Flow cytometric analysis of within-strain variation in polysaccharide expression by *Bacteroides fragilis* by use of murine monoclonal antibodies

DEBORAH A. LUlTON, SHEILA PATRICK*, A. D. CROCKARD, LINDA D. STEWART†, M. J. LARKIN,† EVELYN DERMOTT and T. A. McNElLL

Department of Microbiology and Immunobiology, Queen's University of Belfast, Grosvenor Road, Belfast BT12 6BN and †Division of Genetic Engineering, School of Biology and Biochemistry, Queen's University of Belfast, Northern Ireland

**Summary.** The reactivity of four different monoclonal antibodies (MAbs) with populations of *Bacteroides fragilis* NCTC 9343, enriched by density gradient centrifugation for a large capsule, small capsule and electron-dense layer (EDL) only visible by electronmicroscopy, was examined. The MAbs reacted strongly with polysaccharides present in both the large capsule- and EDL-enriched populations but not in the small capsule-enriched populations. The pattern of labelling was determined by immunoblotting, immunofluorescence and immuno-electronmicroscopy, and flow cytometry. The MAbs labelled cell membrane-associated epitopes in the large capsule- and EDL-enriched populations and cell-free material in the EDL population. By immunoblotting, ladders of repeating polysaccharide subunits were evident in the EDL population but not in the large capsule population. The proportion of cells labelled within each population was determined by flow cytometry. The reactivity of another MAb with the small capsule population was confirmed by flow cytometry. A qualitative indication of epitope expression was obtained by examination of the flow cytometric profiles. Differential expression of the same saccharide epitope was observed both between and within structurally distinct *B. fragilis* populations. The MAbs were species-specific and cross-reacted with several recent clinical isolates. These polysaccharides may be relevant to the virulence of *B. fragilis*.

**Introduction**

*Bacteroides fragilis* is a gram-negative anaerobic species that is an important pathogen, commonly encountered in clinical infections.1 One of the many factors that undoubtedly contribute to its virulence is the expression of particular surface antigens.2 Several authors have described the encapsulating surface structures of *B. fragilis*3–7 but, as yet, their relationship to virulence remains unclear. Individual strains of *B. fragilis* have been shown by electronmicroscopy to be heterogeneous with respect to expression of encapsulating surface structures; cells with a large capsule, a small capsule and a marginal electron-dense layer (EDL) may be separated by Percoll density gradient centrifugation.7 Within-strain antigenic heterogeneity has been shown immunologically with anti-polysaccharide monoclonal antibodies (MAbs).8,9 One MAb reacts with the small capsule but not with the large capsule or EDL.9 The surface carbohydrates of *B. fragilis* have been shown by immunochemical analysis to be antigenically complex. Most strains possess four distinct structural elements that can be detected by immunoblotting—a rough type LPS, a common antigen, a smooth LPS which runs as a series of closely spaced bands, and a high M, antigen which may be capsular polysaccharide.10 How these components relate to the different capsules is not known. The aim of the present study was to obtain MAbs that reacted with the large capsule or EDL populations and to confirm that these structures are antigenically different from the small capsule. Flow cytometry was used to obtain fast and accurate quantitation of bacterial labelling. The reactivity of the MAbs with recent clinical isolates was also determined.

**Materials and methods**

**Bacterial strains**

The strains used in this study were *B. fragilis* NCTC 9343 (National Collection of Type Cultures, Colindale
Avenue, London) and BE3 (Department of Medical Microbiology, Vrije Universiteit, Amsterdam), B. vulgatus NCTC 10583, B. thetaiotaomicron NCTC 10582, B. ovatus ATCC 8483 (American Type Culture Collection), B. distasonis ATCC 8503, and B. gingivalis W83 (Laval University, Quebec, Canada); B. fragilis strains LS1–11, Escherichia coli and Staphylococcus aureus were recent clinical isolates from the Department of Bacteriology, Craigavon Area Hospital, N. Ireland.

Culture methods

Bacteria were grown in minimal medium defined broth. Cultures were incubated at 37°C in an atmosphere of H2 10%, N2 80%, CO2 10% in an anaerobic cabinet MK III (Don Whitley Scientific Ltd, Shipley, W. Yorks). Identification was confirmed with the API20A system.

Separation and enrichment of bacterial populations

Bacterial populations were enriched for different sizes of encapsulating surface structures by Percoll (Pharmacia, Uppsala, Sweden) discontinuous density gradient centrifugation as previously described.

