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Genetic Structure in the Region Near the Sialidase Gene in *Bacteroides fragilis*

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Bacteroides fragilis is a species of anaerobic microorganisms that is most frequently isolated from clinical anaerobic infections. Although *B. fragilis* constitutes less than 1% of the normal human colonic microflora, it is the predominant anaerobic isolate in cases of intra-abdominal abscess and anaerobic bacteremia. Increasing interest has been shown in the enterotoxigenicity and drug resistance of this species in the field of microbiology. However, the virulence factors of *B. fragilis* other than capsular polysaccharide have not yet been identified.

Bacterial sialidase is responsible for cleavage of *N*-acetylneuraminic acid from glycoproteins, glycolipids and polysaccharides in the host tissues, and is considered to be one of the virulence factors, because it has an important role in nutrition and adhesion of the pathogenic microorganism. We have previously reported cloning and sequence analysis of the sialidase gene *nanH* from *B. fragilis* strain YCH46. In this study, we cloned 7.0-kb upstream and 11.5-kb downstream fragments of *nanH*, and we determined their nucleotide sequences. Sequence analysis of the cloned fragments revealed a gene for a TonB-dependent outer membrane receptor protein (named *ompA*) and another gene for a putative outer membrane protein (named *ompB*). In the downstream region of *nanH*, the genes for mucin degradation enzymes, such as β-*N*-acetyl galactosaminidase, two *O*-acetylesterases, β-mannosidase, β-*N*-acetyl glucosaminidase, a putative transporter protein and another β-*N*-acetyl glucosaminidase are organized in this order.

These results show that genes for degradation of sialoglycoconjugates such as mucin and carbohydrate chain on the host cell surface are clustered in the *nanH* region, and the gene cluster is considered to play an important role in growth and survival of *B. fragilis* in host tissues.