.*, 2008; Candela *et al.*, 2008). The use of probiotics to treat a *Campylobacter* infection has not been studied excessively. However, selected *Lactobacillus* strains were able to inhibit *C. jejuni* invasion of human epithelial cells (Wine *et al.*, 2009). In addition, in a later study, it was shown that colonisation of chicken intestinal mucous by particular probiotic strains reduced the adhesion of *Campylobacter* cells *in vitro* (Ganan *et al.*, 2013). These strains may be useful in preventing infection in poultry. However, more research needs to be conducted before these probiotic strains will be used to control this food-borne pathogen.

Some probiotic strains can produce peptides called bacteriocins, which inhibit the growth of pathogenic bacteria (Cotter *et al.*, 2005). Several bacteriocins, such as OR-7 from *Lactobacillus salivarius* and E-760 from *Enterococcus* may significantly control the level of chicken gut colonisation by *Campylobacter*, as bacteriocin-treated chickens had a reduced level of colonisation by *Campylobacter* (Stern *et al.*, 2006; Line *et al.*, 2008). In a later study the use of bacteriocin E-760 for treatment of chickens through drinking water resulted in a
significant reduction of colonisation by *Campylobacter* (Svetoch and Stern, 2010). Additionally, treatment of *Campylobacter*-colonised chickens for more than three days before slaughter resulted in a five to six log reduction of caecal colonisation (Svetoch and Stern, 2010). These findings indicate that bacteriocin treatment prior to slaughter may be an effective strategy for controlling *Campylobacter* infection and colonisation.

## 1.10 Aims and objectives of study

The various methods of bacterial interaction with cellular molecules of the host are paramount in the pathogenesis of many bacterial infections (Casadevall and Pirofski, 2001; Patti *et al.*, 1994). *Campylobacter* attachment to host cells is an important stage in the pathogenesis of *C. jejuni* (Janssen *et al.*, 2008; Zilbauer *et al.*, 2008). With the increase in antibiotic resistance in *Campylobacter*, there is a greater need to further understand the molecular basis of host-pathogen interaction in order to control *Campylobacter* infection. The key to this lies in the inhibition of initial adhesion and colonisation. This, in turn, requires extensive understanding of the adhesins involved in this process. Although we know about the adhesins of *C. jejuni*, our understanding of the molecular basis of the adhesion process is still behind that of other enteropathogens (Poly and Guerry, 2008; Zilbauer *et al.*, 2008).

*C. jejuni* has an extensive glycan repertoire, including highly conserved glycans present in N-linked glycoproteins. N-linked glycoprotein PEB3 may be involved in bacterial attachment, but its role in adhesion has not yet been confirmed. The aim of this study was to develop an *in vitro* assay to evaluate the role of PEB3 and JlpA glycoproteins in adhesion of *C. jejuni* to an analogue of host cell receptors, SBA. The role of capsule in bacterial adhesion was also investigated.

The specific objectives of this work were:

1. Development and evaluation of an *in vitro* ELISA-like assay for the investigation of *C. jejuni* interaction with an analogue of host cell receptors, SBA.

2. Construction and confirmation of *peb3* and *jlpA* mutants in order to investigate the mutants' ability to bind to SBA.

3. Purification of PEB3 after overexpression in *E. coli* in order to identify putative host cell receptors.

4. Investigation of the role of the capsule in adhesion using an acapsulated (kpsM) mutant in an ELISA-like assay.

5. Assessment of gene expression (quantification and comparison of the levels of *peb3* and *kpsM* mRNA expression over time using RT-PCR).

6. Investigation of the inhibitory effect of *E. coli* expressing a recombinant adhesin on binding of *C. jejuni* to an analogue of host cell receptors.

## **CHAPTER 2: Materials and Methods**

## 2.1 Bacterial strains and plasmids

Two C. jejuni strains were used in this study: 11168H, which is a hypermotile strain of C. jejuni NCTC 11168 (Karlyshev et al., 2002), and an acapsulate mutant of this strain, 11168H/kpsM (Karlyshev et al., 2000). E. coli XL1 Blue Supercompetent and E. coli XL2 Blue Ultracompetent cells (Stratagene) were used according to the manufacturer's instructions for cloning and/or protein expression experiments. The plasmids used in this study are listed in Table 2.1.

Plasmids	Description	Source /Reference
pGEM-T Easy	Cloning vector	Promega
рЈМК30	Source of kan' cassette	Van Vliet <i>et al.</i> , 1998
pAV35	Source of cam' cassette	Van Vliet <i>et al.</i> , 1998
pBAD33	Contains pBAD promoter	Guzman et al., 1995
pPGL1	C. jejuni 16 kb fragment (pgl locus) cloned into the BamHI site of pBR322.	Fry <i>et al.</i> , 1998
pRRC	<i>cam</i> <sup>r</sup> cassette cloned into pRR (plasmid with fragments of rRNA gene cluster)	Karlyshev and Wren, 2005
pRRBC	pBAD promoter from pBAD33 cloned into pRRC vector.	Ikeda, 2014

Table 2.1. Plasmids used in this study.

## 2.2 Bacterial growth media and supplements

All culture media made in the laboratory were autoclaved at 121°C for 15 min

prior to use.

#### Columbia Blood Agar (CBA)

Columbia Agar powder (Oxoid) was suspended in distilled water according to the manufacturer's instructions and used for plate cultures of *C. jejuni*. After sterilisation, media was cooled to 50°C and sterile defibrinated horse blood (Oxoid) was added to final concentration of 6%.

## **Brain Heart Infusion Broth (BHI)**

BHI (Oxoid) was used to support the growth of *C. jejuni* in liquid culture. Prior to sterilisation the appropriate amount of powder was suspended in distilled water according to manufacturer's instructions.

## Super Optimal Broth (SOC) Medium

Pre-made SOC media (Invitrogen) was used in the final step of transformation in order to obtain maximal transformation efficiency of *C. jejuni* or *E. coli*. Unopened bottles were stored at 4°C. After opening, SOC medium was stored at - 20°C.

## Luria-Bertani Medium (LB)

LB (Sigma) powder was used for preparation of LB broth according to manufacturer's instructions and autoclaved as appropriate. LB agar (LBA) was prepared similarly except for the addition of 1% (w/v) agar to LB medium. Any necessary antibiotics were added once an appropriate temperature was reached following autoclaving.

## **Mueller-Hinton Broth**

Mueller-Hinton (MH) Broth powder (Oxoid) was suspended in distilled water

according to the manufacturer's instructions and autoclaved. It was used for storage of *C. jejuni* stocks at -80°C.

## Antibiotic Supplements

Ampicillin, kanamycin, chloramphenicol and Skirrow III supplement were obtained from Sigma-Aldrich. Ampicillin was ready to use at stock concentration of 100 mg/ml. 50 mg/ml stock solutions of kanamycin were prepared using distilled water. 34 mg/ml stock solutions of chloramphenicol were prepared using ethanol. Aliquots of antibiotic stocks were stored at -20°C. Skirrow supplement III was prepared using distilled water according to the manufacturer's instructions. Aliquots were stored at -20°C. Final concentration of the components of Skirrow supplement III: Polymyxin B, 2.5 IU/ml; Vancomycin, 10 µg/ml; and Trimethaprim, 5 µg/ml.

## 2.3 Growth and storage of bacterial strains

*Campylobacter* strains were grown under microaerophilic (5% O<sub>2</sub>, 10% CO<sub>2</sub>, 85% N<sub>2</sub>) conditions in a controlled atmosphere incubator (Don Whitley) at 37°C on CBA supplemented with 6% defibrinated horse blood and Skirrow supplement. When necessary, the medium was supplemented with chloramphenicol (10  $\mu$ g/ml) and/or kanamycin (50  $\mu$ g/ml). An aliquot of the resulting bacterial culture was stored at -80°C in MH broth supplemented with 15% glycerol. For liquid cultures, bacterial cells were transferred from the solid media to BHI with Skirrow supplement and incubated shaking (90 rpm) at 37°C.

Based on viable count data, *C. jejuni* grown on BHI at 42°C has following growth stages: exponential or lag phase (0–16 h), retardation or log phase (16–20 h), stationary (20-40 h) and decline phase (40–66 h) (Wright *et al.*, 2009). Two-day old plate culture grown on CBA at 37 °C has around 10% coccoid forms and only from day 3 around 90% of the population becomes coccoid (Ikeda, 2014). Compared to solid media there are around 40% coccoid forms present in two-day liquid culture grown in BHI at 37 °C (Ikeda, 2014).

In order to determine viable c.f.u, bacteria from two-day *C. jejuni* culture plates were suspended in PBS to  $OD_{600}$  1. This was followed by a 10-fold dilution of suspension in PBS and plating 50 µl onto CBA supplemented with Skirrow. Plates were incubated microaerobically at 37°C for 2 days before colonies were counted.  $OD_{600}$  1 corresponded to to  $4x10^9$  c.f.u. of *C. jejuni*.

*E. coli* was grown on LB agar at 37°C or in LB broth under shaking conditions (180–200 rpm). Where necessary, media were supplemented with antibiotics to the following final concentrations: ampicillin, 100  $\mu$ g/ml; kanamycin, 50  $\mu$ g/ml; or chloramphenicol, 10  $\mu$ g/ml. Stocks of *E. coli* were stored at -80°C in LB with 15% glycerol, prepared from fresh one-day-old cultures.

#### 2.4 Chemicals, buffers and solutions

Standard laboratory chemicals were purchased from Fisher Scientific and Sigma Aldrich as AnalaR or Molecular grade, unless otherwise stated. All buffers and solutions were made using distilled water and stored at room temperature, at 4°C or -20°C, according to storage requirements.

## 2.5 Restriction endonucleases and DNA modification enzymes

Restriction endonucleases and Antarctic Phosphatase (AP) were purchased from

New England Biolabs (NEB). T4 DNA Polymerase and T4 DNA Ligase were purchased from Promega. All restriction endonucleases/enzymes were used to digest plasmids and DNA according to the manufacturer's instructions. Each restriction mixture had the appropriate NEB buffer at 1X concentration, and if required it was supplemented with 100  $\mu$ g/ml bovine serum albumin (BSA). Antarctic Phosphatase (AP) (NEB) was used to catalyse the removal of the 5' phosphate groups from linear DNA fragments, thus preventing self-ligation. AP was used according to the manufacturer's guidelines.

T4 DNA polymerase (Promega) was used to form DNA blunt ends: filling-in of 5'-overhangs in the presence of dNTPs (NEB) and removal of 3'-overhangs. The enzyme was used according to protocol with either T4 DNA polymerase reaction buffer or restriction enzyme buffer. These were both appropriate for the reaction. The mixture was incubated according to protocol, followed by inactivation of the reaction mixture at 75°C for 10 min.

T4 DNA ligase was used for ligation of chromosomal DNA fragments with linearised vector, by catalysing the formation of a phosphodiester bond between 5'-phosphate and 3'-hydroxyl termini in DNA. Ligation reactions were set up with the amounts of vector and insert DNA recommended by manufacturer's instruction.

CloneChecker<sup>™</sup> System (Invitrogen) was used in order to determine the presence of target plasmid DNA in recombinant bacterial colonies. "*The Supercoiled Plasmid*" protocol was used for assessing plasmids for the presence of an insert according to manufacturers' specifications.

#### **2.6 General Cloning Techniques**

#### 2.6.1 Crude lysate preparation

Template DNA was prepared by the crude lysis boiling method, in which a single *C. jejuni* colony was boiled using heat block for 30 sec in 4  $\mu$ l of Green solution (CloneChecker<sup>TM</sup> System). The lysate was subsequently diluted in 10  $\mu$ l of TE buffer. For PCR and restriction digestion, 2  $\mu$ l of diluted lysate was used. Distilled water was used for preparation of lysates for *E. coli*. A single colony was re-suspended in 20  $\mu$ l of water and heated at 100°C for 30 sec. Two  $\mu$ l of lysate ware used for PCR or restriction digestion.

## 2.6.2 DNA isolation

Genomic DNA was isolated using Gentra<sup>®</sup> Puregene<sup>®</sup> Yeast/Bacteria Kit (Qiagen) according to the manufacturer's protocol. A two-day-old culture of *C. jejuni* and a one-day-old culture of *E. coli* were used for extraction of chromosomal DNA. Cells were resuspended in 300  $\mu$ l of PBS, centrifuged for 1 min at 11,337 x g (13,000 rpm) and then used for DNA extraction. DNA was eluted from the membrane using an elution buffer or nuclease-free deionised water. Plasmid DNA was purified with Qiagen Plasmid Purification Kit (Qiagen) according to the manufacturer's protocol. Bacterial cells were cultured for one day on agar containing appropriate antibiotics. Cells were resuspended in 300  $\mu$ l PBS, centrifuged for 1 min at 11,337 x g (13,000 rpm) and then used for plasmid purification. Plasmid DNA was eluted from membrane using the elution buffer.

#### 2.6.3 Agarose gel DNA extraction and purification methods

Agarose Gel DNA Extraction Kit (Roche) was used for extracting DNA. Restriction digests were run on 1% agarose gel in order to separate the fragments.

The gel segment with the DNA fragment was cut out using a scalpel and a long wavelength (365 nm) UV source. The gel with DNA fragment was weighed and the appropriate amount of agarose solubilisation buffer was added. The remainder of the procedure was performed in line with the manufacturer's instructions. PCR products and restriction digests were purified using Qiagen's PCR Purification Kit (Qiagen) according to manufacturer's protocol. Purified products were run on agarose gel for confirmation of the product.

## 2.7 Polymerase Chain Reaction

Polymerase Chain Reaction (PCR) was used for a variety of purposes during this study. PCR was performed using a Multigene Gradient Optimax, Labnet 96-well thermocycler using either Phusion<sup>®</sup> High-Fidelity DNA Polymerase (NEB), One*Taq*<sup>®</sup> DNA Polymerase (NEB) or GoTaq<sup>®</sup> DNA Polymerase (Promega). All thermal cycler conditions for each of the DNA polymerases used are listed in Table 2.2. Each PCR mixture contained the DNA template, DNA polymerases and the appropriate buffer, dNTPs (Promega), appropriate forward and reverse primers and nucleotide-free water.

## 2.8 Confirmation and Quantification of DNA

#### 2.8.1 Agarose Gel Electrophoresis

DNA was separated using gel electrophoresis in 1x Tris-Borate EDTA Buffer (TBE) (pH 8.3) (Fisher) at 120V in a Bio-Rad electrophoresis unit. 1% agarose gels (Sigma) and the tank with TBE buffer contained 0.5  $\mu$ g/ml ethidium bromide (Fisher) for visualisation by ethidium bromide fluorescence. Samples were loaded into the gel with bromophenol blue-based loading buffer (NEB). 1 kb molecular weight ladder (NEB) was used as a standard to estimate the DNA fragment sizes.

Gels were visualised under a UV transilluminator, G: BOX (Syngene), and images captured and analysed using GeneSnap software (Syngene). When necessary, DNA samples were quantified using a NanoVue spectrophotometer.

PCR step	Temperature (°C)	Duration of step	Number
			of cycles
Phusion <sup>®</sup> High-Fidelity D	 NA Polymerase with Standar	l d Phusion HF Buffer contai	L ning 1.5
mM MoCh at 1x reaction	concentration.		
		• ·····	
Initial denaturation	98	30 sec	1
Denaturation	98	10 sec	
Annealing	45	30 sec	30
Extension	72	30 sec per kb	
Final extension	72	10 min	1
One <i>Taq<sup>®</sup></i> DNA Polymeras	e with One <i>Taq</i> <sup>®</sup> Standard Re	eaction Buffer containing	
1.8 mM MgCl <sub>2</sub> at 1x reacti	on concentration.		
Initial denaturation	94	30 sec	1
Denaturation	94	30 sec	
Annealing	45	30 sec	30
Extension	68	1 min per kb	
Final extension	68	5 min	1
GoTaq <sup>®</sup> DNA Polymerase	with Colourless GoTaq <sup>®</sup> Rea	action Buffer containing 1.5	mM MgCl <sub>2</sub>
at 1x reaction concentration	n		
Initial denaturation	95	2 min	1
Denaturation	95	30 sec	
Annealing	50	30 sec	30
Extension	72	1 min per kb	
Final extension	72	5 min	1

#### 2.9 Sequencing data analysis

In order to verify that there was no mutation in target genes and plasmids, plasmids with insert were sent for sequencing to Cogenics (Beckman Coulter). Sequence chromatograms were analysed using Chromas 2 software.

## 2.10 Primer design

Primers used in this study were synthesised by Sigma Genosys, UK. For amplification of *C. jejuni*, gene primers were designed using the published nucleotide sequence of the *C. jejuni* strain NCTC 11168 (www.sanger.ac.uk). When designing primers, the following parameters were taken into consideration: G+C content 30–40%, length and melting temperature (Tm). Normally the length of the primers should be about 18–24 bases (Dieffenbach *et al.*, 1993). However, because of the low G+C content of the *Campylobacter* genome, primer length was extended.

## 2.11 Preparation of competent cells

*C. jejuni* were grown as a lawn on CBA overnight under microaerophilic conditions at  $37^{\circ}$ C. Bacteria were suspended in ice-cold buffer containing 272 mM sucrose and 15% glycerol and washed three times with the same buffer. The bacterial suspension was centrifuged for 20 min at 3000 x g (3861 rpm) at 4°C, supernatant removed and pellet resuspended in fresh ice-cold wash buffer. The process was repeated 4 times followed by resuspension of the pellet in 1 ml of icecold wash buffer. Aliquots of competent cells were stored at -80°C. *E. coli* culture was grown as a lawn on LBA overnight at 37°C. Bacteria were inoculated into 10 ml LB with an initial OD<sub>600</sub> of 0.1 and left at 37°C with gentle

shaking. When the culture reached  $OD_{600}$  0.6, the bacterial suspension was

centrifuged for 5 min at 4000 x g (4458 rpm) at 4°C. The supernatant was then removed and the pellet resuspended in 5 ml ultra-purified water. The process was repeated 4 times and finally resuspended in 1 ml of water. Aliquots of competent cells were stored at -80°C.

## 2.12 Electroporation

The electroporation procedure was performed as previously described by Wassenaar *et al.* (1993a). After addition of plasmid DNA to competent cells the mixture was transferred to an ice-cold electroporation cuvette (MBP-Molecular Bioproducts). Electroporation was performed using a BioRad MicroPulser (BioRad) at 2.5 kV, 200  $\Omega$ , and 25  $\mu$ F.

For electroporation of *C. jejuni* the content of the electroporation cuvette was rinsed with 100  $\mu$ l of SOC buffer, and the bacterial suspension was transferred onto a non-selective CBA plate. Following overnight incubation at 37°C under microaerophilic conditions, bacteria were spread onto a CBA plate supplemented with selective antibiotic and incubated for two days. Colonies were re-streaked onto selective CBA plates and incubated for two days. PCR was then used to confirm the presence of the insert.

For *E. coli* electroporation, the contents of the electroporation cuvette were rinsed with 200 µl of SOC buffer, and the bacterial suspension was transferred onto a non-selective LBA plate for 1 h at 37°C. Following incubation for 1 h at 37°C, bacteria were spread onto an LBA plate supplemented with selective antibiotic and incubated overnight at 37°C. Colonies were re-streaked onto selective LBA plates and incubated for one day. PCR was then used to confirm presence of insert.

## 2.13 E. coli transformation using commercial competent cells

Transformations were performed according to the manufacturer's protocol with the following adjustments: 50  $\mu$ l of competent cells, 5  $\mu$ l of ligation mixture and 450  $\mu$ l of SOC medium. Approximately 200  $\mu$ l of transformation mixture was spread onto LB agar plates supplemented with appropriate antibiotics and plates were incubated overnight at 37°C.

XL1 Blue Supercompetent cells (Stratagene), according to the manufacturer, have an average transformation efficiency of  $\ge 5 \times 10^8$  transformants/µg of supercoiled DNA and were resistant to tetracycline. XL2 BLue Ultracompetent (Stratagene) cells have an average transformation efficiency of  $\ge 5 \times 10^9$  transformants/µg of supercoiled DNA and were resistant to tetracycline and chloramphenicol.

## 2.14 PEB3 protein expression

## 2.14.1 Construction of *peb3* knocking-in construct using pRRBC

A pRRBC-peb3 construct was designed for expression of PEB3 protein in *E. coli* and *C. jejuni*. Table 2.3 lists the primer sequences used for expression of PEB3 protein. Primers for pRRBC plasmid contained SD (Shine Dalgarno region), restriction site (*Kpn*I) and histidine (6xHis) tag-encoding sequence (Figure 2.1). A target gene was amplified using High Fidelity Phusion DNA polymerase. PCR conditions are shown in Table 2.2. PCR-amplified product was digested with *Kpn*I and inserted into digested pRRBC plasmid via ligation. Ligation product was used for transformation of *E. coli* XL1cells as described earlier. The transformation mixture was spread on LB agar plates supplemented with chloramphenicol. Selected clones were re-streaked and used for plasmid purification and restriction digestion (*Kpn*I and *Hind*III) in order to confirm the presence of the insert, and then were sent for sequencing using primers pBAD-for

and CamR1.