Preparation of bacterial outer membranes

Outer membranes were prepared as previously described.

Preparation of polysaccharide

Polysaccharide was extracted by the Proteinase K method.

Production of MAb

A BALB/c mouse was immunised with whole cells of a B. fragilis NCTC 9343 population enriched for expression of the EDL. The mouse was inoculated intraperitoneally with 0.5 ml of a bacterial suspension of 1 x 10^8 cfu/ml in 0.01 M phosphate-buffered saline, pH 7.4 (PBS). A further inoculation of 0.2 ml was given 4 days before the mouse was killed. The spleen cells from the mouse were fused with P3X 63 Ag8-653 (NS-0/1) mouse myeloma cells by treatment with polyethylene glycol 16000 (Sigma) 50% in RPMI 1640 (Flow Laboratories, Paisley, Scotland) following a modification of the method of Galfre and Milstein. Hybrid cell lines were selected with hypoxanthine-aminopterin-thymidine in RPMI 1640 medium containing mycione fetal calf serum (Gibco) 20%. Culture supernates were removed and screened by ELISA and immunofluorescence microscopy for IgG to the EDL population of B. fragilis NCTC 9343.

Isotyping

The isotype of the MAb was determined with a mouse MAb isotyping kit (Amersham International plc).

SDS-PAGE was performed on vertical slab 8% gels with the Laemmli buffer system. For outer membrane proteins, samples were mixed with 50 μl of PAGE sample buffer (0.0625 M Tris-HCl, pH 6.8, containing SDS 2% w/v, glycerol 10% v/v, 2-mercaptoethanol 5% v/v and bromophenol blue 0.001% w/v) and heated in a boiling water bath for 10 min. After cooling, samples were loaded on to gels. For polysaccharide, proteinase K extracts (50 μl) were loaded on to gels. Gels were run at a constant current of 50 mA/gel. Immunoblotting was performed as previously described.

Culture of bacteria in vivo

Chambers were constructed, filled with B. fragilis NCTC 9343 and implanted in the peritoneal cavity of a mouse as previously described. The chambers were constructed with 3-μm pore membrane filters (Millipore) which allowed the entry of leucocytes.

Electronmicroscopy

Bacteria were embedded for ultra-thin sectioning as previously described. For negative staining, one drop of bacterial suspension in distilled water was dried on to a formavar carbon-coated 400-mesh copper grid (Agar Aids) which had been glow-discharged. The grids were labelled with immunogold as previously described. The thin sections were stained with uranyl acetate for 10 min. The whole bacteria were negatively stained with a drop of methylamine tungstate (Agar Aids) 2% w/v in distilled water. The bacteria were examined with a Phillips CM 10 transmission electron-microscope.

Dual colour immunofluorescence microscopy

A modification of the staining procedure described by Johnson et al. was used. Separated bacterial populations were suspended in PBS, fixed on multi-test slides (Flow Laboratories) and incubated with MAb supernates. The slides were washed in PBS then incubated with rabbit anti-B. fragilis polyclonal antibody. The slides were again washed and then incubated simultaneously with goat anti-mouse fluoresein conjugate (Sigma) and goat anti-rabbit rhodamine conjugate (Sigma). After a final wash, the slides were examined with a Leitz fluorescence microscope. Random fields of view were selected and the number of bacteria labelled with MAb and polyclonal anti-
serum were counted. The percentage of each population labelled by MAb was calculated relative to the total number of cells labelled with polyclonal antiserum.

Flow cytometric analyses

Cells were prepared by a modification of the method of Nelson et al.\cite{18} PBS that had been filtered three times through 0.22-µm membrane filters was used throughout. Washed, late exponential phase cultures of \textit{B. fragilis} were resuspended to approximately 2 x 10^8 cfu/ml in PBS. Each sample of 1 ml of bacterial suspension was centrifuged at 12 000 g in an Eppendorf 5414 centrifuge for 2 min. The pellets were resuspended in 1 ml of MAb supernate or 1 ml of PBS (control) and incubated at 37°C for 1 h. Samples were washed twice in PBS and mixed with 1 ml of appropriately diluted goat anti-mouse IgG fluorescein conjugate (Sigma) or goat anti-mouse IgM fluorescein conjugate (Serotec). The samples were incubated at 37°C for 1 h, washed twice in PBS and resuspended in 1 ml of paraformaldehyde 1% v/v in PBS.

