JOURNAL OF BACTERIOLOGY, Aug. 2011, p. 4025–4026 Vol. 193, No. 15
0021-9193/11/$12.00 doi:10.1128/JB.05256-11

Draft Genome Sequence of *Bacteroides vulgatus* PC510, a Strain Isolated from Human Feces[▽]

Páraic Ó Cuív,[1] Eline S. Klaassens,[1] A. Scott Durkin,[2] Derek M. Harkins,[2] Les Foster,[2] Jamison McCorrison,[2] Manolito Torralba,[2] Karen E. Nelson,[2] and Mark Morrison[1,3]*

CSIRO Preventative Health Flagship Research Program and Division of Livestock Industries, Queensland Biosciences Precinct, 306 Carmody Road, Queensland 4067, Australia[1]; J. Craig Venter Institute, Rockville, Maryland 20850[2]; and The Ohio State University, Columbus, Ohio[3]

Received 10 May 2011/Accepted 16 May 2011

Although *Bacteroides vulgatus* is one of the most prevalent microorganisms in the human gastrointestinal tract, little is known about the genetic potential of this species. Here, we describe the annotated draft genome sequence of *B. vulgatus* PC510 isolated from human feces.

Bacteroides vulgatus is among the most commonly isolated microbes from the human gastrointestinal tract, and it has been found to constitute part of the core gut microbiota in healthy humans (6, 11). *B. vulgatus* is generally considered to be a beneficial gut commensal, but studies also suggest that important intraspecies variations may exist, with specific strains of *B. vulgatus* shown to be capable of promoting or protecting against colitis (e.g., see references 2, 7, and 12). *B. vulgatus* is also an occasional opportunistic pathogen, and consistent with this it is capable of attaching to and invading colonic epithelial cells and of inducing proinflammatory cytokines (5). In addition, *B. vulgatus* can bind to host structural factors (10), and strains isolated from subjects with ulcerative colitis show increased adhesion to tissue-cultured cells in comparison to that of strains isolated from healthy subjects (8). A key objective of the Human Microbiome Project is to provide information on the pan-genome of key microbial species. *Bacteroides* spp. have been extensively shaped by lateral gene transfer (e.g., see references 1, 9, and 13), and we thus describe here the draft genome sequence of *B. vulgatus* PC510 isolated as part of the Australian Human Gut Microbiome Project to provide a greater insight into the genetic variability of this genus and species.

B. vulgatus PC510 was isolated from a pooled healthy human fecal sample plated on medium 10 (4), with inulin and Hi-maize as the sole carbohydrate sources. We applied a 454 Life Sciences GS FLX system at the J. Craig Venter Institute (JCVI) to generate 4,781,702 bp of DNA sequence at 61× coverage. The individual sequence reads were then assembled into 117 contigs using the Newbler assembler, version 2.3. The contig N50 was approximately 94.2 kb, and the largest contig assembled was approximately 490.4 kb. Then, the JCVI prokaryotic annotation pipeline was used to annotate the DNA sequences.

The G+C content of the draft genome is 42%, with 89.6% of the genome predicted to be coding. The draft genome contains 4,091 genes, with 3,956 protein-coding genes and 63 structural RNAs. As expected, *B. vulgatus* PC510 encodes a diverse array of proteins with predicted roles in carbohydrate metabolism. In particular, we identified arylsulfatases, hexosaminidases, fucosidases, and a sialidase with putative roles in harvesting host glycans, as well as several genomic loci encoding proteins with likely roles in capsule production. The genome sequence also revealed the presence of a putative plasminogen/laminin binding protein, a heme utilization regulon, and an ortholog of a lipoprotein recently implicated in the activation of the NF-κB signaling pathway in an HT-29-based cell line (3).

Finally, we identified integron, transposon, and phage-like elements, suggesting that the genome of *B. vulgatus* PC510 has been extensively shaped by lateral gene transfer, consistent with other *Bacteroides* spp. Further intraspecies analyses may provide important genetic insights into the functional capability of *B. vulgatus*, and future studies should focus particularly on species isolated from subjects with gastrointestinal disorders, including ulcerative colitis and Crohn's disease.