The construct (pRRBC-peb3) with correct (forward) orientation was used for electroporation into *C. jejuni*. In order to check the site of insertion into one of three RNA clusters (Karlyshev and Wren, 2005) the following primers were used: ak233 and pBAD-for, ak 234 and pBAD-up, ak235 and pBAD-up (Table 2.3).

peb3-for ataa GGTACC aagg <i>Kpn</i> 1 SD	aaatact ATGAAAAAAATTATTACTTTATTTGGTGC
peb3-rev aggt GGTACC TTA a <i>Kpn</i> 1 ter	atg atg atg atg atg TTCTCTCCAGCCGTATTTTTAAAAATTTC 6xHis tag

Figure 2.1. Composition of primers used for peb3 gene for pRRBC plasmid. Both primers incorporate Kpnl sites.

Primer Name	Primer sequence (5' to 3')	
peb3 for	ATAAGGTACCAAGGAAATACTATGAAAAAAATTATTACTTTATTTGGTGC	
peb3_rev	AGGTGGTACCTTAATGATGATGATGATGATGATGATGTTCTCTCCAGCCGTATTT TTTAAAAATTTC	
peb3 pBAD-for	ATAATCTAGAAAGGAAATACT ATGAAAAAAATTATTACTTTATTTGGTGC	
peb3_pBAD-rev	AGGTCTGCAGTTAATGATGATGATGATGATGATGTTCTCTCCAGCCGTATTTTTTA AAAATTTC	
peb3_pRRC-for	ATAA TCTAGAAAGGAAATACT ATGAAAAAAATTATTACTTTATTTGGTGC	
peb3_pRRC-rev	AGGTTCTAGATTA ATGATGATGATGATGATG TTCTCTCCAGCCGTATITTTTAAAAATTTC	
ak233	GCAAGAGTTTTGCTTATGTTAGCAC	
ak234	GAAATGGGCAGAGTGTATTCTCCG	
ak235	GTGCGGATAATGTTGTTTCTG	
CamR1	CGTATTGCCAAAATAGTGGTCGAAATACTC	
ak237	TCCTGAACTCTTCATGTCGATTG	
pBAD-for	GATTAGCGGATCCTACCTGAC	
pBAD-up	GCCGTCAAGTTGTCATAATTGGTAACG	

Table 2.3. Primers used for PEB3 expression studies.

2.14.2 Generation of a recombinant *E. coli* strain expressing *pgl* of *C. jejuni* In order to assess if the *pgl* locus of *C. jejuni* could be used to generate a recombinant *E. coli* strain that could express glycosylated glycoproteins, pPGL1 plasmid carrying the entire *pgl* locus of *C. jejuni* 81116 was introduced into *E. coli* strain XL2. Recombinant *E. coli* was grown on LBA plates supplemented with ampicillin, as pPGL1 has an ampicillin resistant cassette.

2.14.3 Construction of recombinant *E. coli* strain expressing non-glycosylated PEB3

pBAD33 plasmid was used for overexpression of non-glycosylated PEB3 in *E. coli. Peb3* primers were designed with *Xba*I and *Pst*I restriction sites and for purification purposes the reverse primer encoded sequence for 6xHis residues (Figure 2.2). The *peb3* gene of *C. jejuni* 11168H was amplified by PCR using High Fidelity Phusion DNA polymerase and primers designed for pBAD33 plasmid (Table 2.3).

peb3\_pBAD-for ataa TCTAGA aaggaaatact ATGAAAAAAATTATTACTTTATTTGGTGC *Xba*l SD peb3-pBAD-rev aggt CTGCAG TTA atg atg atg atg atg atg atg TTCTCTCCAGCCGTATTTTTTAAAAATTTC *Pst*l ter 6xHis tag

Figure 2.2. Composition of primers used for amplification of peb3 gene for pBAD33 plasmid.

PCR product was digested with *Xba*I and *Pst*I enzymes and cloned into pBAD33 vector yielding pBAD\_peb3. Prior to ligation, pBAD33 was treated with the same restriction enzymes as the PCR product. Ligation mixture was used for

transformation into *E. coli* XL1 cells. Transformation mixture was plated onto LB agar supplemented with chloramphenicol. The presence of insert was confirmed with *PfI*MI enzyme digestion. Plasmids with an insert (size of insert 0.8 kb) were sent for sequencing with peb3\_pBAD\_for and peb3\_pBAD\_rev primers. A plasmid with no PCR error in *peb3* was used for further experiments.

# 2.14.4 Construction of a recombinant *E. coli* strain expressing glycosylated PEB3

Glycosylated PEB3 was produced by *E. coli* strain containing pBAD33\_peb3 and pPGL1. pBAD\_peb3 construct was transformed into an *E. coli* strain harbouring pPGL1 plasmid. First competent cells were prepared from *E. coli*/pPGL1 as described in section 2.12.2. Recombinant *E. coli* was grown on LBA plates or in LB broth supplemented with chloramphenicol and ampicillin. Glycosylated PEB3 was produced by *E. coli* strain containing pBAD33\_peb3 and pPGL1. pPGL1 plasmid was transformed into an *E. coli* strain harbouring pBAD\_peb3 plasmid. First competent cells were prepared from *E. coli*/pPGL1 plasmid was transformed into an *E. coli* strain harbouring pBAD\_peb3 plasmid. First competent cells were prepared from *E. coli*/pBAD33\_peb3 as described in section 2.12.2. Recombinant *E. coli* strain harbouring pBAD33\_peb3 as described in section 2.12.2. Recombinant *E. coli* was grown on LBA plates or in LB broth supplemented with chloramphenicol and ampicillin.

## 2.14.5 Expression of recombinant PEB3 in C. jejuni

pRRC plasmid was used for constitutive expression of *peb3* in *C. jejuni*, and for complementation of *peb3* mutation. Primer sequences used for PCR contained *XbaI* restriction sites (Figure 2.3).

The target gene was amplified using High Fidelity Phusion DNA polymerase with the PCR conditions stated in Table 2.2. PCR product (*peb3*) was digested with *Xba*I and inserted into pRRC plasmid via ligation. pRRC plasmid was digested

with *Xba*I and treated with Antarctic Phosphatase prior to ligation. Ligation mixture was used for transformation into *E. coli* XL1 cells as previously described. The transformation mixture was spread on LB agar plates supplemented with chloramphenicol. Selected clones were re-streaked and used for plasmid purification and restriction digestion (*Eco*RV and *PfI*MI) to confirm the presence of the insert and its orientation, and then sent for sequencing using primers peb3-XbaI-for and peb3-XbaI-rev.

peb3-Xbal-for ataa TCTAGA aaggaaatact ATGAAAAAAATTATTACTTTATTTGGTGC *Xba*l SD peb3-Xbal-rev aggt TCTAGA TTA atgatgatgatgatgatg TTCTCTCCAGCCGTATTTTTTAAAAATTTC

**6xHis tag** 

Xbal

ter

Figure 2.3. Composition of primers used for amplification of *peb3* gene for pRRC plasmid. Primers contained *Xba*l restriction sites for insertion into pRRC vector.

The construct with the correct orientation and confirmed sequence was used for electroporation into *C. jejuni*. In order to check the site of insertion into one of three RNA clusters the following primers were used: ak233 and ak237, ak234 and ak237, ak235 and ak237 (Table 2.3). Ak237 and pBAD-up primers were used to check the presence of *cam<sup>r</sup>*. *C. jejuni* with pRRC\_peb3 plasmid was grown on CBA or BHI supplemented with chloramphenicol and Skirrow supplement.

## 2.14.6 PEB3 protein purification

The recombinant *E. coli* strains: pBAD33\_peb3/pPGL and pBAD\_peb3 (with *peb3* 6xHis) were grown in LB broth overnight at 37°C under shaking conditions

and used to inoculate 100 ml LB broth to  $OD_{600}$  0.05–0.1. The cultures were grown under the same conditions until an  $OD_{600}$  of 0.5–0.6 was achieved. Protein expression was induced by the addition of 0.1% L-arabinose (Acros Organics) to exponentially growing cultures which were subsequently incubated for 1 hour at 37°C. The cells were harvested by centrifugation at 4000 x g (4458 rpm) for 10 min at 4°C. Small aliquots were taken before and after induction for preparation of lysates (pellet from a 1 ml culture was suspended in 2X NuPAGE LDS Sample Buffer (Life Technologies)) and incubated for 5 min at 100°C using heat block. The recombinant *C. jejuni* pRRC\_peb3 (with *peb3* 6xHis) was grown overnight in BHI at 37°C under shaking conditions (180 rpm). Bacterial pellets were collected by centrifugation for 10 min at 4000 x g (4458 rpm) at 4°C and either used for protein purification immediately or stored at -80°C.

Recombinant 6xHis-tagged PEB3 was purified from *E. coli* cell lysates using Ni-NTA Fast Start Kit (Qiagen). *E. coli* lacking pPGL1 served as control. Large-scale protein purification (60–100 ml culture volumes) was performed using Qiaexpress Ni-NTA Fast Start Kit (Qiagen) according to the manufacturer's *"Purification of 6xHis-tagged proteins under native conditions"* protocol.

Small-scale protein purification (10–20 ml culture volumes) was performed using Ni-NTA Agarose Magnetic Beads in line with the manufacturer's kit (Qiagen) using "*Purification in single reaction tubes*" protocol. The volume of the final elution was 10–20 µl. The lysates were analysed at the same time as protein fractions using SDS-PAGE and Western blotting (see section 2.14.7). In order to determine protein concentrations, Pierce<sup>TM</sup> BCA Protein Assay Kit (ThermoScientific) was used according to the manufacturer's instructions. A standard bovine serum albumin (BSA) was used as reference.

## 2.14.7 SDS-PAGE and Coomassie Blue staining

Sodium dodecyl sulfate -polyacrylamide gel electrophoresis (SDS-PAGE) was carried out using standard procedure (120V for 1h 30min) with pre-cast polyacrylamide NuPAGE® Novex® 12.5% Bis-Tris Gels (Life technologies). For the SDS-PAGE procedure, samples of lysates and fractions (flow-through, wash and eluates) of purified protein were mixed with NuPAGE LDS Sample Buffer and heated for 2 min at 100°C. The samples and the protein molecular weight marker (Colourplus protein molecular weight marker (NEB) or protein size marker (FisherScientific) were loaded onto gels and run at 120V for approximately 90 min in 1X MOPS Buffer (pH 7.7) (Invitrogen). If necessary, two gels were run, one for Coomassie Blue (Life technologies) staining and another one for Western blotting. Gels were analysed via staining with SimplyBlue<sup>™</sup> SafeStain (Invitrogen) for 1h followed by de-staining with distilled water for minimum of 2 h or overnight. Gels were visualised with GeneSnap software and photographed using a G:BOX SynGene camera.

#### 2.14.8 Western blotting (WB)

After separating proteins on SDS-PAGE, the gel was incubated in transfer buffer for 15 min. Proteins were transferred onto 0.45 µm polyvinylidene difluoride membrane (PVDF) (Millipore) using a semi-dry transfer unit at 15V for 90 min. The PVDF membrane was treated with 100% methanol for 15 sec, washed with ultra-pure water for 2 min and incubated in transfer buffer for 5 min. Following the transfer the membranes were treated using two different protocols described below (depending on an application).

## 2.14.8.1 WB using anti-His antibody

For His-tag detection, membranes were blocked with 5% milk in Tris Buffered Saline with Tween<sup>®</sup> 20 (TTBS) for 1 h and then rinsed with TTBS three times. They were then treated (with gentle shaking overnight at 4°C) with mouse monoclonal anti-His antibody (NEB) (1:1000 dilution) in TTBS. Following an overnight incubation, the membrane was washed three times and a secondary antimouse IgG horseradish peroxidase (HRP)-linked antibody (NEB) (1:10000 dilution) in TTBS was added and incubated with gentle shaking for 2.5 h. After washing the membrane three times for 5 min in TTBS, blots were developed using SuperSignal West Pico Chemiluminescent Substrate (Thermo Scientific). The membrane was visualised using a GeneGnome imaging system (Syngene) with GeneSnap software.

#### 2.14.8.2 WB using SBA lectin

For lectin probing and for detection of glycosylated proteins, blots were blocked in 0.5% PBS with 0.5% Tween<sup>®</sup> 20 (PBST) for 30 min. These were then incubated for 1 h at room temperature with biotinylated SBA (Vector Laboratories) at a concentration of 10  $\mu$ g/ml in 0.2% PBST (PBS with 0.2% Tween<sup>®</sup> 20). Following three brief washes in 0.2% PBST, blots were incubated in HRP-conjugated streptavidin (Sigma) diluted 1 in 1000 in 0.05% PBST at room temperature for 30 min. Following three brief washes in 0.5% PBST, blots were developed using a diaminobenzidine (DAB) HRP substraite staining kit (Vector Laboratories). with nickel enhancement according to the manufacturer's protocol.

## 2.15 Construction of C. jejuni mutants

## 2.15.1 Construction of *peb3* and *jlpA* mutants

Fragments of the genes *peb3* and *jlpA* were PCR-amplified using the primers listed in Table 2.4 and cloned into pGEM-T Easy vector to produce plasmids pGEM\_peb3 and pGEM\_jlpA respectively. The kanamycin cassette was obtained from vector pJMK30 by digestion with *Sma*I. The chloramphenicol cassette was obtained from vector pAV35 by digestion with *Xba*I. In order to disrupt the *peb3* gene, the pGEM\_peb3 plasmid was digested with *Pf*IMI, blunt ended and ligated with the *kan'* cassette producing pGEM\_peb3\_*kan'* construct. The *jlpA* gene was disrupted by insertion of the *cam'* cassette into the *Bsa*BI restriction site of pGEM\_jlpA plasmid, yielding pGEM\_jlpA\_*cam'*. In both cases, the orientation of the antibiotic resistance cassette was the same as that of the target gene to avoid a negative polar effect in the mutants. The derivatives were selected using media supplemented with appropriate antibiotics.

Allelic replacement was confirmed by PCR using gene-specific primers and chromosomal DNA extracted from mutants (Table 2.4).

Primer	Sequence (5'-3')	Used for
peb3_for	ATGAAAAAAATTATTACTITATTTGGTGCATG	Mutation of peb3 gene
peb3 _rev	TTATTCTCTCCAGCCGTATTTTTTAAAAATTTC	
jlpA_for	ATGAAAAAAGGTATTTTTCTCTCTATTGG	Mutation of <i>jlpA</i> gene
jlpA_rev	TTAAAATGACGCTCCGCCCATTAACATAG	1
peb3_Xbal_for	ATAATCTAGAAAGGAAATACTATGAAAAAAA TTATTACTTTATTTGGTGC	Complementation of <i>peb3</i> mutation
peb3_Xbal_rev	AGGTTCTAGATTAATGATGATGATGATGATGT TCTCTCCAGCCGTATTTTTTAAAAATTTC	
ak55-f	CCCCATCAAACCTATGCTAC	Mutation of kpsM gene
ak59-r	GCCTATAAACCTGTAAAGCCTATAC	

Table 2.4. Primers used for mutation of *peb3* and *jlpA*, for complementation of *peb3* and confirmation of *kpsM* mutant.

Insertion of the antibiotic cassette into a target gene was confirmed by the expected increase in size of the PCR product. If the whole plasmid was integrated into the locus this would result in two gene copies: a mutated one producing a large PCR product, and an original one without inserted antibiotic cassette producing a smaller PCR product. The absence of the latter in the mutants confirms that allelic replacement had occurred.

The mutants were designated 11168H/peb3::kan<sup>r</sup> and 11168H/jlpA::cam<sup>r</sup>.

## 2.15.2 Construction of the kpsM mutant

11168H/kpsM::kan<sup>r</sup> strain (Karlyshev et al., 2000) was confirmed using PCR and kpsM-specific primers (Table 2.4). In order to get more clonal isolates, the chromosomal DNA of the 11168H/kpsM::kan<sup>r</sup> strain was purified and used for transformation into *C. jejuni* 11168H. Allelic replacement was confirmed by chromosomal DNA extraction and PCR using gene-specific primers (Table 2.4).

#### 2.15.3 Complementation of peb3 mutant

*Peb3* gene was PCR-amplified using the primers described in section 2.14.5 (Figure 2.3). The product was digested with *Xba*I enzyme and cloned into *Xba*Idigested pRRC plasmid to produce pRRC\_peb3 (Karlyshev and Wren, 2005). The pRRC construct was previously designed for use in complementation studies and gene expression in *C. jejuni*, including expression of genes of non-*Campylobacter* origin (Karlyshev and Wren, 2005). Restriction analysis verified that the gene was transcribed in the same orientation as the *cam'* gene. After transformation of the 11168H/*peb3::kan'* mutant with plasmid pRRC\_peb3, Kan<sup>r</sup> Cam<sup>r</sup> clones were selected. PCR analysis confirmed integration of *peb3* gene into one of the rRNA gene clusters. The complementation derivative was designated 11168H/peb3::kan<sup>r</sup>/peb3<sup>+</sup>.

## 2.16 Binding assay

An enzyme-linked immunosorbent assay (ELISA)-like technique was designed and used for the investigation of adhesins containing glycan moieties.

## 2.16.1 Coating of plates with SBA lectin

SBA lectin was obtained from Sigma. A solution of the SBA lectin was made up in ELISA buffer to a final concentration of 10  $\mu$ g/ml. Stock solution was stored at -20 °C until used.

A 96-well MaxiSorp microtitre plate (Nunc, Fisher) was used as the solid phase for immobilising the ligand. 100  $\mu$ l aliquots of the SBA lectin were immobilised in wells of the ELISA plate at 4°C overnight. Simultaneously, some wells were coated with 100  $\mu$ l of 1% BSA at 4°C overnight to reduce non-specific binding. The following day, wells were washed with 0.2% PBST and then blocked using 250  $\mu$ l blocking buffer (1% BSA in 0.2% PBST). Wells were incubated with BSA at 4°C overnight. Bacteria harvested from two-day *C. jejuni* or one-day *E. coli* culture plates were suspended in PBS to OD<sub>600</sub> 1; 100  $\mu$ l aliquots of bacterial suspension (corresponding to 4x10<sup>8</sup> c.f.u. of *C. jejuni* and 5x10<sup>8</sup> c.f.u. *E. coli*) were applied to the wells and the plate was incubated for 40 min at room temperature. *C. jejuni* grown at 37°C on CBA supplemented with Skirrow were used for all binding assays. When necessary, the medium was also supplemented with kanamycin (50  $\mu$ g/ml) or chloramphenicol (10  $\mu$ g/ml).

## 2.16.2 Detection of bacterial binding to immobilised SBA lectin

After washing with 0.2% PBST, the plate was incubated with 100  $\mu$ l aliquots of biotinylated SBA (10  $\mu$ g/ml) (Vector Laboratories) diluted in 0.2% PBST for 1 h at room temperature. Adhered bacteria were detected with HRP-conjugated streptavidin. 100  $\mu$ l of HRP-conjugated streptavidin at a concentration of 0.05  $\mu$ g/ml in 0.05% PBST was added to the each well and incubated at room temperature for 30 min. The wells were washed and incubated with 100  $\mu$ l TMB (Sigma) substrate solution at room temperature for 10 min. Absorbance was measured at 450 nm after stopping the reaction with 50  $\mu$ l stop solution (1M sulphuric acid) using a FLUOstar OPTIME plate reader (BMG LABTECH). All washing steps between the incubation stages were performed with 0.2% PBST four times. In order to prove specificity of the assay, bacterial cells were incubated in the presence of free lectin or GalNac for 40 min at room temperature.

## 2.16.3 Preparation of acid-glycine extracts

Glycine extraction was performed using the method described by McCoy *et al.*, 1975. Cells of *C. jejuni* grown for two days were harvested from CBA plates and weighed. Cells were then washed twice with 0.7% NaCl and centrifuged at 10,000 x g (12,210 rpm) for 5 min. The pellet was suspended in 0.2M glycine hydrochloride pH 2.2 (Sigma) (0.3g of cells per 10 ml) and stirred at room temperature for 15 min. The suspension was centrifuged at 11,000 x g (12,806 rpm) for 15 min in order to remove cell particles.

The supernatant was dialysed in PBS using 3.5 kDa dialysis tubes (Sigma Aldrich). The acid-glycin extracts were treated with exo-glycosidase then blotted and probed with SBA lectin as described in section 2.14.8.2.