Cells stained with FITC conjugate but without primary antibody were negative controls. An IgM MAb, Bf4, previously shown to react with the small-capsule population\cite{9} was used as a positive control for the fluorescent signal. All samples were sonicated for 20 s at an amplitude of 5 µm (MSE Soniprep 150) to break bacterial aggregates. The sonication time was determined empirically to obtain maximum disruption of bacterial aggregates without cell membrane breakage.

The bacteria were analysed on an EPICS 5 flow cytometer (Coulter Electronics Ltd) equipped with a 5 W argon laser tuned to 488 nm and operating at a power output of 100 mW. Before each analysis, the instrument was calibrated with 1-5-µm fluorescent microspheres (Polysciences). Monodisperse bacterial populations were identified on the basis of size by forward and 90° light scatter signals and gated appropriately. Single parameter log integral green fluorescence (LIGFL) signals were obtained from the gated population. In each sample, 50 000 bacteria were counted and the percentage of positively staining cells was obtained by subtraction of negative control histograms from test histograms with the Immunoprogramme of the instrument.

Results

Characterisation of MAbs and distribution of epitopes in \textit{B. fragilis} populations enriched for different encapsulating structures

MAb \textit{QUBf5}. Immunoblotting of proteinase K extracts with MAb \textit{QUBf5}, of isotype IgG_{2a}, showed a diffuse staining pattern at the top of the blot, corresponding to a high M₇ polysaccharide (fig. 1a, b and c). This polymer was present in smaller amounts in the small capsule population (fig. 1b). A series of discrete bands of repeating polysaccharide subunits was found to extend from the high M₇ polysaccharide to the gel front in the EDL population (fig. 1c). Electronmicroscopy and immunogold labelling with MAb \textit{QUBf5} identified a surface-associated antigen located on the membranes of whole bacteria and on membrane vesicles or blebs. Only a proportion of the bacteria within the large capsule and the EDL populations was labelled (not illustrated). Cells from the small capsule population did not react with MAb \textit{QUBf5} but labelled blebs appeared to be secreted from unlabelled cells (fig. 2A). The \textit{QUBf5} epitope was readily released from the large capsule population in association with membrane blebs (fig. 2B) and from the EDL population as both membrane blebs and cell-free material (not illustrated).

The budding of vesicles from the outer membrane of \textit{B. fragilis} has been observed (fig. 3A). These vesicles may carry encapsulating material (fig. 3B).

MAbs \textit{QUBf6} and \textit{QUBf7}. Two IgG₁ MAbs, \textit{QUBf6} and \textit{QUBf7}, each reacted with high M₇ polysaccharides to give diffuse staining bands at the top of the immunobLOTS (fig. 1d–i). The quantity of labelled polysaccharide was less in the small capsule population (fig. 1e and h). Associated fine ladders of repeating polysaccharide subunits were detected in the EDL population (fig. 1f and i). Heterogeneous labelling of the large capsule (fig. 4A) and the EDL (not illustrated) populations was detected by electronmicroscopy and immunogold labelling with each MAb. Labelled cells were not seen in the small capsule population with either MAb, although some cell-free material was detected by MAb \textit{QUBf7} (fig. 4B). Cell-associated polysaccharides were recognised by each MAb in the large capsule (fig. 4C) and the EDL (fig. 4D) populations as illustrated with MAb \textit{QUBf7}. These
antigens were released from the large capsule population in association with membrane vesicles (fig. 4C) and from the EDL population as membrane vesicles and cell-free material (fig. 4D).

MAb QUBf8. An IgG1 MAb, QUBf8, was shown by immunoblotting to recognise a high-M, polysaccharide which produced a diffuse staining band on the top half of the blot (fig. 1j, k and l). Faint labelling was detected just behind the gel front in the region of the rough LPS. The QUBf8 epitope was most readily detected in the EDL populations where a fine ladder was seen in the middle region of the blot (fig. 1l). As with the other MAbs, the antigen recognised was present in smaller quantities in the small capsule population (fig. 1k). The QUBf8 epitope was shown by thin-section immuno-electronmicroscopy to be expressed on a high proportion of cells from the large capsule and the EDL populations (not illustrated). Negative staining revealed that the polysaccharide was cell associated but could be released from the large capsule population in association with membrane vesicles and from the EDL population as cell-free material (not illustrated).