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ADKO00000000. The version described here is the first version, ADKO01000000. The genome project data are also available at GenBank under the Genome project identifier 42763.

This research was performed as part of CSIRO's contribution to the International Human Microbiome Consortium. The research was funded by CSIRO's Transformational Biology Capability Platform, in support of the Preventative Health Flagship Research Program. We gratefully acknowledge the support provided by CSIRO's OCE Science Leader scheme (to M.M.) and the OCE Postdoctoral Fellow program (to E.S.K.).

We thank CSIRO Human Nutrition for collecting the fecal samples and Daniel Aguirre de Cárcer and Michael Conlon for providing critical reading and suggestions to improve the manuscript.

REFERENCES

1. **Davis, J. J., and G. J. Olsen.** 2011. Characterizing the native codon usages of a genome: an axis projection approach. Mol. Biol. Evol. **28:**211–221.
2. **Frick, J. S., et al.** 2007. Identification of commensal bacterial strains that modulate *Yersinia enterocolitica* and dextran sodium sulfate-induced inflammatory responses: implications for the development of probiotics. Infect. Immun. **75:**3490–3497.
3. **Lakhdari, O., et al.** 2010. Functional metagenomics: a high throughput

* Corresponding author. Mailing address: CSIRO Livestock Industries, Queensland Biosciences Precinct, 306 Carmody Road, Queensland 4067, Australia. Phone: 61 (0)7 3214 2216. Fax: 61 (0)7 3214 2900. E-mail: mark.morrison@csiro.au.

▽ Published ahead of print on 27 May 2011.

screening method to decipher microbiota-driven NF-κB modulation in the human gut. PLoS One **5:**e13092.
4. **McSweeney, C. S., S. E. Denman, and R. I. Mackie.** 2005. Rumen bacteria, p. 23–37. *In* H. P. S. Makkar and C. S. McSweeney (ed.), Methods in gut microbial ecology for ruminants. Springer, Dordrecht, Netherlands.
5. **Ohkusa, T., et al.** 2009. Commensal bacteria can enter colonic epithelial cells and induce proinflammatory cytokine secretion: a possible pathogenic mechanism of ulcerative colitis. J. Med. Microbiol. **58:**535–545.
6. **Qin, J., et al.** 2010. A human gut microbial gene catalogue established by metagenomic sequencing. Nature **464:**59–65.
7. **Rath, H. C., K. H. Wilson, and R. B. Sartor.** 1999. Differential induction of colitis and gastritis in HLA-B27 transgenic rats selectively colonized with *Bacteroides vulgatus* or *Escherichia coli*. Infect. Immun. **67:**2969–2974.
8. **Sato, K., et al.** 2010. OmpA variants affecting the adherence of ulcerative colitis-derived *Bacteroides vulgatus*. J. Med. Dent. Sci. **57:**55–64.
9. **Shoemaker, N. B., H. Vlamakis, K. Hayes, and A. A. Salyers.** 2001. Evidence for extensive resistance gene transfer among *Bacteroides* spp. and among *Bacteroides* and other genera in the human colon. Appl. Environ. Microbiol. **67:**561–568.
10. **Szöke, I., C. Pascu, E. Nagy, A. Ljung, and T. Wadström.** 1997. Binding of extracellular matrix proteins to the surface of *Bacteroides* spp. Anaerobe **3:**91–95.
11. **Tap, J., et al.** 2009. Towards the human intestinal microbiota phylogenetic core. Environ. Microbiol. **11:**2574–2584.
12. **Waidmann, M., et al.** 2003. *Bacteroides vulgatus* protects against *Escherichia coli*-induced colitis in gnotobiotic interleukin-2-deficient mice. Gastroenterology **125:**162–177.
13. **Xu, J., et al.** 2007. Evolution of symbiotic bacteria in the distal human intestine. PLoS Biol. **5:**e156.