#### 2.16.4 Exo-glycosidase treatment

In order to remove terminal GalNAc residues, bacterial cells  $(4x10^8 \text{ c.f.u.})$  and acid-glycin extracts were treated with 20 U/ml of *N*-acetylgalactosaminidase (NEB) for 60 min in 10 µl total reaction volume at 37°C according to the manufacturer's protocol. Following incubation bacterial cells were diluted in PBS to a total volume of 100 µl and used for binding experiments.

## 2.16.5 Fluorescein SBA labelling of C. jejuni and E. coli cells

Fluorescent labelling of cells was performed as described previously (Cole *et al.*, 1984). Fluorescein-labelled SBA (FSBA) (Vector Laboratories) (100  $\mu$ g/ml in PBS) was mixed with an equal volume of bacterial suspension and incubated for 40 min at room temperature. Bacteria were pelleted, washed twice in PBS and centrifuged at maximum speed to remove any unbound lectin. According to manufacturer's specification, FSBA has an appropriate number of fluorochromes bound to provide the optimum staining.

For visualisation, 5  $\mu$ l of the solution with cells was trapped between the slide and the glass coverslip. Samples were observed using a laser scanning confocal microscope (Leica TCS SP2 AOBS) with a 63X oil immersion objective. Higher resolution and increased magnification was obtained using Leica software with digital zoom.

#### 2.17 Inhibition of C. jejuni binding to immobilised SBA lectin

A SBA lectin-coated 96-well microtiter plate was blocked with 1% BSA (as previously described in section 2.16.1). Following the wash step the wells were incubated with a 1-day culture *E. coli/pPGL* suspended in PBS to  $OD_{600}$  1 for 40 min at room temperature. After washing with 0.2% PBST the plate was incubated

with C. *jejuni* suspended in PBS ( $OD_{600}$  1) for 40 min at room temperature. After 3 washes with 0.05% PBST the presence of C. *jejuni* was checked using antibodies specific to C. *jejuni*.

### 2.17.1 C. jejuni detection using anti-Campylobacter antibodies

Two different anti-Campylobacter antibodies (Abs) were used:

1) Mouse anti-Campylobacter Abs (1:10000) with secondary goat anti-mouse HRP (1:5000) (AbD Serotec antibodies) and 2) rabbit anti-PEB1 Campylobacter Abs (1:10000) with secondary anti-rabbit HRP (1:1000) (Antibodies Online). SBA lectin-coated plates were used for incubation of whole cells as described in section 2.16.1, and then the following protocol was used:

100  $\mu$ l of anti-*Campylobacter* Abs was added to the wells and incubated for 60 min at 37°C. After 3 washes, 100  $\mu$ l of secondary Abs was added and incubated for 60 min at 37°C. Following 3 washes, 100  $\mu$ l of TMB was added and incubated for 10 min. The reaction was stopped by addition of 50  $\mu$ l stop solution. Washing of plates and dilution of all antibodies were performed using 0.05% PBST.

#### 2.17.2 DNA quantification of bound C. jejuni using qPCR

## 2.17.2.1 DNA extraction

DNA samples were purified from microtitre plate wells after incubation with E. *coli/*pPGL and/or *C. jejuni* (as described in section 2.17.1) using QIAGEN kit for DNA purification from small volumes (QIAamp UCP Pathogen Mini Kit). Purification was performed according to "*Sample Prep Spin Protocol*". The only protocol modification was that all the reagents used were scaled down by a factor of four. After washing and drying the wells, 100  $\mu$ l of buffer ATL (from the kit) was added. The rest of the procedure was carried out according to the protocol.

Purified DNA samples were stored at -20°C. DNA purity using the A260/280 ratio was found using a spectrophotometer (NanoVue).

#### 2.17.2.2 qPCR

Microbial DNA qPCR assay kit for *flhA* gene (one of the *C. jejuni* virulence genes) (Qiagen) was used to detect the presence of *C. jejuni* cells. All procedures were performed according to the manufacturer's protocol: "*Real-Time PCR Using Microbial DNA qPCR*".

The reaction was conducted in a total volume of 25  $\mu$ l, with 12.75  $\mu$ l master mix (HotStart DNA Polymerase) 1  $\mu$ l DNA samples, 1  $\mu$ l microbial DNA qPCR mixture with pre-dispensed *flhA* gene specific primers and 10.75  $\mu$ l water. Each qPCR run contained a 'no template' control (RNase-free water added instead of DNA), a DNA positive control included in the kit, as well as control DNA purified from 4x10<sup>8</sup> c.f.u. of *C. jejuni* cells. Purified DNA was then diluted several times to correspond to the different number of cells. DNA dilutions corresponding to 1x10<sup>6</sup>, 1x10<sup>5</sup>, 1x10<sup>4</sup>, 1x10<sup>3</sup>, 1x10<sup>2</sup> cells were used. Each control sample was analysed in duplicate. The PCR was run using a CFX96 Real Time Thermocycler System C1000 (Bio-Rad).

The cycle parameters were as follows: an initial PCR activation step for ten min at 90°C was followed by a 2-step cycle: denaturation at 95°C for 15 sec and annealing/extension at 60°C for 2 min. The number of cycles was 40.

#### 2.17.2.3 Data Analysis

An absolute quantification method with a standard curve was used to determine the number of DNA copies in samples, where the number of DNA copies corresponded to the number of cells. Standard curves were plotted using cycle

threshold (CT) values vs number of cells (DNA copies).

## 2.18 RNA isolation and one-step RT-qPCR

## 2.18.1 qPCR primers

RT-qPCR was used for gene expression studies of peb3 and kpsM using the

primers listed in Table 2.5.

Primer name	Primer sequence (5'-3')	Used for
q-16s-for	ACAGGTGCTGCACGGCTGTC	Control
q-16s-rev	TGCTCGGCCGAACCGTTAGC	
Peb3_qpcr_for	GCATCGGCTTGATCTTGTGCG	peb3 expression
Peb3_qpcr_rev	CGTTGTGCCTGAAGGTGCTGG	studies
kpsM_qpcr_for	GCCTGAGTTCCATTCATAAGCTGGG	kpsM expression
kpsM_qpcr_rev	TGGGTAGTTGGGGAGCCTATGAG	studies

Table 2.5. qPCR primers used for gene expression studies.

Primers were designed from *C. jejuni* NCTC 11168 DNA sequences using NCBI web server (http://www.ncbi.nlm.nih.gov/nuccore/AL111168.1). In addition, potential secondary structures and primer-dimer formation were verified using an online tool, Sigma-Genosys DNA calculator. Primers were purchased from Sigma Genosys Ltd. The sequences of the genes of interest were put into Primer BLAST (NCBI) to produce primers. The length of primers designed was between 18 and 21 bp. The amplicon length using these primers should be between 85 and 250 bp. Once the primers were verified with these programs, they were checked through the NCBI BLAST nucleotide tool to ensure the specificity with *C. jejuni*.

For RNA isolation, *C. jejuni* cells were grown for 48 h under microaerophilic conditions at  $37^{\circ}$ C in three separate flasks (biological replicates) in BHI (40 ml). Samples were taken at 14 h, 24 h, 38 h and 48 h intervals. Immediately after removing samples from the flasks RNAprotect Bacteria Reagent (Qiagen) was added to the cultures to stabilise mRNA. The culture and RNAprotect Bacteria Reagent were mixed and incubated for 5 min at room temperature, then centrifuged for 10 min at 5000 x g (4985 rpm). The supernatant was removed and the pellet was either processed immediately or stored at -80°C. The total RNA from each sample was extracted using the RNeasy Mini Kit (Qiagen) according to the manufacturer's protocol (Protocol 7). The purified RNA samples were treated with On-Column DNase Digestion Kit (Qiagen) in order to remove residual DNA contamination. Isolated RNA samples were stored at -80°C or used immediately for quantitative real time PCR (RT-qPCR).

## 2.18.3 Quantification of total RNA

RNA concentration was estimated using a NanoVue spectrophotometer. RNA samples were considered pure with an A260/280 ratio between 1.7 and 2.0 and A260/230 ratio above 2.0. The quality and integrity of total RNA was monitored using the Agilent 2100 Bioanalyzer (Agilent Technologies). RNase-free water was used as a control.

## 2.18.4 RT-qPCR using QuantiFast SYBR<sup>®</sup> Green

One-step RT-qPCRs were performed using QuantiFast SYBR Green RT-PCR Kit (Qiagen) in a total volume of 12.5 µl, containing master mix (QuantiFast SYBR Green RT-PCR Buffer with MgCl<sub>2</sub>, Hot start DNA Polymerase, dNTP mix and

ROX<sup>™</sup> passive reference dye) and QuantiFast RT Mix (containing Omniscript<sup>®</sup> Reverse Transcriptase and Sensiscript<sup>®</sup> Reverse Transcriptase), forward and reverse primers, diluted RNA (50 ng) and RNase-free water.

Primers were added to 100 µM final concentration. Each sample was analysed in technical duplicates and biological triplicates. Every run contained a no template control (RNase-free water added instead of RNA), no primer control (RNase-free water added instead of primers) and a water control, and performed in duplicate. The PCR was run in a CFX96 Real time System C1000 Thermocycler (Bio-Rad). The cycle parameters were as follows: an initial reverse transcription step for ten min at 50°C, and then PCR initial activation step for five min at 95°C followed by two-step cycling: denaturation at 95°C for 10 sec and combined annealing at 60°C for 30 sec. The number of cycles was 35. The 16S rRNA was used as the internal control. The SYBR fluorescence was measured after each cycle and CT values produced from qPCR runs were compared against the control gene. The changes in gene expression (*n*-fold) were calculated from the qRT-PCR data.

## 2.18.5 Analysis using 2<sup>-ΔΔCT</sup> method

The relative change in gene expression was calculated using the Livak and Schmittgen (2001)  $2^{-\Delta\Delta Cl}$  method. Statistical significance was calculated using one-way ANOVA (analysis of variance).

# 2.19 PEB3 probing of Caco-2 cell, THP-1 cell lysates and normal intestine cell lysates

Purified PEB3 protein was used to probe blots with Caco-2 cell lysate (Santa Cruz Biotechnology), THP-1 cell lysate (Santa Cruz Biotechnology) and normal intestine cell lysate (Abcam). 5 µl of each cell lysate was loaded onto SDS-PAGE

gels. After transfer, blots were either incubated with glycosylated PEB3 or nonglycosylated protein for 2 h at room temperature. Control blots were not treated with PEB3 protein. The rest of the procedure was carried out as described earlier (section 2.14.8.1 and/or 2.14.8.2).

## **2.20 Bioinformatics**

Bioinformatics tools were used for restriction mapping and functional analysis. NEBcutter V2.0 tool was used to perform restriction mapping in order to ensure the correct orientation (http://tools.neb.com/NEBcutter2/).

C. *jejuni* nucleotide and amino acid sequences were obtained from databases at the Welcome Trust Sanger Institute website

(http://www.genedb.org/Homepage/Cjejuni).

The National Centre for Biotechnology Information (NCBI) website

(https://blast.ncbi.nlm.nih.gov/Blast.cgi) was used to search proteins similar to

Cj0289c using BLASTP (protein vs protein) and SWISS-PROT database. The

BLAST program was also used to compare the sequences of two different proteins for overlap.

The Artemis program downloaded from the Sanger Institute website (www.sanger.ac.uk) was used to check if the *C. jejuni* genes encoding glycoproteins were known to be adhesins.

PSORT (http://www.psort.org/psortb/) and Softberry

(http://morissardjerome.free.fr/infobiogen/www.softberry.com/berry.html) programs were used for prediction of the subcellular location of putative adhesins.

## 2.21 Statistical analysis

All experiments were repeated a minimum of three times (biological replicates), and data were expressed as mean  $\pm$  SD. Differences were considered significant for P <0.05 (\*, P=0.05-0.01; \*\*, P <0.01-0.001, \*\*\*, P <0.001). Comparison of two groups was made with an unpaired, two-tailed student's t-test. Comparison of multiple groups was made with one way ANOVA

(http://vassarstats.net/anovalu.html).

#### **CHAPTER 3: Results**

## 3.1. Interaction of C. jejuni cells with SBA lectin

In order to investigate the mechanisms and factors involved in *C. jejuni* interaction with host cells, a binding assay based on monitoring bacterial attachment to immobilised analogues of host cell receptors was developed. In this model it is suggested that some N-linked glycosylated proteins may be expressed on the bacterial cell surface, and play the role of an adhesin. As glycan moieties in these glycoproteins contain terminal GalNAc residues recognised by SBA (Linton *et al.*, 2002), the latter could be considered as an analogue of a host cell receptor. Although the *in vitro* interaction of glycoproteins with SBA lectin has been demonstrated previously, the interaction of SBA lectin with whole cells has not.

#### 3.1.1 Validation of the binding assay

Bacterial adhesion was measured using an ELISA-like technique. This technique developed in this study. This *in vitro* model was used to measure bacterial attachment to SBA lectin. Adherent bacteria were detected using biotinylated SBA, which preferentially binds to oligosaccharide structures with terminal GalNAc residues. For detection of biotinylated SBA, the streptavidin-peroxidase polymer was used. Activated streptavidin, conjugated to horseradish peroxidase, is covalently conjugated to a polymer backbone, which increases the biotin binding capacity and amplifies the signal. BSA coated wells were used as a negative control.

A 96-well microtitre plate with immobilised SBA lectin was used for the investigation of bacterial cells producing adhesins containing N-linked glycan moieties. In order to get reproducible data, several experiments were carried out

confirming the specificity and sensitivity of binding (Figure 3.1). Omission of the BSA blocking step lead to false-positive results. No signal was present without bacterial cells or without incubation with biotinylated SBA (Figure 3.1 and Figure 3.2). Immediately after completion, the absorbance was measured and results were analysed using Excel for graphical comparison.



Figure 3.1. Validation of ELISA-like method. After coating a 96-well microtitre plate with immobilised SBA lectin, uncoated sites were blocked by incubation with 1% BSA to reduce non-specific binding. This was followed by incubation with whole bacterial cells. Negative and false-positive controls were obtained by omitting one of the components of the system during the process.

v, added; x, not added.



Figure 3.2. The effect of BSA blocking buffer on the signal. A false positive signal was seen in the wells that were not blocked with BSA. No binding was detected in the wells in which no cells were added. Bars represent mean  $\pm$  SD. Each sample was analysed in technical triplicates. Results are representative of 3 separate experiments that gave comparable results. \*P <0.05 was considered statistically significant. \*\*P <0.01.

All samples in the ELISA assays were tested in technical triplicates, and the mean absorbance was determined. BSA-coated wells were used as a negative control. In order to analyse the results, absorbance in BSA-coated wells (background effect) was subtracted from the absorbance of each sample. Sample absorbance statistically different from the negative control was regarded as positive.

## 3.1.2 Dose-dependent binding of C. jejuni cells to immobilised SBA lectin

After validation of the method the system was successfully tested using *C. jejuni* strain 11168H. The results confirmed specific interaction of *C. jejuni* with immobilised SBA lectin. Incubation of *C. jejuni* cells ( $4x10^8$  cells) produced an absorbance of 1.563 +/- 0.12, whereas at  $4x10^6$  cells the absorbance was 0.440 +/- 0.05 (Figure 3.3). Incubation of cells in the presence of soluble SBA lectin reduced the absorbance from 1.563 +/- 0.12 to 0.867 +/- 0.16 (Figure 3.4).



Figure 3.3. Interaction of *C. jejuni* 11168H with immobilised SBA lectin. Binding of whole cells with SBA lectin was concentration-dependent. The figures below the bars indicate the numbers of cells per well. Bars represent mean  $\pm$  SD. Each sample was analysed in technical triplicates. Results are representative of 3 separate experiments that gave comparable results. \*\*\* P <0.001 was considered statistically significant.



**Bacterial binding** 

Figure 3.4. Interaction of *C. jejuni* 11168H with immobilised SBA in the presence of soluble SBA lectin. Free soluble SBA lectin at the concentration of 0.1  $\mu$ M inhibits binding of whole *C. jejuni* 11168H cells. Bars represent mean  $\pm$  SD. Each sample was analysed in technical triplicates. Results are representative of 3 separate experiments that gave comparable results. \*\* P <0.01 was considered statistically significant.
As can be seen from the results, bacterial binding is concentration-dependent. Although there is reduction in binding there are still significant residual binding present. Incubation of bacterial cells in the presence of soluble SBA lectin inhibits binding, which suggests that binding is specific to SBA lectin.

## 3.1.3 Generation of E. coli that expresses SBA-reactive molecules

In order to confirm that the glycosylation gene cluster (pgl locus) can be used to generate recombinant E. coli that binds SBA lectin, PGL1 plasmid carrying the entire N-linked protein glycosylation apparatus (pgl gene cluster) of C. jejuni 81116 (Fry et al., 1998) was introduced into E. coli XL2 strain. Restriction analysis confirmed the presence of pPGL1 plasmid in E. coli (Figure 3.5). In order to further confirm that the developed model of attachment was specific and was based on the surface-located GalNAc moieties, binding experiments were repeated using E. coli carrying pPGL1 plasmid. Due to the absence of glycosylation acceptor proteins in strain E. coli XL2, the pgl system was found to be able to glycosylate bacterial lipo-polysaccharide, resulting in exposure of GalNAc residues to the cell surface (van Sorge et al., 2009). Confirmed E. coli /pPGL1 strain (designated as E. coli/pPGL in this thesis) was used in ELISA experiments. The interaction of surface-located GalNAc moieties on the surface of E. coli/pPGL with SBA lectin confirmed the specificity of this developed assay, as E. coli lacking pgl did not interact with immobilised SBA. The mean absorbance in the wells incubated with E. coli/pPGL cells was 2.293 +/- 0.09, whereas in the presence of free GalNAc absorbance was 0.859 +/- 0.04 (Figure 3.6). The results confirmed that E. coli/pPGL cells are capable of binding to immobilised SBA lectin in a GalNAc-dependent fashion.



**Figure 3.5. Restriction analysis of pPGL1 plasmid.** Digestion of plasmid was performed using and *Sph*I (Lane 2) and *Eco*RV (Lane 3). The expected sizes of fragments using with *Eco*RV-15.0 kb and 5.6 kb. Digestion with *Sph*I produces two fragments of 18.7 kb and 1.8 kb size. Lane1: 1 kb DNA ladder.



Figure 3.6. Attachment of *E. coli/*pPGL to immobilised SBA lectin. *E. coli* with the pPGL insert binds SBA lectin. Binding is inhibited by incubation with GalNAc at 25  $\mu$ M. No binding of the recipient strain *E. coli* XL2 was detected. Bars represent mean  $\pm$  SD. Each sample was analysed in technical triplicates. Results are representative of 3 separate experiments that gave comparable results. \*\*\* P <0.001 was considered statistically significant.

In order to further confirm interaction between *C. jejuni* or *E. coli*/pPGL with SBA lectin, the bacterial cells were incubated with fluorescein-labelled SBA (FSBA). After incubation of cells with FSBA as described in the Materials and Methods (section 2.16.5), the cells were examined by fluorescence microscopy. Both *C. jejuni* 11168H and *E. coli* XL2/pPGL cells (but not the recipient *E. coli* XL2) fluoresced green, indicating that SBA lectin binds to the surface of the cells (Figure 3.7).

A



**Figure 3.7. Confirmation of SBA binding to the surface** *C. jejuni* and *E. coli/pPGL* cells. Confocal microscopy of *C. jejuni* 11168H (A) and *E. coli/pPGL* (B and C) cells after treatment with FSBA. Representative of several images taken of cells from 2 slides (x630 magnification). Resolution of *C. jejuni* was difficult due to the small size of bacteria.

Fluorescence microscopy with FSBA as a probe clearly demonstrated fluoresceinlabelling of the cell surface of *E. coli*/pPGL, but not in *E. coli* lacking the *pgl* locus (data not shown), confirming the presence of the SBA ligand GalNAc on the surface of the recombinant *E. coli* strain. The results also confirmed that *C. jejuni* cell surface glycoproteins interacted with the SBA lectin and that the detection of N-linked glycans is possible using a confocal microscope. Together, these results indicated that *E. coli* XL2/pPGL express GalNAc residues on the surface of the cells.

### 3.1.4 Specificity of binding of C. jejuni to SBA lectin

Incubation of a suspension of *C. jejuni* 11168H cells with immobilised SBA resulted in bacterial attachment. This binding was found to be specific, as demonstrated by the inhibitory effects of both soluble GalNAc and a soluble form of SBA, in a dose-dependent manner. Inhibition was detected in the presence of 0.1  $\mu$ M soluble SBA lectin, the lowest concentration used (Figure 3.8). Absorbance of the control (without soluble SBA lectin) was 1.388 +/- 0.09, whereas cells incubated in the presence of soluble SBA lectin at 0.1  $\mu$ M concentration produced an absorbance of 0.706 +/- 0.01. The presence of soluble GalNAc resulted in an inhibitory effect with concentrations of 75  $\mu$ M (the minimum inhibitory concentration) and above, giving a mean absorbance in the wells of 1.241 +/- 0.07 compared to 1.476 +/- 0.04 in the control (Figure 3.9). A decrease in absorbance indicates fewer bound cells to the immobilised SBA lectin, compared with control values.

