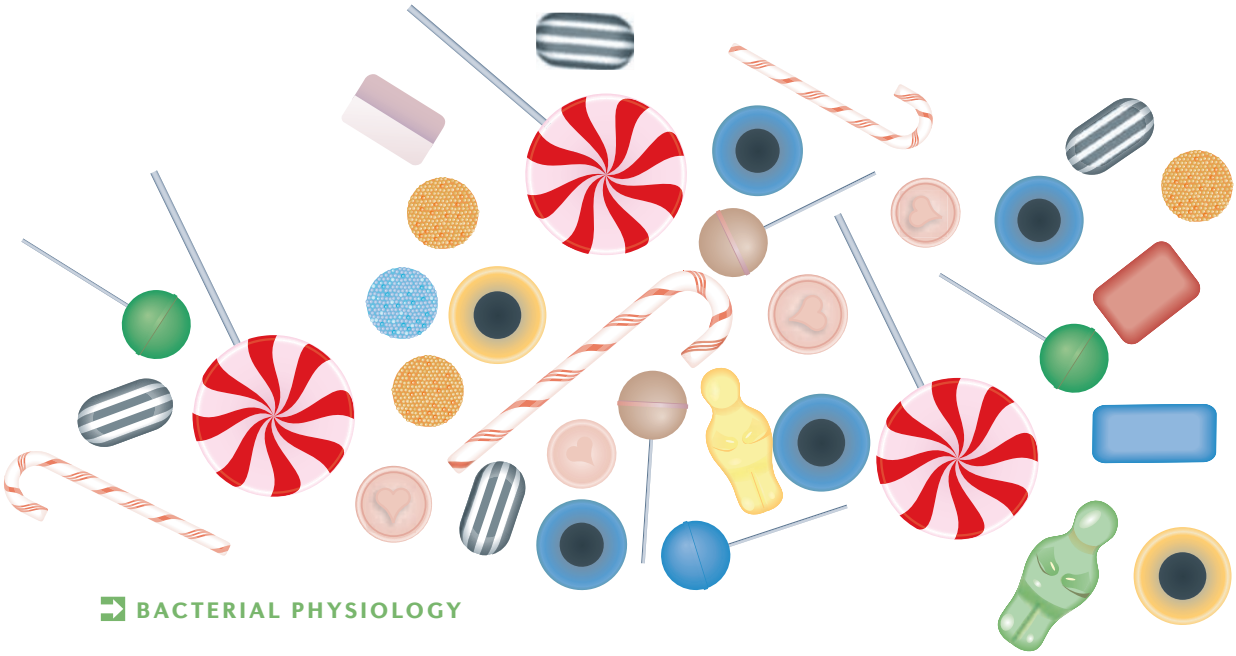
Nature Reviews Microbiology | AOP, published online 11 May 2009; doi:10.1038/nrmicro2151



Simon Bradwick

BACTERIAL PHYSIOLOGY

Sugar-coating friendly bacteria

The human intestinal microbiota contributes to host metabolism, development and immunity. Members of the *Bacteroides*, one of the most abundant genera of intestinal bacteria, have evolved several adaptations to survive in this competitive environment. Protein glycosylation is rare in bacteria and only a few general glycosylation systems have been identified. A study published in *Cell* now describes the discovery and characterization of a general O-glycosylation machinery in *Bacteroides* spp. that is essential for colonization of the mammalian intestine.

Bacteroides spp. encode a repertoire of genetic systems for harvesting and metabolizing carbohydrates from the intestine. One species, *Bacteroides fragilis*, produces enzymes that gather fucose sugars from host mucosal glycans and incorporates this exogenous fucose into its own capsular polysaccharides and glycoproteins. To determine the nature of the glycoproteins to which exogenous fucose residues are added, the authors purified the fucosylated proteins, before carrying out two-dimensional PAGE and tandem mass spectrometry. They identified 48 different proteins and, using a range of techniques, confirmed that 8 of these proteins were glycosylated. They generated antiserum that was specific to the glycan component of one of these proteins, and found that the antiserum also recognized each of the other purified glycoproteins, indicating that their glycans are similar or identical. Glycosylation occurs either on asparagine residues (N-linkage) or serine and threonine residues (O-linkage), and in this case it was shown that the glycans were O-linked at a specific three amino acid motif. Biochemical analysis indicated that the eight glycoproteins were secreted and were localized to the periplasm and outer membrane.

In *B. fragilis* the capsular polysaccharides are assembled at the inner face of the cytoplasmic membrane, transported across the membrane by a flippase and then oligomerized by a polymerase. The authors reasoned that the O-glycosylation machinery would probably be encoded in an operon that contained a flippase but not a polymerase, as no polymerization step is necessary for O-glycosylation. A genome search identified such a region, which contained a putative flippase, five putative glycosyltransferase enzymes and other genes likely to be involved in oligosaccharide synthesis. Deletion of all nine genes in this region (which spanned BF4298–BF4306) blocked fucosylated glycoprotein synthesis; as such, the authors named this the *lfg* (locus of *fragilis* glycosylation) region. Other *Bacteroides* species have similar regions to *lfg*, and glycoproteins of several species were shown to be glycosylated at the same conserved motif.

Finally, the authors found that although an *Δlfg* strain of *B. fragilis* was able to achieve similar growth to wild-type *B. fragilis* in monoassociation studies in a gnotobiotic mouse model, it was not able to compete with the wild-type strain for colonization of the mouse intestine when co-inoculated. These findings indicate that the general O-glycosylation system is essential for *B. fragilis* to colonize its ecological niche.

Andrew Jermy

> “…general O-glycosylation of proteins is essential for *B. fragilis* to colonize its ecological niche.”

ORIGINAL RESEARCH PAPER Fletcher, C. M. *et al.* A general O-glycosylation system important to the physiology of a major human intestinal symbiont. *Cell* **137**, 321–331 (2009)
FURTHER READING Szymanski, C. M. & Wren, B. W. Protein glycosylation in bacterial mucosal pathogens. *Nature Rev. Microbiol.* **3**, 225–237 (2005)