Immunoblotting of outer membrane extracts

The immunoblotting patterns of Sarkosyl-extracted outer membranes were similar to those obtained by proteinase K extraction (fig. 1). No additional bands were identified in the outer-membrane preparations, indicating that protein antigens were not detected by any of the MAbs.

Confirmation of MAb specificity by immunofluorescence microscopy and flow cytometry

The pattern of labelling of the large capsule, small capsule and EDL populations with the MAbs was confirmed by immunofluorescence microscopy and flow cytometry. Strong labelling was associated with the small capsule populations in the case of MAb Bf4 and with the large capsule and the EDL populations in the case of the other MAbs (table I and fig. 5). The proportion of bacteria labelled within the populations was also measured (table I). For microscopy, populations were labelled at the same time with a rabbit
polyclonal anti-\textit{B. fragilis} anti-serum (which labelled all the bacteria) and with each of the MAbs. Secondary antibodies of anti-mouse antibody conjugated to fluorescein and anti-rabbit antibody to rhodamine were used to assess the labelling. For flow cytometry, bacteria were identified on the basis of size by forward and 90° light-scatter signals. Bacterial populations labelled with the nucleic acid-specific fluorochrome propidium iodide and identified in the flow cytometer by a red fluorescent signal were identical to those identified by size (unpublished result). Bacteria labelled with the MAbs were identified by the fluorescent

### Table I. Variation in MAb labelling in different populations of \textit{B. fragilis} NCTC 9343

<table>
<thead>
<tr>
<th>MAb</th>
<th>Method of analysis</th>
<th>Mean (SEM) percentage of population labelled*</th>
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<tr>
<td></td>
<td></td>
<td>Large capsule</td>
</tr>
<tr>
<td>Bf4</td>
<td>IFM</td>
<td>3 (1)*</td>
</tr>
<tr>
<td></td>
<td>FC</td>
<td>9 (5)†</td>
</tr>
<tr>
<td>QUBf5</td>
<td>IFM</td>
<td>16 (5)</td>
</tr>
<tr>
<td></td>
<td>FC</td>
<td>23 (8)</td>
</tr>
<tr>
<td>QUBf6</td>
<td>IFM</td>
<td>14 (5)</td>
</tr>
<tr>
<td></td>
<td>FC</td>
<td>37 (5)</td>
</tr>
<tr>
<td>QUBf7</td>
<td>IFM</td>
<td>47 (12)</td>
</tr>
<tr>
<td></td>
<td>FC</td>
<td>73 (9)</td>
</tr>
<tr>
<td>QUBf8</td>
<td>IFM</td>
<td>19 (14)</td>
</tr>
<tr>
<td></td>
<td>FC</td>
<td>77 (11)</td>
</tr>
</tbody>
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IFM, immunofluorescence microscopy; FC, flow cytometry.
* Each IFM value represents the mean of percentages from three experiments.
† Each FC value represents the mean of percentages from three experiments for MAbs QUBf7 and 8 and four experiments for the other MAbs.
signal from an anti-mouse fluorescein-conjugated secondary antibody. Flow cytometry consistently gave higher percentage labelling than fluorescence microscopy for most of the MAbs.

Flow cytometric profiles, which relate to the intensity of fluorescent signal, were obtained consistently in consecutive experiments. Representative profiles are illustrated in Fig. 5. MAb QUBf8, labelling the large capsule population, was an exception; although a biphasic profile was consistently obtained, the relative sizes of the two peaks varied. MAbs QUBf5, 6 and 8 all had a biphasic profile when labelling the large capsule population and a much broader profile with the EDL population. A single peak was obtained with MAb QUBf7 for both the LC and EDL populations, and with MAb Bf4 for the small capsule population. A small peak at high fluorescent intensity was also apparent in the large capsule population with MAb Bf4. A low level of fluorescent signal was obtained with MAbs 5–8 and the small capsule population.

Cross-reaction of the MAbs with other isolates

The reactivity of MAbs QUBf5, 6, 7 and 8 with other Bacteroides spp. and with E. coli was tested by immunofluorescence microscopy. None of the MAbs cross-reacted with B. vulgatus, B. thetaiotaomicron, B. ovatus, B. distasonis, B. gingivalis, E. coli or S. aureus. All reacted with B. fragilis strain BE3. The specificity of MAb Bf4 was described previously. Several recent clinical isolates, LS1–11, were screened for reactivity with each of the MAbs. The results are presented in Table II.