Moreover, the bound cells could be detached in the presence of soluble forms of SBA lectin or GalNAc. The absorbance in wells that were first incubated with bacterial cells and then treated with 5 mM SBA lectin was 0.195 +/- 0.04, which

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was lower compared to the absorbance in the wells that were treated with 5 mM GalNAc (absorbance was 0.596 +/- 0.01. Both of these were far reduced compared with the control value of 1.676 +/- 0.21. SBA lectin detached bound cells more efficiently (by 8.5 times) compared to the same molar concentration of GalNAc (2.8 times) (Figure 3.10).

Together, the results from the inhibition of attachment and detachment experiments suggest that competitive inhibition of binding is more pronounced with SBA lectin than with GalNAc. Further confirmation of specificity of binding was obtained by treatment of bacterial cells with an exoglycosidase. *C. jejuni* glycoproteins bind to SBA lectin due to GalNAc residues in the glycan component, thus whole bacterial cells were treated with Nacetylgalactosaminidase to remove terminal GalNAc. This resulted in a remarkable reduction of the ability of bacterial cells to attach (Figure 3.11), suggesting that the GalNAc moieties are a requirement for bacterial binding.



Figure 3.8. Effect of different concentrations of soluble SBA lectin on binding of *C. jejuni* 11168H. Cells were incubated with different concentrations of free (soluble) SBA lectin. No free SBA lectin was added to control samples. Bars represent mean  $\pm$  SD. Each sample was analysed in technical triplicates. Results are representative of 3 separate experiments that gave comparable results. \*\* P <0.01 was considered statistically significant. \*\*\* P < 0.001



Figure 3.9. Effect of different concentrations of soluble GalNAc on binding of *C. jejuni* 11168H. Cells were incubated with different concentrations of free (soluble) GalNAc. No GalNAc was added to control samples. Bars represent mean  $\pm$  SD. Each sample was analysed in technical triplicates. Results are representative of 3 separate experiments that gave comparable results. \*\* P <0.01 was considered statistically significant. \*\*\* P <0.001







Figure 3.11. The effect of exoglycosidase on binding. Reduction of binding upon treatment of bacteria with GalNAc-specific exoglycosidase. Bacterial cells were incubated with exoglycosidase (20 U/ml) for 1h under microaerophilic conditions at  $37^{\circ}$ C in 10 µl total reaction volume. Following incubation cells were diluted in PBS and used in binding experiment. Bars represent mean ± SD. Each sample was analysed in technical triplicates. Results are representative of 3 separate experiments that gave comparable results. \*\*\* P <0.001 was considered statistically significant.

**3.2** *Peb3* gene is involved in the attachment of whole cells to SBA lectin Previous studies have suggested a possible location of PEB3 protein on the bacterial cell surface (Pei *et al.*, 1991; Linton *et al.*, 2002). The ability of purified PEB3 protein to bind SBA lectin due to the presence of a GalNAc-containing glycan moiety has also been demonstrated (Linton *et al.*, 2002). As PEB3 is a glycoprotein, which can be involved in the binding of *C. jejuni* to immobilised SBA, a *peb3* mutant was constructed and its binding properties were investigated using a developed binding assay.

### 3.2.1 Construction and confirmation of peb3 mutant

A PCR was used to amplify the gene of interest, *peb3*, using primers peb3\_for and peb3 rev and *C. jejuni* 11168H genomic DNA. After amplification, the PCR

product was purified and run on an agarose gel (Figure 3.12). PCR product was cloned into pGEM-T Easy vector by ligation and transformed into *E. coli* cells. After transformation *E. coli* colonies were verified for the presence of *peb3* gene using PCR with *peb3* primers. The orientation of *peb3* gene in the pGEM\_peb3 plasmid was checked in several clones.





Two restriction maps were constructed using NEBcutter program using *Hind*III and *Psi*I enzymes (Figure 3.13, A and B). In forward orientation the sizes of generated fragments were 1130 bp, 388 bp and 2427 bp, whereas in the reverse orientation the sizes of fragments were 603 bp, 388 bp and 2954 bp. Restriction analysis was conducted to confirm the forward orientation. Double digestion generated three fragments of expected sizes (1.1 kb, ~0.4 kb and ~2.4 kb). The clone in forward orientation (with the same orientation as *peb3* gene) was used for the insertion of the *kan<sup>r</sup>* gene.

The pJMK30 vector was the source of the *kan'* cassette. Figure 3.14A shows the restriction map of pJMK30. Expected sizes of fragments after digestion with

*Bam*HI should be around 2684 bp and 1499 bp. Fragment sizes after digestion were verified using gel electrophoresis (Figure 3.14 B).



B

**Figure 3.13. Restriction maps of pGMT\_peb3.** pGEM\_peb3 digested with *Hind*III/*Psi*I in forward orientation (A) and reverse orientation (B). "b" fragment: the gene of interest–*peb3.* Image produced by NEBCutter v2.



B

**Figure 3.14. Verification of pJMK30 plasmid.** A. pJMK30 restriction map with 2 cutters showing the *Bam*HI restriction sites flanking the kanamycin cassette. Image produced by NEBCutter v2. B. Gel electrophoresis analysis of pJMK30 digested with *Bam*HI. The approximate sizes of the bands were identified by comparison with the DNA ladder. Lane 1: 1 kb DNA ladder; Lane 2: pJMK30 digested with *Bam*HI.

*PfI*MI-digested pGEM\_peb3 plasmid was blunt-ended and ligated with *Bam*HI blunt ended *kan'* fragment. The pGEM\_peb3\_*kan'* was transformed into *E. coli* competent cells using the technique as described in the Materials and Methods (section 2.15). Two restriction maps of pGEM\_peb3\_*kan'* plasmid with a different orientation of *kan'* cassette were constructed using *Sph*I restriction enzyme (Figure 3.15). In the forward orientation of *kan'* cassette the sizes of fragments were 2038 bp and 3421 bp (Figure 3.15A), whereas in the reverse orientation of *kan'* cassette the sizes of fragments were 4869 bp and 579 bp (Figure 3.15B). Transformation of the ligation mixture into *E. coli* XL2 produced colonies on LB agar supplemented with kanamycin. Several clones were confirmed for the presence of *kan'* insert by digestion with *Sph*I. Clone with pGEM\_peb3\_*kan'* plasmid with forward orientation of *kan'* was confirmed by restriction analysis (Figure 3.16).

The pGEM\_peb3\_kan<sup>r</sup> plasmid with confirmed forward orientation of the kan<sup>r</sup> was used for transformation into *C. jejuni* via electroporation as described in the Materials and Methods (section 2.12). Colonies were checked for the presence of kan<sup>r</sup> using PCR and *peb3* primers and DNA of three mutants and the WT. The expected size of the PCR product in the mutant would be around 2.3 kb (actual size of *peb3* = 0.753 kb + 1.5 kb kan<sup>r</sup>). The difference of 1.5 kb between *peb3* gene bands of WT and mutants indicates the presence of *kan<sup>r</sup>* in mutants (Figure 3.17).





B

Figure 3.15. Restriction maps of pGEM\_peb3\_kan<sup>r</sup> with two possible orientation of kan<sup>r</sup> cassette. A. Forward orientation of kan<sup>r</sup>. B. Reverse orientation of kan<sup>r</sup>. Image produced by NEBCutter v2.



Figure 3.16. Gel electrophoresis analysis of pGEM\_peb3\_kan<sup>r</sup>. pGEM\_ peb3\_kan<sup>r</sup> construct digested with *SphI*. Lane 1: uncut plasmid; Lane 2: digested plasmid; Lane 3: 1 kb DNA ladder.



Figure 3.17. Confirmation of *peb3* mutant (11168H/*peb3::kan'*). Gel electrophoresis analysis of three clonal isolates. Lane 1: 1 kb DNA ladder; Lane 2: wild type 11168H; Lanes 3–5 – three clonal isolates of 11168H/*peb3::kan'*.

# **3.2.2 Mutation of** *peb3* **resulted in a reduced ability of cells to bind to SBA** Clonal isolates of *C. jejuni* 11168H/*peb3::kan<sup>r</sup>* mutant were tested using the binding assay to check if mutation of *peb3* affected the ability of cells to bind to immobilised SBA. The mutation in *peb3* resulted in a reduction of binding in all three independent clonal isolates (Figure 3.18).

The results from this experiment also showed that the *peb3* mutation did not completely eliminate binding, suggesting that other glycoprotein(s) may be involved in specific interactions with this analogue of a host cell receptor. This hypothesis was supported by the reduction of residual binding of the 11168H/ *peb3::kan'* mutant in the presence of soluble SBA lectin (Figure 3.19). In order to confirm the involvement of the *peb3* gene in binding, complementation of *peb3* mutation was performed next.







Figure 3.19. Effect of soluble SBA lectin on binding of 11168H/peb3::kan' mutants. Comparison of binding of three clonal isolates of 11168H/peb3::kan' mutant cells to immobilised SBA lectin in the presence and absence of soluble SBA lectin. Bars represent mean  $\pm$  SD. Results are representative of 3 separate experiments that gave comparable results. \*\* P <0.01 was considered statistically significant.

### 3.2.3 Complementation of peb3 restored binding ability of C. jejuni

In order to check whether *peb3* gene function could be restored after insertional inactivation, the *peb3* gene was PCR-amplified and inserted into the pRRC vector. The pRRC construct was previously designed for use in complementation studies in *C. jejuni* that can be achived by insertion a copy of the gene of interest into one of the three rRNA gene clusters without any negative impact (Karlyshev and Wren, 2005).

This was performed in order to prove the involvement of the *peb3* gene in adhesion of *C. jejuni* to SBA lectin. Figure 3.20A shows the restriction map of pRRC plasmid (digestion with *Sal*I should produce 846 bp and 4999 bp fragments). Purified and digested plasmid was verified using gel electrophoresis and compared with the expected sizes of fragments (Figure 3.20B).

*Peb3* gene was PCR-amplified using *peb3* primers (with *Xba*I restriction site in primer sequences). PCR product was purified and run on the gel together with digested pRRC plasmid to verify the presence of product (Figure 3.21).





B

A

**Figure 3.20. Verification of pRRC plasmid.** A. pRRC restriction map with 2 cutters showing the *Sal*I restriction sites. B. Gel electrophoresis analysis of pRRC digested with *Sal*I enzyme. Lane 1: uncut pRRC; Lane 2–5: different samples of pRRC digested with *Sal*I; Lane 6: 1 kb DNA ladder.



**Figure 3.21. Gel electrophoresis analysis of PCR product (***peb3***) and pRRC plasmid.** Lane 1: PCR product (*peb3*) of ~0.8 kb; Lane 2: purified PCR product; Lane 3: pRRC plasmid digested with *Xba*I; Lane 4: 1 kb DNA ladder.

Purified PCR product (*peb3*) was used for insertion into *Xba*I-digested pRRC vector by ligation. The product of ligation was used for transformation into *E. coli* competent cells. Recombinant *E. coli* colonies were verified for the presence of *peb3* using restriction analysis. Figure 3.22A shows the restriction map of pRRC\_peb3. The pRRC\_peb3 plasmid with confirmed insert (Figure 3.22B, Lane 7) was used for checking the orientation of the *peb3* gene, as it was difficult to identify the orientation using *Pflm*I and *Eco*RV. Digestion with these enzymes gave relatively similar fragments on the gel in both orientations (forward orientation 4653 bp, 1415 bp and 577 bp; reverse orientation 4908 bp, 1160 bp and 577 bp). Two restriction maps of pRRC\_peb3 with different orientations of the *peb3* gene were constructed using digestion with *Pfl*MI and *Bam*HI enzymes. In forward orientation of *peb3* the sizes of fragments are 5244 bp, 855 bp and 539 bp (Figure 3.23A). In reverse orientation of the *peb3* gene the sizes of fragments

are 5503 bp, 850bp and 280 bp (Figure 3.23B). Restriction analysis verified that the gene was in the same orientation as the  $cam^{r}$  gene (Figure 3.24).



**Figure 3.22.** Restriction analysis of clonal isolates of pRRC\_peb3 digested with *PfImI* and *Eco*RV. A. Map in forward orientation of *peb3*. "b" fragment: the gene of interest-*peb3*. B. Restriction digestion of different clonal isolates. Expected sizes of fragments without insert: 5.2 kb and 0.5 kb; with insert: 4.6 kb, 1.4 kb and 0.5 kb. Lane 1: 1 kb DNA ladder; Lane2: empty pRRC; Lane 3–7: pRRC\_peb3 plasmids purified from different clonal isolates. Plasmid in Lane 7 has an insert.



A

**Figure 3.23. Restriction maps of pRRC\_peb3 construct.** Restriction enzymes used are *PfIMI* and *BamHI*. A. Forward orientation of *peb3*. B. Reverse orientation of *peb3*. "b" fragment: the gene of interest– *peb3*. Image produced by NEBCutter v2.



**Figure 3.24. Gel electrophoresis analyses of digested pRRC\_peb3 construct**. Restriction digestion with *PflMI* and *BamHI* confirmed forward orientation of *peb3* gene. Lane 1: digested pRRC\_peb3; Lane 2: 1 kb DNA ladder.

Competent cells were prepared from 11168H/*peb3::kan<sup>r</sup>* mutant cells (from clonal isolate 1). The pRRC\_peb3 plasmid was used for transformation into 11168H/*peb3::kan<sup>r</sup>* strain via electroporation as described in the Materials and Methods (section 2.12). After transformation of the 11168H/*peb3::kan<sup>r</sup>* mutant with plasmid pRRC\_peb3, *Kan<sup>r</sup>* Cam<sup>r</sup> clones were isolated. PCR analysis confirmed integration of the *peb3* gene into one of the rRNA gene clusters. Each clone was analysed using the following sets of primers ak233/ak237, ak234/ak237, and ak235/ak237. Ak237 is a *cam<sup>r</sup>* gene-specific PCR primer, whereas the three other primers (ak233, ak234, ak235) correspond to the regions adjacent to the three potential insertion sites on the chromosome (Figure 3.25). Integration of *peb3* in clones 1, 2 and 4 was confirmed. No integration of *peb3* in clone 3 was found (Figure 3.26, Lanes 8–10). The complementation derivative was designated 11168H/*peb3::kan<sup>r</sup>/peb3<sup>+</sup>*.

As can be seen in Figure 3.26, in some cases PCR products with more than one primer pair could be detected. It has been shown previously that sometimes  $cam^{r}$ 

gene could integrate into two RNA clusters on the same chromosome. However this has no effect on cell growth or function (Karlyshev and Wren, 2005). The ability to bind to SBA lectin in the complementation derivative was fully restored (Figure 3.27), indicating expression of a functionally active PEB3 protein. These results confirm the involvement of the *peb3* gene in bacterial binding to SBA lectin.



Figure 3.25. Organisation of the three rRNA gene clusters in strain NCTC 11168. Three possible products of allelic replacement resulting from recombination of pRRC with the genome (diagram taken from Karlyshev and Wren, 2005).



Figure 3.26. PCR analysis of four insertion derivatives (clones) resulting from transformation of strain 11168H with pRRC. Primers used were ak233/ak237, ak234/ak237, and ak235/ak237. Lane 1: 1 kb ladder; Lane 2: clone 1 (ak233/ak237); Lane 3: clone 1 (ak234/ak237); Lane 4: clone 1 (ak235/ak237); Lane 5: clone 2 (ak233/ak237); Lane 6: clone 2 (ak234/ak237); Lane 7: clone 2 (ak235/ak237); Lane 8: clone 3 (ak233/ak237); Lane 9: clone 3 (ak234/ak237); Lane 10: clone 3 (ak235/ak237); Lane 11: clone 4 (ak233/ak237); Lane 12: clone 4 (ak234/ak237); Lane 13: clone 4 (ak235/ak237).



**Figure 3.27. Comparison between WT 11168H, 11168H/***peb3::kan'* and 11168H/*peb3::kan'* /*peb3+* to bind to immobilised SBA lectin. Reduced ability of 11168H/*peb3::kan'* mutant to bind immobilised lectin compared to original 11168H strain is restored in a complemented derivative 11168H/*peb3::kan'* /*peb3+*. Bars represent mean ± SD. Each sample was analysed in technical triplicates. Results are representative of 3 separate experiments that gave comparable results. \*\* P <0.01 was considered statistically significant.

**3.3 Mutation of** *jlpA* **doesn't affect the ability of cells to bind SBA lectin** Since deletion of *peb3* resulted in a reduction, but not the complete elimination of binding, the involvement of other glycoprotein adhesins was suggested. It has been shown previously that putative adhesin JlpA is an N-linked glycoprotein (Scott *et al.*, 2009). Therefore it was expected that mutation of *jlpA* would reduce the binding ability of *C. jejuni*. To verify this hypothesis, we constructed a *jlpA* mutant and tested the effect of this mutation on attachment.

### 3.3.1 Construction and confirmation of jlpA mutant

PCR was used to amplify *jlpA* using primers jlpA\_for and jlpA\_rev and *C. jejuni* 11168H genomic DNA. After amplification, the PCR product was purified and

run on agarose gel to verify the presence of the amplified gene (Figure 3.28). Amplified *jlpA* was used for insertion into pGEM-T Easy vector by ligation. The product of ligation was used for transformation into *E. coli* XL2 competent cells. *E. coli* colonies were verified for the presence of *jlpA* using PCR. Several clones of pGEM\_jlpA were used for checking the orientation of the *jlpA* gene.



Figure 3.28. Purified PCR product (*jlpA*). Gel electrophoresis analysis of purified PCR product. Lane1: PCR product (*jlpA*) of  $\sim$ 1.2 kb; Lane 2: 1 kb DNA ladder.

Two restriction maps were constructed using the NEBcutter program (Figure 3.29, A and B). Enzymes used were *Bsm*AI and *Bsa*BI. In forward orientation the generated sizes of fragments were 2280 bp, 1083 bp and 776 bp, whereas in reverse orientation the sizes of generated fragments were 1700 bp, 1663 bp and 776 bp. Restriction digests were run on agarose gel to confirm the forward orientation. The clone in forward orientation was used for the insertion of the *cam*<sup>*r*</sup> cassette. The pAV35 vector was the source of the *cam*<sup>*r*</sup> cassette. Figure 3.30A shows the restriction map of pAV35. Expected sizes of fragments after digestion with *Bam*HI were 2961 bp and 850 bp, which were verified using gel electrophoresis (Figure 3.30B). The pGEM\_jlpA plasmid was blunt-ended using *Bsa*BI and ligated with blunt-ended *cam*<sup>*r*</sup> cassette.



**Figure 3.29. Restriction map of pGEM\_jlpA.** pGEM\_jlpA digested with *Bsm*AI and *Bsa*BI in forward orientation (A) and reverse orientation (B). "a" fragment: gene of interest-*jlpA*. Image produced by NEBCutter v2.

Using *Cla*I and *Xba*I restriction enzymes, two restriction maps of pGEM\_jlpA\_*cam*<sup>r</sup> were constructed with different orientation of *cam*<sup>r</sup> cassette (Figure 3.31). In forward orientation of *cam*<sup>r</sup> cassette the sizes of fragments were 4524 bp and 427 bp, whereas in the reverse orientation of *cam*<sup>r</sup> cassette the sizes of fragments were 3992 bp and 989 bp.



A

B

**Figure 3.30. Verification of pAV35 plasmid.** A. pAV35 restriction map with 2 cutters showing the *Bam*HI restriction sites flanking the chloramphenicol cassette (fragment "b"). B. Gel electrophoresis analysis of pAV35. Lane 1: 1 kb DNA ladder; Lane 2: pAV35 digested with *Bam*HI; Lane 3: uncut pAV35



**Figure 3.31. Restriction maps of pGEM\_jlpA\_***cam*<sup>'</sup> **construct digested with** *Cla***I and** *Xba***I.** A. Forward orientation of *cam*<sup>'</sup>; B. Reverse orientation of *cam*<sup>'</sup>. Chloramphenicol cassette fragment "c" and *jlpA* fragment "b". Image produced by NEBCutter v2.

Transformation of ligated pGEMT\_jlpA +  $cam^r$  into *E. coli* XL1 led to the growth of colonies on LB agar (supplemented with chloramphenicol). Several clones with the presence of the  $cam^r$  insert were confirmed by digestion with *Cla*I and *Xba*I. The clone with plasmid pGEMT\_jlpA\_*cam<sup>r</sup>* with forward orientation of *cam<sup>r</sup>* was confirmed by restriction analysis, with 4.5 kb and 0.5 kb fragment sizes (Figure 3.32, Lane 7) and used for transformation into *C. jejuni*.



