

Classic Spotlight: *Bacteroides thetaiotaomicron*, Starch Utilization, and the Birth of the Microbiome Era

George A. O'Toole

Department of Microbiology and Immunology, Geisel School of Medicine at Dartmouth, Hanover, New Hampshire, USA

The revolution in the study of the human microbiome has increased our understanding of the central role of gut bacteria in terms of human nutrition, development of the human immune system, and the evolving nature of early gut microbiota. A key player in all of these processes is an anaerobic, Gram-negative group of microbes, the *Bacteroides* spp., and the best studied of this group is *Bacteroides thetaiotaomicron*. *Bacteroides* spp. use carbohydrates as a source of carbon and energy. A series of papers in the *Journal of Bacteriology* (JB) by Abigail Salyers and colleagues first established the role of polysaccharide utilization in *B. thetaiotaomicron* (or *B. theta* for short) and the role of sugar metabolism in the ability of this microbe to colonize the intestine.

In papers dating back to 1989, the Salyers lab used genetic and biochemical approaches to identify and characterize outer surface starch binding proteins and outer surface and periplasmic enzymes involved in the binding and breakdown of starch and other polysaccharides by *B. thetaiotaomicron* (1–3). As importantly, the successful search for mutants defective in polysaccharide degradation established the transposon Tn4351 as a useful genetic tool for this organism (1). A series of subsequent papers in JB described and further characterized the *sus* genes (for starch utilization system) and their products in catabolism of starch and related polysaccharide by *B. thetaiotaomicron* (see, for example, references 4, 5, 6, and 7). These collective studies showed that there is a starch utilization locus encoding numerous proteins involved in the binding, digestion, and import of starch and its digestion products. This locus served as the prototype for the numerous polysaccharide utilization loci subsequently identified in *Bacteroides* spp., each dedicated to the utilization of a distinct plant or host glycan. Another key contribution of the Salyers group related to polysaccharide utilization was establishing a link between the colonization of a germfree mouse intestine and a regulatory mutant defective in two polysaccharide utilization pathways, thereby demonstrating a key role for polysaccharide degradation in establishing a host niche (8). Studies of *B. thetaiotaomicron* and related *Bacteroides* spp., including work using these microbes as probiotics to treat human disease, continue to build on this fundamental research described in JB. Finally, it has become clear that *B. thetaiotaomicron* dedicates an enormous portion of its genome to

polysaccharide utilization, and thus one could easily argue that the contributions of Abigail Salyers and her group to the mechanistic understanding of polysaccharide utilization in *Bacteroides* spp., largely published in the pages of JB, had the field poised to interpret the findings of more recent genome-level studies of these important gut microbes.

REFERENCES

1. Anderson KL, Salyers AA. 1989. Genetic evidence that outer membrane binding of starch is required for starch utilization by *Bacteroides thetaiotaomicron*. *J Bacteriol* 171:3199–3204.
2. Anderson KL, Salyers AA. 1989. Biochemical evidence that starch breakdown by *Bacteroides thetaiotaomicron* involves outer membrane starch-binding sites and periplasmic starch-degrading enzymes. *J Bacteriol* 171:3192–3198.
3. Shipman JA, Cho KH, Siegel HA, Salyers AA. 1999. Physiological characterization of SusG, an outer membrane protein essential for starch utilization by *Bacteroides thetaiotaomicron*. *J Bacteriol* 181:7206–7211.
4. Reeves AR, Wang GR, Salyers AA. 1997. Characterization of four outer membrane proteins that play a role in utilization of starch by *Bacteroides thetaiotaomicron*. *J Bacteriol* 179:643–649.
5. Reeves AR, D'Elia JN, Frias J, Salyers AA. 1996. A *Bacteroides thetaiotaomicron* outer membrane protein that is essential for utilization of maltotriose and starch. *J Bacteriol* 178:823–830.
6. Smith KA, Salyers AA. 1991. Characterization of a neopullulanase and an alpha-glucosidase from *Bacteroides thetaiotaomicron* 95-1. *J Bacteriol* 173:2962–2968.
7. D'Elia JN, Salyers AA. 1996. Contribution of a neopullulanase, a pullulanase, and an alpha-glucosidase to growth of *Bacteroides thetaiotaomicron* on starch. *J Bacteriol* 178:7173–7179.
8. Cheng Q, Hwa V, Salyers AA. 1992. A locus that contributes to colonization of the intestinal tract by *Bacteroides thetaiotaomicron* contains a single regulatory gene (*chuR*) that links two polysaccharide utilization pathways. *J Bacteriol* 174:7185–7193.

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Address correspondence to georgeo@dartmouth.edu.

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