Populations of B. fragilis NCTC 9343 grown in vivo in the mouse for 7 days showed heterogeneous immunogold labelling with MAbs QUBf7 and 8 (not illustrated).

Discussion

The exact nature of the polysaccharides produced by B. fragilis is not yet clear. LPS of B. fragilis was characterised chemically and immunochemically by Kasper et al. and Weintraub et al. The extraction

Table II. Reactivity of B. fragilis MAbs with a range of recent clinical isolates of B. fragilis

<table>
<thead>
<tr>
<th>MAb</th>
<th>Number of isolates* which showed positive fluorescence with MAb</th>
</tr>
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<tbody>
<tr>
<td>Bf4</td>
<td>11</td>
</tr>
<tr>
<td>QUBf5</td>
<td>5</td>
</tr>
<tr>
<td>QUBf6</td>
<td>4</td>
</tr>
<tr>
<td>QUBf7</td>
<td>6</td>
</tr>
<tr>
<td>QUBf8</td>
<td>5</td>
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* A total of 11 isolates (LS1–11) was screened with each MAb.
and separation procedures used in both studies resulted in
the selection of only the rough form of *B. fragilis*
LPS. Further assays by gel electrophoresis of the crude
aqueous phase obtained by phenol-water extraction or
the PCP-insoluble fraction repeatedly failed to detect
the ladder-like pattern characteristic of O-antigen.22
However, Poxton and Brown10 extracted LPS from *B.
fragilis* by the classical aqueous phenol technique and
demonstrated that, in most strains, LPS was present
as predominantly smooth type. SDS-PAGE analysis
revealed regularly spaced ladder patterns of smooth
LPS molecules possessing increasing numbers of O-
antigen repeating units. Linko-Kettunen et al. produced
MAbs to the LPS of *B. fragilis*.22 Each MAb
recognised a common galactose-containing determi-
nant present in the outer core of the rough LPS.23 The
absence of the long chains of repeating polysaccharide
units led the authors to conclude that *B. fragilis* LPS
resembled the rough type LPS of gram-negative bacteria.24

The MAbs described in the present study all reacted
with saccharide epitopes. By immunoblotting, MAb
QUBf5 reacted with *B. fragilis* antigens to produce a
ladder in the middle of the blot similar to the ladder
which Poxton and Brown suggested was the O-
antigen.10 MAbs QUBf6 and QUBf7 were specific for
different high-M₄ polysaccharides. MAb QUBf8 la-
belled high M₄ polysaccharide and also some low M₄
material which stained in a similar position to the core
region of the rough LPS from other bacteria. This
indicates that the Bf8 epitope may be present on a
core or anchoring region of the polysaccharide.

Therefore, by using whole bacteria as antigens for
both immunisation and MAb screening, we obtained a
broader range of MAbs, including one which may be
to the O-antigen.

Immuo-electronmicroscopy showed that these
MAbs labelled epitopes primarily associated with the
large capsule and EDL, but not the small capsule. In
the case of the large capsule population, MAbs QUBf5–8
recognised epitopes present on both the bacterial surface and extracellular vesicles. The mem-
brane vesicles either remained within the fibrous
network of the large capsule or were sloughed off.
Since extracellular vesicles may have associated
capsular or EDL material, it remains unclear whether
the saccharide epitopes are associated with the
membrane bilayer or the encapsulating structures.
Deslauriers et al. observed the release of similar
extracellular vesicles from intact *Porphyromonas (Bac-
teroides) gingivalis* cells.25 The extracellular vesicles
described consisted of a membrane bilayer and were
thought to contain some periplasmic material.
The release of extracellular OM vesicles has previously
been described in *E. coli* growing under lysine
limitation26 and also under normal growth condi-
tions.27 Such a release of membrane vesicles or slime
may be important in virulence. The antigenic sites
located on extracellular structures could result in the
deposition of opsonin, either C3 or specific antibody,
at a distance from the bacterial cell, thus reducing the
effectiveness of the host immune response.

The reaction of each of the anti-polysaccharide
MAbs with a proportion of recent clinical isolates and
bacteria grown *in vivo* suggests that these polysacchar-
ides may be relevant to the virulence of *B. fragilis*.