**Figure 3.32.** pGEMT\_jlpA + *cam'* construct digested with *ClaI* and *XbaI*. Gel electrophoresis analysis of pGEMT\_jlpA + *cam'*. Lane 1: uncut plasmid; Lane 2: 1 kb DNA ladder; Lanes 3–8: digested plasmids from different clonal isolates. Plasmid in Lane 7 has *cam'* in forward orientation.

Colonies were checked for the presence of  $cam^r$  insertion using PCR and jlpA primers. The expected size of the PCR product in mutant would be around 2 kb (actual size of jlpA = 0.8 kb + 1.1 kb  $cam^r$ ). The difference of 1.1 kb between jlpA gene bands of WT and mutants indicates the presence of  $cam^r$  in mutants (Figure 3.33).



Figure 3.33. Confirmation of 11168H/*jlpA::cam<sup>r</sup>* mutant. Gel electrophoresis analysis of three clonal isolates. Lanes 1–3: mutants 11168H/*jlpA::cam<sup>r</sup>*; Lane 4: WT *C. jejuni* 11168H; Lane 5: 1 kb DNA ladder.

# 3.3.2 Effect of jlpA mutation on binding ability of cells to SBA lectin

Three clonal isolates of the *jlpA* mutant were checked using the binding assay (Figure 3.34). Mutation of the *jlpA* gene did not affect the ability of *C. jejuni* cells to bind to immobilised SBA lectin. Surprisingly, none of the three independent clonal isolates showed any difference when compared with the control recipient strain 11168H. This indicates that JlpA is not involved in SBA lectin binding (this is consistent with specificity of this protein for Hsp90 $\alpha$ ). Reduction of the residual binding of 11168H/*jlpA::cam<sup>r</sup>* mutant in the presence of soluble SBA lectin confirmed the specificity of the mutant binding (Figure 3.35).



Figure 3.34. Mutation of *jlpA* had no effect on binding of cells to immobilised SBA lectin. Three clonal isolates of the jlpA mutant  $(11168H/jlpA::cam^r)$  were checked for the ability to bind SBA lectin using ELISA. Bars represent mean  $\pm$  SD. Each sample was analysed in technical triplicates. Results are representative of 3 separate experiments that gave comparable results.





### 3.3.3 Functional analysis of N-linked glycoproteins

Results obtained with *peb3* and *jlpA* mutants indicate the existence of some unknown GalNAc-containing adhesins. We found that Peb3, but not JlpA, is involved in binding to SBA, which is consistent with specificity of this protein for Hsp90a. All known N-linked glycoprotein gene sequences were examined as putative adhesins using Artemis software. According to the GenBank genome annotation, out of 38 N-linked glycoproteins only *cj0143* had an adhesin family signature making this protein an important candidate for future studies. Adhesion family fingerprint provides a signature for the adhesins.

In addition, two bioinformatic prediction programs were used to predict the cell localisation of known N-linked glycoproteins. PSORT and Softberry were chosen as they are based on the different prediction methods that help to give a combined result. During analysis of the sequences of known N-linked glycoproteins, Cj0143 protein was predicted to be periplasmic by both programs, which indicates that it potentially may carry dual action as a transport protein and adhesin, similar to PEB1 (Leon-Kempis *et al.*, 2006). In addition, both protein localisation prediction programs indicated that another N-linked glycoprotein (Cj0114 protein) might be located to the outer membrane or a secreted protein, suggesting it is also an important candidate for future studies.

### 3.4 Production of capsule has a negative effect on binding

The role of the capsule in bacterial attachment depends on the nature of a bacterial pathogen, and on the structural features of the capsules and adhesins. In order to investigate the role of *Campylobacter* capsule on the interaction with analogues of host cell receptors, an acapsulated (*kpsM*) mutant was tested using the *in vitro* ELISA-like binding assay.

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### 3.4.1 Confirmation of the kpsM mutant

A previously constructed non-polar *kpsM* mutant of *C. jejuni* was used in this study (Karlyshev *et al.*, 2000). The mutant was constructed by inserting a *kan'* gene containing an internal promoter, but lacking a transcriptional terminator. The presence of the *kan'* cassette in the gene was verified using PCR with primers that flank the insertion site (ak55-f and ak59-r). Two DNA templates were used, one being *C. jejuni* 11168H genomic DNA (control) and another DNA from 11168H/*kpsM::kan'* mutant. The PCR products were run on a gel to verify the presence of the amplified genes (Figure 3.36). The size of *kan'* cassette is 1.5 kb, the size of *kpsM* gene is 0.7 kb. In total the size of PCR product using 11168H/*kpsM::kan'* mutant DNA should be around 2.2 kb, which is what we found in the mutant.



Figure 3.36. Confirmation of 11168H/kpsM:: kan' mutant using PCR. PCR product was analysed by gel electrophoresis. Lane 1: 1 kb DNA ladder; Lane 2: 11168H/kpsM:: kan' mutant, Lane 3: 11168H.

In order to get more kpsM clonal isolates, chromosomal DNA of

11168H/kpsM::kan' was used for transformation into C. jejuni 11168H.

Transformation involved plating onto plates with kanamicyn selecting only those transformants that acquired a mutated copy of the target gene and any potential 'spontaneous' mutations in *kpsM* would still retain the gene inactive (due to insertional gene inactivation).

After transformation, clonal isolates were checked for the presence of *kan*<sup>r</sup> cassette using PCR (Figure 3.37). Confirmed clonal isolates were later used in a binding assay. In order to exclude the chance of spontaneous mutations occurring in the mutant, three independent clonal isolates were analysed.



**Figure 3.37. Gel electrophoresis analysis of 11168H**/*kpsM:: kan<sup>r</sup>* **clonal isolates.** PCR was used for confirmation of insertion of *kan<sup>r</sup>* cassette in 3 clonal isolates of the *kpsM* mutant. Lane 1: control (confirmed *kpsM* mutant); Lanes 2–4: three clonal isolates.

**3.4.2 Mutation of** *kpsM* resulted in an increased ability of cells to bind to SBA Clonal isolates of 11168H/*kpsM::kan<sup>r</sup>* were used in the binding assay together with the recipient strain 11168H in order to evaluate whether there was any

difference in binding between WT and mutants. The results shown in Figure 3.38 demonstrate a significantly higher affinity of binding of the non-capsular mutant of strain 11168H. This result, confirmed by the analysis of three independent clonal isolates of this mutant, suggests an interference effect of the *C. jejuni* capsule on bacterial interaction with host cell receptors. The fact that the phenotypic change was confirmed in all three of them suggests that the change observed is attributed to that particular mutation. Furthermore, confirmation of the phenotypic change in several mutants is a common practice used in the investigation of other bacteria, including *Campylobacter*. This is often considered to be an alternative to complementation, which is notoriously difficult in *Campylobacter* due to the lack of universal shuttle vectors. Results of binding assay provide strong and convincing evidence that the observed changes are indeed attributed to *kpsM* mutation.





One clonal isolate was also used for inhibition studies using soluble SBA lectin and GalNAc. Inhibition of binding was detected from 0.01  $\mu$ M SBA lectin, the lowest concentration used. Absorbance of the control was 2.202 +/- 0.10, whereas cells incubated in the presence of SBA lectin at 0.01  $\mu$ M concentration produced an absorbance of 1.647 +/- 0.06 (Figure 3.39). Soluble GalNAc also showed an inhibitory effect, with concentrations of 20  $\mu$ M and above yielding an absorbance of 2.054 +/- 0.11. The absorbance of the control (*C. jejuni* 11168H/*kpsM::kan<sup>r</sup>*) sample was 2.398 +/- 0.11 (Figure 3.40).

Further confirmation of specific binding was obtained by treatment of bacterial cells with an exoglycosidase. *C. jejuni* glycoproteins bind to SBA lectin due to GalNAc residues in the glycan component. Whole bacterial cells (*C. jejuni* 11168H/kpsM::kan') were treated with *N*-acetylgalactosaminidase to remove terminal GalNAc. This resulted in a remarkable reduction in the ability of bacterial cells to attach (Figure 3.41).







Figure 3.40. Effect of different concentrations of soluble GalNAc on binding of *C. jejuni* 11168H/kpsM::kan'. Cells were incubated with different concentrations of soluble GalNAc. No GalNAc was added to the control sample. Bars represent mean  $\pm$  SD. Each sample was analysed in technical triplicates. Results are representative of 3 separate experiments that gave comparable results. \*\* P <0.01 was considered statistically significant. \*\*\* P <0.001.



Figure 3.41. Reduction in binding of 11168H/kpsM:: kan<sup>r</sup> mutant upon treatment of bacteria with GalNAc-specific exoglycosidase. Reduction of binding upon treatment of bacteria with GalNAc-specific exoglycosydase. Bacterial cells were incubated with exoglycosidase for 1h under microaerophilic conditions at 37°C. Bars represent mean  $\pm$  SD. Each sample was analysed in technical triplicates. Results are representative of 3 separate experiments that gave comparable results. \*\*\* P <0.001 was considered statistically significant.

### 3.5 Peb3 and capsule-related genes are differentially expressed

Since the results of these experiments show that capsule and PEB3 adhesin have antagonistic effects on bacterial attachment, it was hypothesised that these structures may be differentially expressed. In order to test this hypothesis, comparative analysis of the dynamics of *kpsM* and *peb3* gene expression at different growth stages in a liquid culture using real-time PCR was performed.

### 3.5.1 Quality checking of RNA samples

The changes in expression levels of *peb3* and *kpsM* genes were studied by RTqPCR. In order to assess gene expression changes, cell cultures were incubated for 48 h. Samples were taken at 14 h, 24 h, 38 h and 48 h. Optical density was measured at each time point to assess the rate of cell growth (Table 3.1). RNA from each sample was purified as described in Materials and Methods (section 2.18.2). In order to assess the integrity/purity of RNA, samples were analysed using an Agilent 2100 bioanalyser and RNA 6000 LabChip kit. The software automatically calculated the ratio of the peak areas of the ribosomal bands 16S/23S for bacterial samples. This information, in addition to the separation analysis (electropherograms), was used as a parameter to estimate the quality of the RNA preparation. An ideal total RNA preparation would result in a 16S/23S ratio of 2. Variability in this ratio may indicate partial degradation of the sample by ribonuclease contamination during the purification procedure. In the case of complete sample degradation these bands would disappear.

The twelve samples (three biological replicates at each time point) were sequentially separated on the chip through a single separation channel and the resulting electropherograms are shown alongside the gel-like image (Figure 3.42).

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#### **Biological replicates**



B



#### Figure 3.42. The integrity/purity of RNA samples analysed using the Agilent 2100

**bioanalyser**. Data displayed as electropherograms: (A)samples 1–12) as well as a gel-like image (B). The presence of distinct 16S and 23S peaks (A) and bands (B) can be observed in all samples. Total RNA samples were purified from 3 biological replicates at 14 h, 24 h, 38 h and 48 h.

A

**Table 3.1.** *C. jejuni* optical density at 600 nm (OD<sub>600</sub>) measured over 48 h. Cells were growing in BHI supplemented with Skirrow supplement (n=3). These data are representative of 3 separate experiments.

Time	Biological replicate	Biological replicate	Biological replicate
	1	2	3
0 h	0.08	0.07	0.07
14 h	0.45	0.46	0.44
24 h	0.72	0.69	0.71
38 h	0.75	0.81	0.77
48 h	0.47	0.56	0.59

#### 3.5.2 Relative expression of *peb3* and *kpsM* genes

The expression of *peb3* and *kpsM* of *C. jejuni* 11168H was measured (using qPCR) from samples cultured under microaerophilic growth conditions at  $37^{\circ}$ C in liquid media at 14, 24, 38 and 48 h. The intervals used for measuring the expression of both genes in liquid media represented the growth stages of the culture: lag, logarithmic, stationary and decline phases (Ikeda, 2014). In order to determine the level of expression, one housekeeping gene, 16S RNA, was used. All biological and technical replicates from each time point were analysed at the same time. The expression studies showed that *peb3* expression does not change dramatically over the first 38 h; however, there was a 3-fold increase in expression of *peb3* at 48 h (Figure 3.43A). In contrast, there was a reduction in *kpsM* expression after 24 h (Figure 3.43B). There was no significant change in *kpsM* gene expression after 24 h. It is suggested that the relative change in the expression of *peb3* and *kpsM* over the period of 48 h showed that *kpsM* gene expression decreased over time compared to expression of *peb3*.



B

A



Figure 3.43. Increase of *C. jejuni peb3* gene expression (A) and decrease of *kpsM* gene expression (B) over time in a liquid culture. Gene expression levels relative to 16S rRNA were determined as described in Materials and Methods (section 2.18.5). Bars represent mean  $\pm$  SD. Results are representative of three individual experiments. \* P <0.05. \*\* P <0.01.

### **3.6 Expression and purification of His-tagged PEB3 from** *E. coli* and *C. jejuni* Since mutation in *peb3* reduces the binding ability of bacterial cells to immobilised SBA, it would be interesting to purify PEB3 and investigate the binding properties of glycosylated PEB3. An attempt to construct a system for regulated expression of a His-tagged fusion derivative of PEB3 in *C. jejuni* using pRRBC was performed.

## 3.6.1 Construction of a plasmid (pRRBC) for inducible expression of PEB3 in *C. jejuni*

The pRRBC vector was earlier constructed from pRR plasmid and an arabinoseinduced promoter derived from pBAD33 plasmid (Ikeda, 2014). pRR plasmid was constructed via insertion of fragment of rRNA gene clusters into pGEM-T Easy vector (Karlyshev and Wren, 2005). XbaI-digested pRR and pBAD (isolated from pBAB33 by digestion with ClaI and Sall) were ligated to form an intermediate construct called pRRB. Insertion of cam' cassette from pAV35 into pRRB resulted in an arabinose-inducible plasmid pRRBC, which is specific for Campylobacter (Ikeda, 2014). The pRRBC vector was verified using primers camR1, pBAD-for and pBAD-up (Table 2.1). The native KpnI site was used to insert peb3 into pRRBC. A DNA fragment containing the peb3 gene was PCR-amplified using C. ieiuni 11168H genomic DNA and primers peb3\_his-for and peb3\_his-rev. Peb3 primers were designed with the KpnI restriction site. Reverse primer had a hexahistidine tag sequence for purification purposes. The PCR product was purified and analysed by gel electrophoresis (Figure 3.44). Amplified DNA fragment was cloned into pRRBC. In order to assess the presence of insert in pRRBC-peb3 plasmid, restriction digestion was performed using KpnI (to demonstrate

similarity of the insert size to that of the PCR product) (Figure 3.45, Lanes 2, 6

and 10).



Figure 3.44. Gel electrophoresis of purified PCR product (*peb3*). Lane 1: 1 kb DNA ladder; Lane 2: amplified PCR product of expected size ~0.8 kb.

The orientation of pRRBC-peb3 was determined by restriction digestion using *Hind*III. Two restriction maps were constructed using the NEBcutter program (Figure 3.45A and B). Digestion with *Hind*III produced 4 fragments, two of which were the same size. Thus only three fragments could be observed on the gel. In forward orientation of *peb3* the generated sizes of fragments were 5890 bp, 822 bp, 550 bp and 609 bp, whereas in reverse orientation the sizes of generated fragments were 5597 bp, 1118 bp, 550 bp and 609 bp. The forward and correct orientation was detected in clone 3 (Figure 3.45C).



A



В



**Figure 3.45. Restriction analysis of pRRBC-peb3.** Restriction maps of pRRBC digested with *Hind*III in forward orientation (A) and reverse orientation (B). Fragment "c" is *peb3* gene. (C) Restriction analysis of 3 recombinant clones (pRRBC-peb3). Lanes 1, 5, 9: plasmids digested with *Hind*III; Lanes 2, 6, 10: plasmids digested with *Kpn*I; Lanes 3, 7, 11: undigested plasmids; Lanes 4, 8: 1 kb DNA ladder. Clone 3 has *peb3* in forward orientation (the sizes of fragments are 5.8 kb, 0.8 kb and 0.6 kb).

The plasmid with the correct orientation of *peb3* was used for the transformation into *C. jejuni* 11168H cells via electroporation. The transformants were then selected on CBA plates supplemented with the selective antibiotic, chloramphenicol. The transformants were verified by PCR (Figure 3.46) using GoTag master Mix and primers pBAD-up and ak237 (for *cam*<sup>7</sup>), which amplify the region in the *cam*<sup>7</sup> cassette through the gene of interest to the pBAD region. The transformants were PCR-analysed using pBAD-for primer and three other primers (ak233, ak234, and ak235) corresponding to the regions adjacent to the three potential insertion sites on the chromosome (rRNA clusters I, II and III respectively). The results of the analysis (Figure 3.47) demonstrated that recombination occurred in one of the three rRNA clusters (rRNA cluster I) in two clones.







**Figure 3.47. PCR analysis of two derivatives (clone 1 and 2) to assess the site of insertion in** *C. jejuni* **11168H.** Verification of allelic replacement using pBAD-for and ak233/ak234/ak235. The presence of pRRBC-peb3 was shown using primers ak233 and pBAD-for (cluster I) The 2.4 kb amplicon confirms the presence of the system. There were no products from using primers ak234/pBAD-for and ak235/pBAD-for. Lane 1: control (pBAD-up and ak237); Lanes 2 and 5: pRRBC-peb3 plasmid with ak233 and pBAD-for; Lanes 3 and 6: pRRBC-peb3 plasmid with ak234 and pBAD-for; Lanes 4 and 7: pRRBC-peb3 plasmid with ak235 and pBAD-for. Lane 8: 1 kb DNA ladder.

#### 3.6.2 Use of pRRBC-peb3 construct for over-expression of C. jejuni peb3 in E.

coli

pRRBC-peb3 was constructed for a specific regulated expression for *C. jejuni*. In order to test the effect of the expression system, a pRRBC construct was used for over-expression of *peb3* in *E. coli*. The *peb3* gene was put under the control of a tightly-regulated promoter pBAD in vector pRRBC. The gene was induced by addition of L-arabinose in *E. coli* liquid culture and, after induction, fusion protein was purified and analysed using SDS-PAGE. In order to check whether arabinose affects the expression of *peb3* in *E. coli*, pRRBC-peb 3 was grown in liquid media in biological duplicates, one of which was used as a control (no arabinose was added). The rate of growth (assessed by optical density) was measured in both and was shown to decrease in the induced liquid culture compared to the non-induced control.



Figure 3.48. Coomassie-stained SDS-PAGE gel showing 6xHis-tagged PEB3 purified under native conditions. The fusion protein was present in both eluates, however in eluate 1 (Lane 4) there are some contaminant bands present. Lane 1: marker (P7709V); Lane 2: flow through; Lane 3: wash; Lane 4: eluate 1; Lane 5: eluate 2. Results are representative of 3 separate experiments.

The *E. coli* strain that harboured pRRBC-peb3 plasmid with correct orientation of *peb3* (Figure 3.45, clone 3) was used for PEB3 protein purification (Figure 3.48). However, it was not possible to purify glycosylated PEB3 from *C. jejuni* using pRRBC construct, as several attempts to purify PEB3 protein using *C. jejuni* liquid culture were unsuccessful.

### 3.6.3 Expression and purification of glycosylated and non-glycosylated Histagged PEB3 from *E. coli* using pBAD33 and pPGL1 plasmids

The *E. coli* strain that harboured the pRRBC-peb3 plasmid with the correct orientation of *peb3* was used for PEB3 protein purification. However, it was only possible to purify non-glycosylated PEB3. In order to purify glycosylated PEB3 from *E. coli*, construction of the system containing two plasmids (pBAD33 and pPGL1) was considered. This system allowed the expression and purification of N-linked glycosylated proteins from *E. coli*. The pBAD\_peb3 system allowed purification of non-glycosylated PEB3, whereas *E. coli* harbouring both pBAD\_peb3 and pPGL1 plasmids allowed purification of glycosylated PEB3 from *E. coli*.

#### 3.6.3.1 Construction of pBAD\_peb3

PCR was used to amplify the gene of interest, *peb3*, using primers designed for pBAD33 plasmid. After amplification, the PCR product was purified and analysed by gel electrophoresis (Figure 3.49). PCR product was digested and used for ligation into pBAD33 plasmid, yielding pBAD\_peb3. *E. coli* colonies (transformants) were verified for the presence of *peb3* using restriction analysis.



Figure 3.49. Purified PCR product (peb3). PCR was run using C. jejuni DNA and specific primers. Gel electrophoresis of purified peb3 PCR product. Lane1: 1 kb DNA ladder; Lane 2: PCR product (peb3) of ~0.8 kb.