In contrast with the large capsule population, in the
EDL population the saccharide epitopes were not
firmly surface-associated. Polysaccharides are abun-
dantly released from these cells as free material,
probably in the form of slime (fig. 4d) similar to that
observed in other bacteria and described as excreted
viscous substances that are not anchored in the
bacterial outer membrane.28

Interestingly, the ladder pattern observed by im-
umnoblotting was associated only with the EDL
population. These ladders are considered to represent
polysaccharide molecules of varying chain lengths,
each step up the ladder corresponding to the addition
of one repeating subunit. Perhaps the polysaccharides
from cells in the EDL population are of varying chain
lengths, or they are more susceptible to breakage of
the chain. Where the polysaccharides remain solely
cell- or vesicle-associated, in the case of the large
capsule population, the chains may remain large and
intact.

There was a low level of labelling of the small
capsule population detectable by flow cytometry,
immunoblotting and immunogold electronmicroscopy
with negative stain. There are a number of possible
explanations of this. Firstly, as the MAb only labelled
extracted and secreted material and not whole cells, it
is possible that the antigenic sites are masked by other
structures. However, electronmicroscopy and
immunogold labelling of thin sections gave a negative
result and, therefore, did not support this hypothesis.
Secondly, a low proportion of cells from the large
capsule or EDL population may have been present in
the sample. Thirdly, the polysaccharides may be
expressed at a low level because of incomplete
repression of the genes involved in controlling polysac-
charide synthesis. A few labelled outer membrane
vesicles were observed in the small capsule population
(fig. 2a).

Flow cytometry provided further confirmation of
the labelling pattern of the four MAbs QUBf5–8 and
of MAb Bf4 which reacted with the small capsule. It
also allowed a more rapid and accurate measurement
of the proportion of bacteria labelled within a given
population.

The generally higher percentage labelling obtained
by flow cytometry, when compared with fluorescence
microscopy, may be due to the greater sensitivity of
the flow cytometer which detects fluorescence signals
not readily visible by eye. Alternatively, it may be due
to the harsher fixation procedure used for microscopy.
This may cause the loss of some antigenic sites.

The significance of the fluorescent intensity profiles
obtained by flow cytometry is at yet unclear, although
they were consistently reproducible. The twin peaks
obtained with MAbs 5, 6 and 8 and the large capsule population may represent different populations within the large capsule population. Whether this occurs as a natural phenomenon or as a result of the treatment of bacteria during the labelling procedure is under investigation. These MAbs gave a broad profile when labelling the EDL population. The electronmicroscopy results show that polysaccharides labelled by these MAbs are released as cell-free material from the EDL population. Therefore, the broad profile may represent a continuum from cells from which most of the polysaccharide has been released as free material, to those in which most of it remains associated with the bacterial cell. Ørskov and Ørskov noted that even the mildest extraction procedures, such as cautious suspension of E. coli in saline, gives a suspension containing capsular material and LPS. More discrete bacterial cell. Ørskov and Ørskov noted that even the mildest extraction procedures, such as cautious suspension of E. coli in saline, gives a suspension containing capsular material and LPS. More discrete peaks (e.g., small capsule population with MAb B14) may relate to the closer association of the polysaccharide with the cell surface.

We have shown previously that the EDL population agglutinates erythrocytes from a number of different animal species. The present study shows that a proportion of the bacteria within these populations share common epitopes. The polysaccharides recognised by the MAbs may not be involved in haemagglutination. Alternatively, the polysaccharides may have different properties in the large capsule and EDL populations. This might relate in some way to the variation in polysaccharide chain length detected by immunoblotting only in the EDL population.

The factors governing the differential expression of the same saccharide epitopes in the large capsule, the small capsule and the EDL populations of B. fragilis are unclear. Ørskov and Ørskov described form variation in E. coli K1 strains. In the same K1 antigen cultures two types of colony were found with different reactivity towards a K1 antiserum. It was suggested that antigenic phase variation occurred in E. coli O26/B6. Two distinct phenotypic variants, which showed differences in reactivity with a core-specific MAb, were identified by flow cytometry. Similar antigenic variation may occur in B. fragilis and may be important in the virulence of this bacterium.

Structural differences, observed by electronmicroscopy, within individual strains of B. fragilis are reflected by differences in antigenicity. There is also, antigenic variation within structurally homogeneous populations of B. fragilis. Therefore, it seems likely that antigenic variation may occur in B. fragilis and the epitopes expressed by individual cells may reflect the selective pressures imposed on the population at a given time. The stability of epitope expression in relation to the virulence of B. fragilis is the subject of current investigations.

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References