Two restriction maps were constructed using NEBcutter program with and without insert using *PfI*MI enzyme (Figure 3.50, A and B). Expected sizes of fragments with insert: 3.0 kb, 2.1 kb, 0.9 kb and without insert: 3.2 kb and 2.1 kb. Restriction digests were analysed by gel electrophoresis to confirm the presence of an insert. Digestion with *PfI*MI generated three fragments of expected sizes (3.0 kb, ~2.1 kb and ~0.9 kb) (Figure 3.51). Clones with insert were sent for sequencing using primers peb3\_pBAD-for and peb3\_pBAD-rev. Clone 1 and 3 had mutations, but not clone 2. Thus, clone 2 was used for purification of non-glycosylated PEB3 and for further experiments.



A



B

Figure 3.50. Restriction maps of pBAD33 (A) and pBAD\_peb3 (B) digested with *PfI*MI. On map B, "b" fragment is the gene of interest – *peb3*.



Figure 3.51. Restriction digestion analysis of pBAD33 and pBAD\_peb3 construct using *PfIMI* enzyme. Restriction digests were analysed using gel electrophoresis. Lane1: 1 kb DNA ladder; Lane 2: digested pBAD33; Lanes 3–5: pBAD\_peb3 digested with *PfIMI* confirming insertion of *peb3* gene in three clones (3.0 kb, ~2.1 kb and ~0.9 kb).

#### 3.6.3.2 Construction of pBAD\_peb3/pPGL

pPGL1 plasmid was transformed into an *E. coli* strain harbouring plasmid pBAD\_peb3. The transformation mixture was plated on LB plates supplemented with chloramphenicol and ampicillin, in order to make sure that both plasmids were present. Clones were used for plasmid purification and assessed for the presence of both plasmids via gel electrophoresis (Figure 3.52A). The purified plasmid extracts were digested with *Pf*/MI enzyme and run on a gel along with the uncut samples (Figure 3.52B). The expected fragment size of the digested sample was as follows; for plasmid extract without pPGL1 three fragments of 3.0 kb, 2.1 kb and 0.9 kb and for plasmid extract with both plasmids five fragments of 11.7 kb, 8.8 kb, 3.0 kb, 2.1 kb and 0.9 kb. Clone 3 (Figure 3.52B, Lane 6) was used for PEB3 protein purification experiments, as it had the correct size and number of fragments.



Figure 3.52. Confirmation of the presence of two plasmids (pBAD\_peb3 and pPGL) in three clonal isolates after transformation of pBAD\_peb3 into *E.coli*/pPGL strain using gel electrophoresis analysis. A- Lane 1-3: uncut purified plasmids from three clonal isolates; Lane 4: 1 kb DNA ladder. B. Restriction digestion analysis using *PfI*MI of three clonal isolates with two plasmids. Sample in Lane 6 has both pBAD\_peb3 and pPGL. Lanes 1, 3, 5: uncut plasmids; Lanes 2, 4, 6: digested plasmids; Lane 7: uncut pPGL1; Lane 8: digested pPGL1; Lane 9:1 kb DNA ladder.

#### 3.6.3.3 Over-expression and purification of PEB3 using E. coli pBAD\_peb3

#### and E. coli pBAD\_peb3/pPGL

pBAD\_peb3 *E. coli* strains with and without pPGL1 were used for liquid media cultures with a starting point of OD<sub>600</sub> 0.1. PEB3 was over-expressed by addition of 0.1% arabinose and the proteins were purified under native conditions. The protein samples were run on a SDS-PAGE. As can be observed from Figure 3.53, two forms of PEB3 (glycosylated and non-glycosylated) were obtained using these strains. The size of glycosylated PEB3 (~27 kDa) was slightly larger than non-glycosylated PEB3 (~25.5 kDa).



Figure 3.53. Small scale protein purification after over-expression of PEB3 using *E.coli* pBAD\_peb3 and *E.coli* pBAD\_peb3/pPGL strains. SDS-PAGE analysis of proteins purified from pBAD\_peb3 *E. coli* strains with and without pPGL1. Lane 1: lysate after induction (pBAD\_peb3); Lane 2: flow-through (pBAD\_peb3); Lane 3: wash (pBAD\_peb3); Lane 4: eluate (pBAD\_peb3); Lane 5: lysate after induction (pBAD\_peb3/pPGL); Lane 6: flow-through (pBAD\_peb3/pPGL); Lane 7: wash (pBAD\_peb3/pPGL); Lane 8: eluate (pBAD\_peb3/pPGL); Lane 7: wash (pBAD\_peb3/pPGL); Lane 8: eluate (pBAD\_peb3/pPGL); Lane 9: marker. Results are representative of 3 separate experiments.



Figure 3.54. Large scale protein purification after over-expression of PEB3 using *E.coli* pBAD\_peb3 and *E.coli* pBAD\_peb3/pPGL strains. Identification of glycosylated and nonglycosylated proteins using SDS-PAGE. Lane 1: marker; Lane 2: lysate after induction (pBAD\_peb3); Lane 3: flow-through (pBAD\_peb3); Lane 4: wash 1 (pBAD\_peb3); Lane 5: wash 2 (pBAD\_peb3); Lane 6: eluate (non-glycosylated PEB3 with size ~25.5 kDa); Lane 7: lysate after induction (pBAD\_peb3/pPGL); Lane 8: flow-through (pBAD\_peb3/ pPGL); Lane 9: wash 1 (pBAD\_peb3/ pPGL); Lane 10: wash 2 (pBAD\_peb3/ pPGL); Lane 11: eluate (pBAD\_peb3/pPGL). Results are representative of 2 separate experiments. In order to obtain larger quantities of both proteins, large scale protein purification was performed as described in Materials and Methods (section 2.14.6). The protein samples were analysed using SDS-PAGE and Western blotting. Coomassie staining showed both glycosylated and non-glycosylated proteins (Figure 3.54). Western blot analysis using anti-His Abs showed the presence of the tagged fusion protein (Figure 3.55, A and B).

#### 3.6.3.4 Exoglycosidase treatment of glycosylated PEB3

In order to confirm the difference between the two forms of protein (one glycosylated and another non-glycosylated, used as control), both fractions were subject to treatment with exoglycosidase. Treated and untreated samples were subject to SDS-PAGE and Western blot analysis (Figure 3.55). On Figure 3.55A and 3.55B it can be observed that after treatment with exoglycosidase, the size of glycosylated PEB3 (PEB3 glyco) is slightly smaller compared to the non-treated sample. This observation confirms that this protein is indeed glycosylated. The blot was probed with SBA lectin (biotinylated for detection) to determine if binding between glycosylated PEB3 and SBA lectin occurred. It can be clearly observed that exoglycosidase digests glycosylated PEB3, as it is not observed on the blot that was probed with SBA lectin (Figure 3.55C, Lane 4). This is another confirmation that *E. coli* pBAD\_peb3/pPGL can be used for the expression of glycosylated PEB3 and *E. coli* pBAD\_pep3 for the expression of non-glycosylated protein.



Figure 3.55. SDS-PAGE and Western blot analysis of glycosylated and non-glycosylated PEB3 before and after exoglycosiadase treatment. A. Coomassie-stained gel showing PEB3. B. Western blotting using Anti-His Abs. C. Western blotting using biotinylated SBA lectin for probing. Lane 1: undigested non-glycosylated PEB3; Lane 2: digested non-glycosylated PEB3; Lane 3: undigested glycosylated PEB3; Lane 4: digested glycosylated PEB3; Lane 5: marker. Results are representative of 2 separate experiments.

#### 3.6.4 Over-expression of PEB3 in C. jejuni

Due to the lack of sugar uptake systems present in *C. jejuni*, it was not possible to obtain PEB3 using a pRRBC construct. Taking the above results into consideration, a slightly altered approach was used to obtain a construct using the pRRC plasmid, which allowed purification of PEB3 from *C. jejuni*.

#### 3.6.4.1 Construction of pRRC\_peb3 plasmid

pRRC plasmid was previously designed to be used as plasmid for gene expression studies in *C. jejuni* (Karlyshev and Wren, 2005). All procedures were performed as described in section 3.2.3 (complementation of the *peb3* gene), with exception

of the last stage, in which plasmid was transferred into WT *C. jejuni* competent cells using electroporation. After transformation of the 11168H with plasmid pRRC peb3, Cam<sup>r</sup> clones were selected.

PCR analysis confirmed integration of the *peb3* gene into one of the rRNA gene clusters. Each clone was analysed using the following set of primers ak233/ak237, ak234/ ak237, and ak235/ak237. Gel electrophoresis analysis confirmed integration of *peb3* in clone 2. Integration of *peb3* in clones 1 and 3 was not confirmed (Figure 3.56). The obtained derivative was designated 11168H/pRRC peb3.



Figure 3.56. PCR analysis of three insertion derivatives to check the site of insertion in 11168H. Lanes1,4 and 7: primers ak233/ak237; Lanes 2, 5 and 8: ak234/ak237; Lanes 3, 6 and 9: ak235/ak237; Lane 8: 1 kb DNA ladder.

3.6.4.2 Expression and purification of glycosylated PEB3 from C. jejuni using

#### pRRC\_peb3 construct

The 11168H/pRRC\_peb3 C. jejuni strain was grown overnight. The protein was

purified from the pellet as described in Materials and Methods (section 2.14.6)

using small scale purification. Purified fractions were analysed using SDS-PAGE and Western blotting. Equal amounts of fractions were applied onto the gel (Figure 3.57).

Both proteins, one from *E. coli* pBAD\_peb3/pgl and another from pRRC\_peb3, were glycosylated and have the same molecular weight. Both proteins were detected using anti-His Abs and biotinylated SBA lectin (Figure 3.58). These results show that *E. coli* pBAD\_peb3/pPGL construct can be used for purification of larger quantities of glycosylated PEB3 protein. After large scale purification, the PEB3 protein was used for further experiments.



Figure 3.57. SDS-PAGE analysis of PEB3 purified from *C. jejuni*/pRRC\_peb3 and *E. coli* pPAD\_peb3 /pPGL Lane 1: marker; Lane 2: lysate from 11168H/pRRC\_peb3; Lane 3: flow-through from 11168H/pRRC\_peb3; Lane 4: wash from11168H/pRRC\_peb3; Lane 5: eluate (PEB3) from11168H/pRRC\_peb3; Lane 6: eluate (PEB3) from *E. coli* pBAD\_peb3/pPGL. Results are representative of 2 separate experiments.



Figure 3.58. Western blot analysis of PEB3 purified from *C. jejuni*/pRRC\_peb3 and *E. coli*/pPABD\_peb3 /pPGL. A. Western blotting using SBA lectin. B. Western blotting using anti-His Abs. Lane 1: marker; Lane 2: PEB3 purified from *C. jejuni*/pRRC\_peb3; Lane 3: PEB3 purified from *E. coli*/pBAD\_peb3/pPGL. Results are representative of 2 separate experiments.

3.7. Interaction of PEB3 and *E. coli/pPGL* with the lysates of human cells In order to determine the receptors to which PEB3 protein binds, Western blots using host whole cell lysates were probed with PEB3. Glycan moieties of PEB3 contain terminal GalNAc residues that can specifically bind to lectin-like host cell receptors. *Campylobacter* has the ability to interact with C-type lectins (including MGL receptors) produced by host cells (van Sorge *et al.*, 2009). MGL receptors specifically recognise terminal GalNAc residues and are expressed on macrophages and DC (Higashi *et al.*, 2002; van Vliet *et al.*, 2008). Other host cell receptors may be present on the surface of normal intestinal cells.

#### 3.7.1 No interaction of PEB3 with proteins of human whole cell lysates

Human cell lysates used were normal intestinal cells, Caco-2 cells and THP-1 cells. The choice of these particular whole cell lysates was due to the fact that there is a possibility that PEB3 might interact with lectins present on either intestinal cells (normal intestinal cells and Caco-2 cells) or with lectins present on immune cells (THP-1 is a human monocytic cell line). Lysate samples were run on SDS-PAGE gels and transferred onto membranes according to manufacturers' instructions. After transfer, blots were probed with purified PEB3 and then with anti-His Abs, in order to identify binding of PEB3 to protein bands of whole cell lysates. Several attempts to identify any difference between blots that were treated with glycosylated PEB3 (purified from *E. coli* pBAD\_peb3/pPGL) and controls that were not treated with PEB3 were not successful (Figure 3.59). The same concentration of PEB3 was used across all blotting experiments.

inactivation of binding sites of the host cells during denaturing the host cell

lysates. However, it is not possible to predict in advance if this may have an effect on binding sites.



Figure 3.59. Comparison of blots treated and not treated with purified PEB3 protein. Samples were run on a 12.5% polyacrylamide gel before Western blot transfer. After incubation with PEB3, both blots were incubated with anti-His Abs in order to identify PEB3 attachment. Lane 1: THP-1 lysate; Lane 2: human intestinal cell lysate; Lane 3: SBA lectin; Lane 4: PEB3 glyco. Results are representative of 3 separate experiments.

Another reasons for no difference being observed between blots may be due to a low PEB3 protein yield used for probing the blots. In order to identify the reason for low PEB3 protein yield purified from *E. coli*, Western blot analysis of lysates before and after induction was performed (Figure 3.60). Induced and non-induced cultures were used for protein purification and Western blotting. It seems that the reason for obtaining a low PEB3 yield is due to low expression of the PEB3 protein. PEB3 can be observed in induced culture cell lysates, but not in flowthrough, suggesting that PEB3 binds to the column. However there were no problems present during the purification process itself, since there was no loss of protein during the purification process – the wash fractions were empty. Therefore the reason for low yield is thought to be due to low expression of PEB3 (Figure 3.60, A and B). Since no lysate was run after the induction procedure in the previous experiment, a further Western blotting experiment was performed in order to confirm that PEB3 protein was not lost during the purification process. Fractions before and after induction were also analysed in order to compare the presence of PEB3 in induced culture (Figure 3.61).



Figure 3.60. Western blot analysis of PEB3 protein expression using induced and noninduced *E.coli* pBAD\_peb3/pPGL. Samples were run on 12.5% polyacrylamide gel before Western blot transfer. M: marker (picture taken before transfer); Lane 1: lysate before induction; Lane 2 on A: supernatant (without induction); Lane 2 on B: supernatant after induction (with induced protein); Lane 3: flow-through; Lane 4: wash 1; Lane 5: wash 2; Lane 6: eluate1; Lane 7: eluate 2; Lane 8: marker. Equal amounts of products were loaded on the gel in order to compare the intensity of the bands. Results are representative of 2 separate experiments



**Figure 3.61. Analysis of PEB3 protein expression using Western blotting**. Samples were run on a 12.5% polyacrylamide gel before Western blot transfer. Lane 1: marker; Lane 2: lysate before induction; Lane 3: lysate after induction; Lane 4: clear lysate (it has induced protein); Lane 5: flow-through; Lane 6: wash 1; Lane 7: wash 2; Lane 8: eluate 1; Lane 9: eluate 2. Equal amounts of products were loaded on the gel in order to compare the intensity of the bands. Band in Lane 2 is probably histidine rich protein of *E. coli*. Results are representative of 2 separate experiments. Band present in Lane 2 is probably histidine rich protein of *E. coli*.

#### 3.7.2 E. coli/pPGL whole cells interact with human whole cell lysates

It was previously shown that *E. coli*/pPGL expresses glycosylated bacterial lipopolysaccharide, resulting in exposure of GalNAc residues on the cell surface (van Srorge *et al.*, 2009). The ELISA binding assay results, as well as confocal microscopy, confirmed that *E. coli*/pPGL is capable of binding to immobilised SBA lectin. Blots of human cell lysates were probed with whole *E. coli*/pPGL cells in order to check if surface GalNAc residues interact with human whole cell lysates.

The same amount of human whole cell lysates was used as in section 3.7.1. After blotting, the membrane was blocked, treated with *E.coli*/pPGL cells and then treated with biotinylated SBA lectin, in order to show the interaction of glycoproteins on whole bacterial cells with cell lysate proteins. Purified glycosylated PEB3 from *E. coli* was loaded onto the gel as control to confirm that the method works (Figure 3.62).

There are some differences in the intensity of bands between two blots, as well as the presence of extra bands in the blot that was treated with whole *E. coli*/pPGL cells. In order to check if the presence of pPGL plasmid affects the interaction of whole *E. coli* cells with lysates, both *E. coli* wild type strain and *E.coli*/pPGL were used to probe blots with normal intestinal cell lysates.

The difference observed as on Figure 3.62 was also observed in these results, between blots that were treated with the *E. coli* recipient strain and *E. coli*/pPGL, with bands being more intense in the blot that was incubated with *E. coli*/pPGL whole cells (Figure 3.63). This demonstrates the interaction of *E. coli*/pPGL cells with human cell lysates.



Figure 3.62. Comparison of blots treated and not treated with whole *E. coli/*pPGL cells. Samples were run on 12.5% polyacrylamide gel before Western blot transfer. After incubation of the blot with whole cells, both blots were incubated with biotinylated SBA lectin in order to identify any attachment of cells. Lane 1: marker; Lane 2: Caco-2 lysate; Lane 3: THP-1 lysate; Lane 4: normal intestinal cell lysate; Lane 5: purified PEB3 glyco. Results are representative of 2 separate experiments.



Figure 3.63. Comparison of blots treated with whole *E. coli*/pPGL cells (A) and *E. coli* recipient cells (B). Samples were run on 12.5% polyacrylamide gel before Western blot transfer. After incubation of blot with whole *E. coli* cells (with or without pPGL), both blots were incubated with biotinylated SBA lectin in order to identify any attached cells. Lane 1: marker; Lane 2: normal intestinal cell lysate.

After confirmation of binding of *E. coli/*pPGL to whole cell lysates, another binding experiment was performed in the presence of soluble SBA ( $0.2 \mu$ M) or soluble GalNAc (20 mM) in order to see if any inhibition of binding could be observed. After incubation with whole cells in the presence or absence of inhibitors, blots were probed with SBA lectin conjugate (Figure 3.64). As can be observed from the blot pictures, GalNAc did not have an inhibitory effect. However, inhibition of binding by SBA lectin was detected in blots with THP-1 cell lysate. The majority of bands on the blot (lane with THP-1 lysate) that was treated with *E. coli*/pPGL in the presence of soluble SBA lectin are absent. This indicates that *E. coli* binds specifically to THP-1, through SBA lectin.



Figure 3.64. Western blot analysis of whole cell lysates. After transfer, blots were incubated with *E. coli*/pPGL cells only (A), incubated with *E. coli*/pPGL cells in the presence of GalNAc (B) and incubated with *E. coli*/pPGL cells in the presence of SBA lectin (C). Lane 1: THP-1 lysate; Lane 2: normal intestinal cell lysate; Lane 3: PEB3 protein (control). Blots represent those obtained in two different experiments.

#### 3.8 E. coli/pPGL cells inhibit binding of C. jejuni to immobilised SBA

Since *E. coli*/pPGL whole cells were found to be able to bind SBA lectin, it was interesting to investigate if these cells could potentially compete with *C. jejuni* for attachment in our model of adhesion. If confirmed, this could be a useful model for the development of novel probiotics based on competition with pathogens for binding to specific host cell receptors. Thus, *E. coli*/pPGL was used for inhibition of binding of *C. jejuni* to SBA lectin. As the *C. jejuni* capsule may interfere with attachment, an acapsulated strain 11168H/*kpsM* was used for all inhibition studies.

# **3.8.1 Detection of inhibition of binding of** *C. jejuni* cells using quantitative **ELISA**

The 96-well plate coated with SBA lectin and anti-*Campylobacter* Abs were used in order to check inhibition of binding of *C. jejuni* cells. Coating was performed as described in Materials and Methods (section 2.16.1). After blocking with BSA, *E. coli*/pPGL cells were incubated in the wells in order to bind to SBA. As *E. coli*/pPGL binds to SBA lectin in the same way as *C. jejuni*, incubation of *E. coli*/pPGL cells in the SBA-coated plate would block binding sites. This would result in an inability of *C. jejuni* cells to bind to immobilised SBA, or a very reduced amount of binding.

The detection of inhibition of binding was not possible using the earlier developed binding assay (Materials and Methods section 2.16) due to the fact that it detects the presence of both *Campylobacter* cells and *E. coli*/pPGL cells. In order to check whether *Campylobacter* cells bind to SBA after incubation with *E. coli*/pPGL, mouse anti-*Campylobacter* Abs were used. First the optimal dilution of primary and secondary Abs was determined. After coating of a 96-well

microtitre plate with immobilised SBA lectin, uncoated sites were blocked by incubation with 1% BSA to reduce non-specific binding. This was followed by incubation with whole bacterial cells. All samples in the ELISA assays were tested in triplicates, and the mean absorbance was determined. BSA-coated wells were used as negative controls.

After validation of the method the system was successfully tested using *C. jejuni* cells. The results confirmed specific interaction of *C. jejuni* with immobilised SBA lectin. It has been demonstrated that bacterial binding is concentration-dependent, and incubation in the presence of soluble SBA lectin inhibits binding, which proves that binding is specific for SBA and can be detected using mouse anti-Campylobacter Abs (Figure 3.65 and Figure 3.66).



Figure 3.65. Interaction of *C. jejuni* 11168H with immobilised SBA lectin, detectable using mouse anti-*Campylobacter* Abs. Binding of whole cells with SBA lectin was concentration-dependent. The figures below the bars indicated the numbers of cells per well. Bars represent mean  $\pm$  SD. Results are representative of 3 separate experiments that gave comparable results. \*\*\* P <0.001 was considered statistically significant.



Figure 3.66. Binding in the presence of soluble SBA lectin using mouse anti-Campylobacter Abs. Soluble SBA lectin at a concentration of 0.1  $\mu$ M inhibits binding of whole C. jejuni 11168H cells to immobilised SBA lectin. Bars represent mean  $\pm$  SD. Results are representative of 3 separate experiments that gave comparable results. \*\*\* P <0.001 was considered statistically significant.

The observed dose-binding response is very similar in results described in Section 3.1.2. Both results (Figure 3.3 and Figure 3.65) show the same effect with similar results for  $4 \times 10^6$  c.f.u. and  $4 \times 10^7$  c.f.u., followed by a greater increase in  $4 \times 10^8$  c.f.u. It is known that SBA is composed of four subunits with one carbohydratebinding site per subunit (Sletmoen *et al.*, 2009). It is possible that smaller number of bacterial cells do not bind all available carbohydrate-binding sites. In order to check the inhibition of binding, SBA-coated wells were incubated with *E. coli/*pPGL or recipient strain *E. coli* XL2 (as a negative control) cells, and after washing wells were incubated with *C. jejuni* cells. Wells without *C. jejuni* cells served as a control, to check any interaction of mouse anti-Campylobacter Abs with *E. coli* and *E. coli/*pPGL cells. Table 3.2 shows the order in which the cells were added to the SBA-coated wells. Control wells (sample 1) were incubated with PBS and then with *C. jejuni*. Results from this experiment are shown in Figure 3.67.

Sample	First Incubation	Second Incubation	
1	PBS	C. jejuni	
2	E. coli/pPGL	C. jejuni	
3	E. coli XL2	C. jejuni	
4	E.coli/pPGL	PBS	
5	E. coli XL2	PBS	

Table 3.2. Incubation of ELISA plate with bacterial cells. Each sample was run in triplicate.



Figure 3.67 Mouse anti-Campylobacter Abs detect both C. jejuni and E. coli/pPGL. No signal in the wells that were incubated only with E. coli XL2. Bars represent fold change in absorbance (mean  $\pm$  SD of n = 3). Results are representative of 3 separate experiments that gave comparable results. \*\*\* P <0.001 was considered statistically significant, compared to the control (in this case, the well with only C. jejuni).

The well with only *C. jejuni* cells was used as a positive control, and absorbance values from other wells were compared to this, with the fold change given. Wells in which *E. coli/pPGL* were added showed an unexpected increase in absorbance (and therefore increase in binding) than *C. jejuni*, showing that the anti-*Campylobacter* Ab was not specific to *C. jejuni* and cross-reacted with *E*. *coli/*pPGL (Figure 3.67). Thus, it was not possible to detect inhibition of binding using this Ab. Several attempts to get information from the manufacturer about specificity of this antibody were unsuccessful. The manufacturer only provided the following description "recognises *Campylobacter jejuni* whole bacteria". The absorbance of the wells with *E. coli*/pPGL was 0.7 times higher than absorbance of the wells with *C. jejuni*. Since there was no signal detected in wells incubated with *E. coli* XL2 cells, it suggests that the Ab binds a common site of *C. jejuni* and *E. coli*/pPGL. It is proposed that the anti-*Campylobacter* Ab binds lipopolysaccharide present on the cell surface of either *C. jejuni* or *E. coli*/pPGL.

The use of more specific anti-*Campylobacter* Abs was considered. Antibodies against PEB1 antigen were chosen to check if there was any inhibition of binding of *C. jejuni* to SBA by *E. coli*/pPGL. First, the optimal dilutions of primary and secondary Abs were determined. After validation of the method, the system was successfully tested using *C. jejuni* cells. All samples in the ELISA assays were tested in triplicates, and the mean absorbance was determined. BSA-coated wells were used as negative control.

Before performing inhibition studies, first the cross reactivity of anti-PEB1 Abs with *E. coli* XL2 and *E. coli*/pPGL was checked. In the same type of experiment as above, incubation of cells in the presence of soluble SBA was performed to check the specificity of binding. Although a decrease in binding was demonstrated when *C. jejuni* was incubated with soluble SBA (compared to *C. jejuni* alone), an increase in binding was observed in wells with *E. coli*/pPGL, compared with the control *C. jejuni* cells (Figure 3.68). From these results it was concluded that anti-PEB1 Abs interacted with both *C. jejuni* and *E. coli*/pPGL cells, but not *E. coli* XL2 cells.

As both anti-*Campylobacter* Abs were interacting with *E. coli*/pPGL cells, it was not possible to detect if *E. coli*/pPGL could inhibit binding using an ELISA. There is a possibility that both Abs were raised against whole cells and not a specific antigen, which was not specified by the manufacturers. The lipopolysaccharide on the cell surface of *E. coli*/pPGL may have interacted with both anti-

Campylobacter Abs.



Figure 3.68. Anti-PEB1 Abs detect both *C. jejuni* and *E. coli/*pPGL cells. No signal was present in the wells that were incubated only with *E. coli* XL2. Soluble SBA inhibited binding of both cell types. Bars represent fold change in absorbance (mean  $\pm$  SD of n = 3). \*\*\* P <0.001 was considered statistically significant, compared to the control (in this case, the well with only *C. jejuni*).

#### 3.8.2 Detection of inhibition of attachment of C. jejuni using qPCR

Since the use of ELISA was not successful to assess if *E. coli/*pPGL could inhibit the binding of *C. jejuni* to immobilised SBA lectin, the use of qPCR-based *C. jejuni* detection was considered. Incubation of ELISA wells with *E. coli/*pPGL and/or *C. jejuni* cells was performed as described in Table 3.2 above (Sample 1 and Sample 2). Following incubation, the DNA of attached cells was purified

from each well of a microtitre plate as described in the Materials and Methods (section 2.17.2). There were 4 replicates for each sample, making 8 samples in total. At the same time, DNA was purified from *C. jejuni* corresponding to  $4 \times 10^8$  c.f.u. and used as control for PCR. The DNA concentration and quality of each sample was determined by measuring the absorbance at 260 nm using a NanoVue spectrophotometer. The ratio between the absorbance at 260 nm and 280 nm provided an estimate of DNA purity with respect to contaminants that absorb at a different wavelength.

After DNA purification and measurement of concentration, the number of reactions required for each procedure was calculated, and the master mix was prepared. Cycles were programmed as described in the Materials and Methods (section 2.17.2.2). In order to check the presence of C. jejuni cells the flhA gene. which encodes the flagellar biosynthesis protein was amplified using qPCR. The number of DNA copies calculated to be present at the start of the reaction equalled the number of cells, as there was only one copy of *flhA* gene present in the genome of Campylobacter. The amplified product was detected using targetspecific fluorescent hydrolysis probes. Earlier purified control DNA from C. *jejuni* was diluted several times to correspond to the different number of cells  $(1\times10^{6}, 1\times10^{5}, 1\times10^{4}, 1\times10^{3}, 1\times10^{2})$ . To determine the number of DNA copies in samples an absolute quantification method was used. CT values of diluted samples were used in a plot of the standard curve, with CT values vs the number of cells (DNA copies). The average of each control sample was used to plot the standard curve. Using this standard curve, the number of cells in each sample was determined (Table 3.3). In order to assess if E. coli/pPGL inhibited the binding of C. jejuni to immobilised SBA, the number of cells in both groups were compared and the difference was analysed (Figure 3.69).

**Table 3.3.** *E. coli*/pPGL inhibited binding of *C. jejuni* cells to immobilised SBA lectin. *C. jejuni* was incubated either with or without *E. coli*/pPGL bound to immobilised SBA lectin. The number of *C. jejuni* cells in each sample was determined using a standard curve.

Samples	Replicates	СТ	Number of cells
C. jejuni cells only	1	29.4	1529
	2	29.19	1791
	3	29.80	1131
	4	29.54	1376
<i>C. jejuni</i> and incubation with <i>E. coli/</i> pPGL	1	28.52	2969
	2	30.32	764
	3	30.47	682
	4	30.16	862



Figure 3.69. E. coli/pPGL pre-incubation affects binding of C. jejuni cells to immobilised SBA lectin. E. coli/pPGL incubation in SBA-coated ELISA plates were followed by incubation with C. jejuni cells. Bars represent the number of C. jejuni cells determined by qPCR (mean  $\pm$ SD). Wells that were pre-incubated with E. coli/pPGL had a smaller number of C. jejuni cells compared with wells containing only C. jejuni. \*\* P <0.01 was considered statistically significant.

The average number of cells in four samples that were not pre-incubated with *E. coli*/pPGL was 1456, which was two times higher than the average number of cells in the wells that were pre-incubated with *E. coli*/pPGL (769). 'The CT value in replicate 1 was not similar to the CT values obtained from the other 3 replicates. It was thought that this sample produced an anomalous result and therefore was discounted from the analysis. The high concentration found may have been due to contamination of the sample. From these preliminary results it is suggested that *E. coli/pPGL* was able to inhibit binding of *C. jejuni* cells to immobilised SBA. However, further studies would be need to be conducted to confirm these findings.

#### **CHAPTER 4: Discussion**

## 4.1 Interaction of *C. jejuni* cell surface glycans with analogues of host cell receptor

Pathogens may produce different types of adhesins that are differentially regulated and may be expressed at different stages of disease (Gerlach and Hensel, 2007). As stated earlier in Chapter 1, there are several in vitro cell culture-based methods available to study Campylobacter adhesion to host cells. Even though cell culture methods are commonly used for studying adhesiondefective mutants, they have some disadvantages. In addition to being time consuming, laborious and complicated, these techniques may give variation in results due to the use of different bacterial strains and cultured cell lines. Therefore, it may be useful to complement cell culture with non-cell culture methods, which are based on the binding of bacterial cells to inanimate surfaces. Studies involving Campylobacter binding to non-tissue surfaces have previously been carried out to identify the interaction of bacterial cells with specific receptors. For example Konkel et al. (1997) were able to observe binding of C. *jejuni* cells to immobilised fibronectin under the fluorescent microscope using acridine orange staining. This approach allows the identification of the occurrence of bacterial adhesion to proteins that are attached to a surface. Another approach used in the same study to assess bacterial interaction with the receptor was the radioactive labelling of fibronectin (Konkel et al., 1997). Western blotting is another method used for the identification of adhesin receptors. For example, the JlpA receptor was identified using anti-Glutathione S-transferase (GST) antibodies to JlpA-GST (Jin et al., 2003). ELISA may also be used to evaluate binding. In the study conducted by van Sorge et al. (2009) the bacterial cells were

first immobilised to the plate surface and then probed with the specific receptor, human macrophage galactose-type lectin (MGL). Successful binding of MGL was identified using anti-MGL antibodies. Each of the above methods when combined may complement each other and lead to better results.

In this study an *in vitro* model of bacterial attachment using a non-cell culture based method was developed. The assay enabled the assessment of bacterial binding to an immobilised analogue of putative host cell receptors, SBA lectin. *C. jejuni* expresses N-linked glycoproteins with a terminal  $\alpha$ -linked GalNAc residue that may interact with SBA lectin, as well as the lectins present on the surface of host cells. The purpose of using SBA lectin was to demonstrate, if a positive interaction was found, that *C. jejuni* is likely to additionally bind animal cell lectins. The assay was also used to determine whether capsule was involved in bacterial binding to SBA lectin.

The two-day culture (mid-log growth stage) (Ikeda, 2014) was selected, as it was the phase in bacterial growth in which they are highly metabolically active (i.e. enzyme activity and gene synthesis), and thus it served to mimic bacterial dynamics inside a host. The *in vitro* infectious process depends on the growth phase of *Campylobacter*. Bacteria from mid-log growth culture were shown to have a higher invasion rate compared to bacteria in early stationary growth phase (Konkel *et al.*, 1992b; Hu and Kopeko, 1999). It was assumed that this growth phase should be optimal for the bacterial ability to adhere to SBA lectin. In addition, using the same growth stage for each binding experiment provided consistency in the physiological state of each *Campylobacter* strain.

Using the binding assay developed in this study it was demonstrated that bacterial attachment was dose-dependent, since a reduced number of bacterial cells led to a reduced signal. The interaction of SBA lectin with *C. jejuni* cells was also
confirmed using fluorescence microscopy. The specificity of interaction was confirmed by treatment of whole cells with exoglycosidase specific for terminal GalNAc residues, as well as by inhibition of binding in the presence of free soluble SBA lectin and soluble GalNAc. In addition, treatment of cells that were already bound to the immobilised SBA lectin with exoglycosidase resulted in detachment of cells. These experiments confirmed that bacterial binding was the result of interaction with the  $\alpha$ -linked GalNAc of bacterial N-linked glycans. It was previously shown that expression of the C. jejuni pgl cluster that encodes the bacterial N-glycosylation system in E. coli results in the modification of LPS molecules on the surface of E. coli (van Sorge et al., 2009). The results confirmed that the introduction of the pgl locus into E. coli resulted in the generation of an SBA-reactive E. coli strain. This was confirmed with both the binding assay and with fluorescence microscopy. Bacterial cells were incubated with FSBA, which resulted in green fluorescing cells visible under a microscope, indicating that the SBA lectin binds to the surface of the cells. FSBA binding to glycoproteins of Campylobacter and recombinant E. coli provided a more direct indication of the interaction between these strains and SBA lectin. The main advantages of the use of FSBA were its simplicity and the quick confirmation of interaction between bacterial cells and SBA lectin. The presence of soluble GalNAc inhibited binding of recombinant E. coli cells to SBA lectin, confirming the specificity of binding. The results showing that E. coli lacking pgl did not interact with SBA lectin or FSBA further corroborate this.

The results obtained demonstrate the role of *C. jejuni* glycoprotein adhesins in the host-pathogen interaction. However, in order to develop a successful lectin-based *in vitro* assay for large-scale commercial application, further research with different *C. jejuni* strains and lectin types should be performed along with tests to

ensure durability of the assay after storage and within different laboratories. Although the developed system was used to test attachment of *C. jejuni* to SBA lectin, this method could also be used for the investigation of the interaction of other bacterial species and strains with purified host cell receptors or their analogues.

#### 4.2 The roles of glycoproteins PEB3 and JlpA in adhesion to SBA lectin

In this study it was shown that some N-linked glycoproteins interact with immobilised SBA. However, it was still unclear which glycoprotein was interacting with the analogue of the host cell receptor. Among the N-linked glycoproteins that can act as an adhesin is PEB3, a highly immunogenic protein that was previously shown to have an affinity for SBA lectin (Pei *et al.*, 1991; Young *et al.*, 2002; Linton *et al.*, 2002). In this study, in order to investigate the involvement of PEB3 protein in adhesion the *peb3* gene was mutated. Any observed differences in binding between the wild type and *peb3* insertional knockout could indicate the involvement of PEB3 in *C. jejuni* binding to SBA lectin. In addition, the ability of the *peb3* mutant to grow on agar plates suggests that *peb3* is not an essential gene for survival *in vitro*, although this may be different *in vivo*.

Following inactivation of *peb3*, the mutant was tested using the developed binding assay. The results showed a difference in the amount of binding to immobilised SBA lectin between the mutant and wild type strains. Several experiments provided consistent results that demonstrated a reduced binding of the *peb3* mutant. Complementation of *peb3* mutation using the pRRC delivery plasmid resulted in restoration of binding and confirmation that a functional PEB3 is required for binding. However, mutation of *peb3* did not completely eliminate

binding, suggesting that the presence of other cell surface structures may compensate the role of inactivated PEB3 protein. This hypothesis was supported by inhibition of the residual binding of the *peb3* mutant in the presence of free soluble SBA lectin.

PEB3 was among the first identified glycosylated proteins of Campylobacter (Linton et al., 2002), however the biological role of this protein is still not clear. PEB3 has 52% amino acid sequence identity with the putative adhesin Paa from E. coli (97% coverage with E-value 3e-83 ( $3 \times 10^{-83}$ ). Paa annotation suggests that the protein is involved in initial bacterial adhesion and may have specificity toward heparin sulfate receptors on the host cell surface (Batisson et al., 2003). PEB3 is predicted to contain a sulphate-binding domain which may be associated with microbial adherence, however, purified wild type PEB3 did not show any interaction with sulphated oligosaccharides (Min et al., 2009). PEB3 might carry a dual function as an adhesin and transport protein (Rangarajan et al., 2007; Min et al., 2009), similar to protein PEB1 (Leon-Kempis et al., 2006). Despite knowledge that both of these proteins are major antigenic proteins of C. jejuni (Pei et al., 1993), mutation of peb3 in this study may not have completely abrogated cell binding but instead may have resulted in a deficiency of the transport functions of PEB3, which were not examined here.

Results from this study imply that PEB3 is involved in the interaction with GalNAc-specific lectin receptors on the host cells. It is known that there are many structurally different glycans present on the surface of human pathogens, which target glycan-binding protein lectins, such as C-type lectins. Some of them, including MGL, share binding specificity with SBA, used in this study. Thus the interaction of PEB3 with the lectins present on immune cells may assist in evasion of the host immune response, similar to other pathogens, where they specifically

target C-type lectin receptors to escape immune surveillance (Cambi *et al.*, 2005; Lugo-Villarino *et al.*, 2011).

Due to the presence of residual binding with the *peb3* mutant, insertional mutagenesis of *ilpA*, which encodes a confirmed glycoprotein adhesin, was performed. An isogenic *jlpA* mutant was constructed via insertion of the chloramphenicol resistance cassette instead of the kanamycin cassette, to allow the generation of a double (e.g. peb3-jlpA) mutant. However, mutation in the jlpA gene did not reduce C. jejuni binding to immobilised SBA lectin, thus the creation of a double mutant was not necessary. Among the possible reasons explaining these results was the absence of *jlpA* expression in vitro. It is also possible that JlpA did not interact with SBA due to instability of JlpA in the 11168H strain. Earlier it was reported that NCTC11168 JlpA is glycosylated only at one site compared with other strains, which may affect the stability of the glycoprotein (Scott et al., 2009). Even though it was reported that jlpA mutation affects adhesion of C. jejuni to human epithelial cells, other studies have shown that the ilpA mutation had no effect on binding to host cells (Flanagan et al., 2009: Novik et al., 2010). This discrepancy might be the result of different cell lines, which were used for different experiments, suggesting that only certain host cells produce JlpA receptors.

Since the binding of *jlpA* mutants was not affected, and presence of residual binding in the 11168H/*peb3::kan<sup>r</sup>* mutant strain was demonstrated, this suggests the presence of other unknown GalNAc-containing adhesins in *C. jejuni*. In this study, two further N-linked glycoproteins were identified as putative adhesins using bioinformatics tools. Out of 38 known N-linked glycoproteins one was predicted to be secreted and another one had an adhesin family signature. These

proteins may be involved in interaction with SBA lectin and it is suggested that this should be the target for future studies.

In addition, there was a possibility that LOS of *C. jejuni* could also be involved in the interaction with SBA lectin. LOS is known to be involved in adhesion, invasion and evasion of the host immune response (Louwen *et al.*, 2008; Guerry *et al.*, 2000). In addition, it was also shown that *C. jejuni* strains that have a terminal GalNAc residue in LOS interact with MGL (van Sorge *et al.*, 2009). However LOS of NCTC11168 does not have a terminal GalNAc structure, thus it is unlikely that the presence of residual binding was due to LOS.

#### 4.3 Role of capsule in the host-pathogen interaction

Capsule is a well-known virulence factor in various pathogens, including *Campylobacter* spp. Although *C. jejuni* CPS is known to be an essential virulence factor, the role of capsule in pathogen-host interaction has not been extensively studied. In order to investigate whether the presence of the capsule affects binding of *C. jejuni* cells to the immobilised analogue of a host cell receptor, an acapsulated mutant of 11168H was tested using the same binding assay. A previously constructed *kpsM* mutant was first confirmed for the presence of the kanamycin cassette in the *kpsM* gene using PCR with specific primers. The isogenic acapsulated mutant showed an increase in binding to immobilised SBA suggesting a negative effect of capsule on bacterial attachment. The inhibition of binding in the presence of free soluble SBA lectin and soluble GalNAc also confirmed specificity of binding. In addition, the specificity of the interaction was also confirmed by treatment of whole cells with exoglycosidase, indicating that binding occurs due to glycoproteins that have GalNAc residues.

We have found that PEB3 protein and capsule have different effects on binding of *C. jejuni* cells to SBA lectin. The presence of capsule in some pathogens may shield bacterial surface structures, such as adhesins (Schembri *et al.*, 2004), which is what may be occurring in our study. It has been shown that the F1 capsule of *Yersinia pestis* prevents interaction of fimbrial adhesins with receptors on the host cell (Runco *et al.*, 2008). Similarly, in another pathogen, *Klebsiella pneumonia*, capsule prevents adhesins from binding to epithelial cells (Sahly *et al.*, 2000). We therefore performed gene expression studies for *kpsM* and *peb3* genes using RT-PCR in order to see if these genes are differentially regulated.

Gene expression studies using samples obtained from liquid culture media exhibited some variation between biological replicates. However, after repeating the experiment a number of times it was possible to get consistency in the results. Campylobacter is able to turn CPS expression on and off (Bacon et al., 2001), which may suggest that the presence or absence of capsule might be important at different stages of infection or in the bacterial life cycle. Results of RT-PCR studies showed an increase of peb3 and a decrease of kpsM gene expression over time, suggesting that a shielding effect by the capsule may be essential at the initial stages of infection, hiding bacterial cell surface structures from the immune system. Subsequent down-regulation of CPS production during colonisation may lead to exposure of other bacterial cell surface structures required for the attachment and/or evasion of the host immune response. Reduction in expression of CPS was earlier reported in C. jejuni cells that were co-cultured with epithelial cells (Corcionivoschi et al., 2009). Together these findings suggest variable modulation of CPS expression during infection.

The presence of capsule in some pathogens aids in immune response evasion (Raffatellu et al., 2005; Unkmeir et al., 2002). For example, in Salmonella spp.

the presence of capsule inhibits expression of host IL-8 via capsule-mediated inhibition of TLR signalling (Raffatellu *et al.*, 2005). A similar effect was present in *Neisseria meningitides*, where capsule inhibits TLR2 activation, and aids in adhesion to phagocytes (Unkmeir *et al.*, 2002). Similarly, in *C. jejuni*, it was shown that an acapsulated mutant or strain with modification of MeOPN induced expression of IL-6, IL-10 and TNF- $\alpha$  in mouse DCs when compared with the wild type strain (Rose *et al.*, 2012). A more recent study reported that the presence of CPS in the wild type resulted in reduced activation of both TLR2 and TLR4 (Maue *et al.*, 2013). These findings suggest that CPS helps *Campylobacter* to evade the host immune response during the initial stages of infection, which in turn helps to establish colonisation of the host.

# 4.4 The role of N-linked glycoproteins in binding to host cell receptors

Since the mutation of the *peb3* gene resulted in a reduction in bacterial binding, the binding abilities of purified PEB3 protein were investigated. In order to optimise purification of PEB3, His-tagged PEB3 was constructed. The use of the His-tag allowed the identification of the protein after purification using antibodies toward histidine. In addition, the presence of His-tag would also help to identify the PEB3 interaction with host cell receptors in the assay. The pRRBC plasmid was used to regulate *peb3* over-expression. This is the first regulated gene expression system for *C. jejuni* (Ikeda, 2014). The pRR was used as the basis in pRRBC to enable integration into the *C. jejuni* genome, as it encodes for several *Campylobacter*-specific non-coding rRNA gene clusters. As these sites are highly conserved and redundant, the insertion of the construct should therefore not have a major effect on the cell function (Karlyshev and Wren, 2005). It was assumed that the use of the pRRBC system would allow the purification of glycosylated

PEB3 from *C. jejuni*. In order to show if the system was functional, it was first successfully tested within *E. coli*. The disadvantage of this system was the inability to induce expression of the *peb3* gene in *C. jejuni* due to the absence of arabinose transporters within *C. jejuni* to induce the construct. *Campylobacter* metabolism depends mainly on amino acids rather than sugars, which are the main source of energy for *E. coli* (Guccione *et al.*, 2008; Stahl *et al.*, 2012). Thus, using the pRRBC system it was only possible to express non-glycosylated PEB3 from recombinant *E. coli*. To create a system that would allow arabinose induction in *C. jejuni* the use of the *E. coli* sugar transport gene *araE* was considered. The *araE* encodes a component of the high-affinity L-arabinose transport system and it is one of the operons of the L-arabinose regulon (Englesberg and Wilcox, 1974). In order to improve the pRRBC system, attempts to add an *araE* in pRRBC were performed (data not shown). Unfortunately, this work could not be completed due to time constraints.

Meanwhile, another approach was used to obtain glycosylated forms of PEB3. Taking into account the absence of a sugar transporter within *C. jejuni*, the use of two plasmids (pBAD33 and pPGL1) enabled purification of glycosylated PEB3 from *E. coli*. The pBAD33 plasmid (Guzman *et al.*, 1995) that contains the P<sub>BAD</sub> promoter of the L-arabinose operon and its regulatory gene *araC* facilitated expression and subsequent purification of non-glycosylated PEB3 from *E. coli* using the pBAD\_peb3 construct. Introduction of pBAD\_peb3 into the recombinant *E. coli*/pPGL strain allowed regulatory expression and purification of glycosylated PEB3 from *E. coli*. Following induction with arabinose, the rate of growth (according to OD<sub>600</sub>) of the induced culture was decreased compared to the uninduced culture. This was explained by divergence of energy to target protein synthesis. The advantage of this system was the ability to purify C-

terminal His-tagged glycosylated PEB3 from *E. coli* rather than from *C. jejuni*. To confirm that recombinant *E. coli* with the pBAD\_peb3/pPGL construct expressed glycosylated PEB3 protein, it was compared to PEB3 purified from *C. jejuni*. Using the pRRC system the purification of His-tagged fusion PEB3 protein from *C. jejuni* was successfully performed. The pRRC plasmid was designed for constitutive expression and it had previously been suggested that it could be used for isolation of functional protein complexes (Karlyshev and Wren, 2005). Comparison of the two proteins using Western blotting, as well as exoglycosidase treatment, verified that the pBAD\_peb3/pPGL system could be used for expression and purification of glycosylated PEB3 protein.

Purified glycosylated PEB3 was used in attempts to identify receptors in different types of human whole cell lysates. The fact that *Campylobacter* interacts with human intestinal cells was the reason for investigating the effect with normal intestinal cell lysates as well as Caco-2 cell lysates. In addition, the use of THP-1 cell lysate was considered. THP-1 cells are known to mimic monocytes and macrophages, resembling them in morphology and differentiation properties (Tsuchiya et al., 1980). THP-1 cells were selected because N-linked glycoproteins interact with MGL receptors on macrophages. Unfortunately, it was not possible to identify any interaction of purified PEB3 with the receptors of host cells using Western blotting. This might be due to inactivation of binding sites of the host cells during denaturing the host cell lysates. However, some Western blotting experiments suggest that after denaturation proteins still retain active epitopes allowing their detection using specific antibodies (Jin et al., 2003). Moreover, some proteins retain full enzymatic activity after denaturation and PAGE. The phenomenon is actually a basis of Zymography when many protein activities can still be detected after denaturing gel electrophoresis (Karlyshev et al., 2014).

Furthermore, commercially available lysates of host cells, which were specifically designed for blotting, were used in these assays. Therefore, the experimental design used in this thesis was appropriate, as SDS gel electrophoresis was used as the first step in an attempt to detect host cell receptors, which is quite a challenging task. Future work may involve blotting with native proteins as well as other approaches.

Another reason explaining absence of interaction of purified PEB3 with the receptors of host cells might be due to production of a low yield of purified glycosylated PEB3. This might be caused either by low PEB3 expression, low binding in the column during large scale protein purification, or elution problems. Two purification methods were used, including column and beads, with various amendments to the methodology including increasing the volume of liquid culture as well as incubation time. However, all variations still produced low yields of the protein. As a means to check if there was a loss of protein during the purification procedure, a number of experiments were performed using recombinant and wild type E. coli (as wild type E. coli does not produce PEB3). These experiments confirmed that the low yield of protein was not caused by the loss of protein during the purification process. Among the possible reasons for low protein yield it is suggested that the protein was either unstable or toxic to the cells in higher concentrations. Another possible reason that prevented the detection of binding was the potential loss of the His-tag residue due to degradation during incubation of blots.

Previously, recombinant PEB3 protein was expressed and purified from *E. coli* using different constructs (pET*peb3* / pACYC*pgl* and pET*peb3* / pNBpgl) (Linton *et al.*, 2005; van Sorge *et al.*, 2009). In both cases PEB3 protein was designed to incorporate a 6-His residue tag in the C-terminal, to express the protein on the

surface of E. coli cells. In this study the same approach was applied for expression of the PEB3 on the surface of the E. coli cells (6-His residue tag incorporated onto the C-terminal) but using different constructs (pBAD peb3/ pPGL1). Although it was possible to express glycosylated protein using E. coli, the yield of protein was unfortunately not high enough to identify its interaction with putative host cell receptors. It is not clear if other cited studies managed to express this protein at higher levels, thus comparison of efficiency of our construct was not possible. Identification of any potential host cell receptors using whole cell lysates was not possible due to the low yield of PEB3 protein. Therefore, recombinant E. coli cells harbouring pPGL plasmid were used to check the presence of any interaction between receptors of the host cell. E. coli/pPGL is able to glycosylate bacterial lipopolysaccharide, resulting in exposure of GalNAc residues on the cell surface. The developed binding assay results, as well as confocal microscopy, confirmed GalNAc-dependent binding of recombinant E. coli to immobilised SBA lectin. Thus, it was hypothesised that GalNAc residues on the surface of E. coli/pPGL cells may interact with host cell receptors. Blots with human whole cell lysates were probed with whole E. coli/pPGL cells to check whether glycosylated bacterial lipopolysaccharides would interact with human whole cell lysates. E. coli/pPGL expressing GalNAc residues were shown to interact with whole cell lysates immobilised on a PVDF membrane. No interaction was detected when a recipient E. coli strain was used. The interaction of E. coli/pPGL expressing surface GalNAc residues with THP-1 whole cell lysates was found to be specific. as it was inhibited in the presence of free SBA lectin.

SBA lectin has the same binding specificity as C-type lectins (including MGL receptors) produced by host cells. GalNAc residues are specifically recognised by SBA and human MGL receptors, which are expressed by macrophages and DCs

(Higashi et al., 2002; van Vliet et al., 2008a). MGL binding to GalNAc limits the migration of immature DCs (van Vliet et al., 2008b), which may result in antigen presentation and uptake in MHC class II (Napoletano et al., 2007; van Vliet et al., 2007). It was previously shown that MGL is able to recognise a GalNAccontaining antigen of the helminth parasite *Schistosoma mansoni* and it was suggested that human DCs use MGL to internalise soluble egg antigen (SEA) of *S. mansoni* (van Vliet et al., 2005). MGL receptors can also recognise members of the filoviridae family (Takada et al., 2002). *N. gonorrhoeae* LOS phenotype C was the first described bacterial ligand to human MGL (van Vliet et al., 2009). *N. gonorrhoeae* LOS phenotype C also carries terminal GalNAc residues (Yamasaki et al., 1991a; Yamasaki et al., 1991b). Targeting different C-type lectins (including MGL) enables *N. gonorrhoeae* to shift the immune response in favour of bacterial survival, via alteration in DC cytokine production (van Vliet et al., 2008a).

Previously it was reported that *C. jejuni* N-linked glycans limit cytokine production, as the absence of a functional MGL ligand (GalNAc) induces secretion of IL-6 by DCs (van Sorge *et al.*, 2009). The role of human MGL receptors in *C. jejuni* infection is not clear. However, *C. jejuni* interaction with MGL is N-glycan-mediated and may subvert the host immune response. As stated earlier, interaction of *C. jejuni* cell surface structures with C-type lectins may result in evasion of host immune response like in other pathogens (Cambi *et al.*, 2005; Lugo-Villarino *et al.*, 2011). Results of blotting experiments with human whole cell lysates indirectly suggest that N-linked glycoproteins are involved in the interaction with host immune cells. However, further studies using cell line cultures need to be performed to support this hypothesis.

#### 4.5 The use of E. coli/pPGL as an inhibitor of binding

The use of carbohydrate-binding antagonists may be an attractive approach for anti-adhesion therapy. In particular, the use of adhesin analogues as anti-adhesive agents may be beneficial for Campylobacter infection control. This strategy is based on the premise that some soluble molecules can mimic adhesins present on the bacterial cells and compete for adhesion with host cell receptors (Ofek et al., 2003). In this study it is hypothesised that surface structures of E. coli/pPGL may inhibit binding of C. jejuni to immobilised SBA. Previously this system has been used for engineering diverse glycan structures that can be transferred onto recombinant proteins in E. coli through an N-linkage (Linton et al., 2005). It was earlier suggested that pgl gene locus-generated polysaccharides are incorporated into recombinant E. coli LPS or enterobacterial common antigen (ECA), which indicates that N-linked glycosylation and glycolipid biosynthesis have similar mechanisms (van Sorge et al., 2009). In addition, similarity between E. coli and C. jejuni biosynthesis pathways were shown, when E. coli WecA protein, involved in glycolipid synthesis, substituted the activity of C. jejuni PglC in N-linked glycosylation (Linton et al., 2005). As E. coli/pPGL has high affinity to SBA lectin, it may be used to block binding sites to prevent adhesion of C. *ieiuni*. To test this hypothesis, *in vitro* inhibition experiments were conducted. In order to assess the anti-adhesive properties of recombinant E. coli strain against C. *iejuni*, E. coli/pPGL cells were pre-incubated with immobilised SBA, followed by incubation of C. jejuni cells.

The use of anti-*Campylobacter* antibodies to check inhibition proved ineffective due to the cross-reactivity with the *E. coli*/pPGL strain. However, preliminary results of qPCR confirmed that *E. coli*/pPGL strain indeed was able to inhibit *C. jejuni* binding to the analogue of host cell receptors, as the number of *C. jejuni* 

cells was fewer in the wells that were pre-incubated with *E.coli*/pPGL compared with wells that only had *C. jejuni*.

These findings look promising, as they can be used for further development of inhibitors of *C. jejuni* attachment to host cell receptors and hence for the treatment or prevention of *Campylobacter* infection.

### **4.6 Conclusion**

The results of this study demonstrate the feasibility of a new technique for measuring *C. jejuni* binding to SBA lectin. This novel technique was validated through microscopy, competitive inhibition studies and exoglycosidase treatment. Additionally, it was tested successfully using *C. jejuni* strain 11168H and its isogenic mutants: 11168H/peb3, 11168H/jlpA and 11168H/kpsM. The study confirmed PEB3 as one of the cell surface glycoproteins required for

bacterial interaction with an analogue of host cell receptors. In contrast, JlpA glycoprotein adhesin was shown not to be involved in this interaction. The study confirms the existence of GalNAc-containing cell surface structures able to interact with SBA lectin other than what is currently known in the published literature.

The results of the developed binding assay indirectly suggest that PEB3 plays a role in the interaction with receptors present on macrophages and DCs, which may lead to evasion of the host immune response. Additionally, it was shown that the presence of capsule has an interfering effect on bacterial attachment and that the genes involved in capsule and PEB3 adhesin biosynthesis are differentially regulated *in vitro*. It is likely that the developed methods could be applied to study *C. jejuni* interactions with other putative host cell receptors.

Additionally, in this study the *C. jejuni* N-linked glycosylation machinery was used to produce a glycosylated recombinant protein in *E. coli*. Using a recombinant *E. coli* strain producing LPS-like surface molecules it was shown that whole cells specifically interact with THP-1 cell lysate and are able to inhibit binding of *C. jejuni* cells to analogue of host cell receptors. The elucidation of the specific interactions of *C. jejuni* with analogues of host cell receptors could result in the development of inhibitors, which will prevent bacterial attachment, leading to the development of novel specific antibacterials.

#### 4.7 Future Work

In the course of this study, other N-linked glycoproteins – Cj0143 and Cj0114 – that may act as an adhesins, were identified. It would therefore be interesting to study the cj0143 and cj0114 knock-out mutants similar to the *peb3* and *jlpA* mutants in order to establish their adhesive properties. Following confirmation of interaction between SBA lectin and these proteins and subsequent purification of both proteins one could study their interaction with host cell receptors using host cell lysates and/or cell culture.

Although in this study PEB3 was shown to play a role in adhesion, it has not been possible yet to demonstrate the interaction directly with any host cell receptors. Thus, further attempts at expression and purification of this protein should be considered.

Purification of PEB3 could be achieved by incorporation of a 6-His residue tag onto the N-terminus, instead of the C- terminus. A higher yield of PEB3 protein would allow investigation of its interaction with host cell receptors. It could also be used in adhesion and inhibition assays using cell culture methods. In order to get detailed structure crystalisation of recombinant protein might be considered.

Moreover, in order to confirm that PEB3 is indeed an adhesion factor, the use of a knock-out mutant and complemented derivative in binding experiments using cell line cultures may be performed. The production of antibodies against PEB3 protein would be the next logical step. The use of antibodies would allow examination of inhibition of PEB3 binding to epithelial or immune cells. Following confirmation of PEB3 binding to host cells, identification of PEB3 host cell receptors will be of interest.

The results of gene expression studies demonstrated that peb3 and kpsM are differentially regulated in liquid culture. It would be interesting to investigate whether peb3 and kpsM are also differentially regulated during the infection process. Based on these results and previous research in this field it is suggested that capsule and N-linked glycoproteins are involved in the interaction with immune cells. As *in vivo* studies of immune responses to *C. jejuni* are complex, kpsM and peb3 mutants and the effects of wild type strains of *C. jejuni* could be studied on cell lines of macrophages or DCs first. This approach should help to develop a better understanding of the response generated by immune cells. These results provide the first evidence that recombinant *E. coli* cells with a functional *pgl* locus may inhibit *C. jejuni* binding to an analogue of a host cell receptor. Further studies could test these results using other methods such as cell culture and microscopy.

Additionally, it would be interesting to test if the interaction between whole *E*. *coli* recombinant cells and DCs or THP-1 cells could be reproduced using cell culture methods. Also the ability of recombinant glycoproteins to detach already attached *C. jejuni* cells should be investigated.

The recombinant *E. coli* glycoproteins may act as analogues of adhesins by masking bacterial adhesins and blocking their access to host cell receptors.

Another approach in antimicrobial development would include further research to test if these recombinant glycoproteins successfully and continually mask bacterial adhesins, and can therefore be used as a basis for the development of novel antibacterials.

Improved understanding of bacterial adhesins is the key to the development of appropriate adhesion blockers. Effective production and delivery of these adhesion blockers to the host could lead to a major pharmaceutical breakthrough.

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## Appendix

#### **Published abstracts and articles**

#### Abstracts

Rubinchik, S., Seddon, A. and Karlyshev, A.V. (2012) "Development of a novel *in vitro* assay for investigation of *Campylobacter jejuni* attachment to host cell receptors" was presented at CampyUK 2012 Conference in London (UK), 6<sup>th</sup> January 2012.

Karlyshev, A.V., Seddon, A. and Rubinchik, S. (2012)

"The role of *Campylobacter* surface N-link glycosylated proteins and capsule in interaction with host cell receptors" was presented at II International Conference on Antimicrobial Research – ICAR2012 in Lisbon (Portugal), 21<sup>st</sup>–23<sup>rd</sup> November 2012.

Rubinchik, S., Seddon, A. and Karlyshev, A.V. (2013) "Effect of capsule on interaction of *Campylobacter jejuni* cells with an analogue of a host cell receptor" was presented at the 17<sup>th</sup> International Workshop on Campylobacter, Helicobacter and related organisms (CHRO) 2013 in Aberdeen (UK), 15<sup>th</sup>-19<sup>th</sup> September 2013.

# Published articles

Rubinchik, S., Seddon, A. and Karlyshev, A. V. (2012) 'Molecular mechanisms and biological role of *Campylobacter jejuni* attachment to host cells', *European Journal* of Microbiology and Immunology, 2 (1), pp.32–40.

Rubinchik, S., Seddon, A. and Karlyshev, A. V. (2014) 'A negative effect of *Campylobacter* capsule on bacterial interaction with an analogue of a host cell receptor', *BMC Microbiology*, 14:141.

### Presentation

S. Rubinchik (2011) '*Campylobacter* adhesins as novel antibacterial targets: *in vitro* models and mechanisms of attachment'. PowerPoint presentation. Postgraduate Research Seminar Day, Kingston University London.