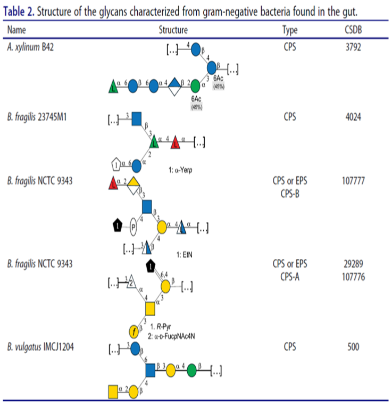


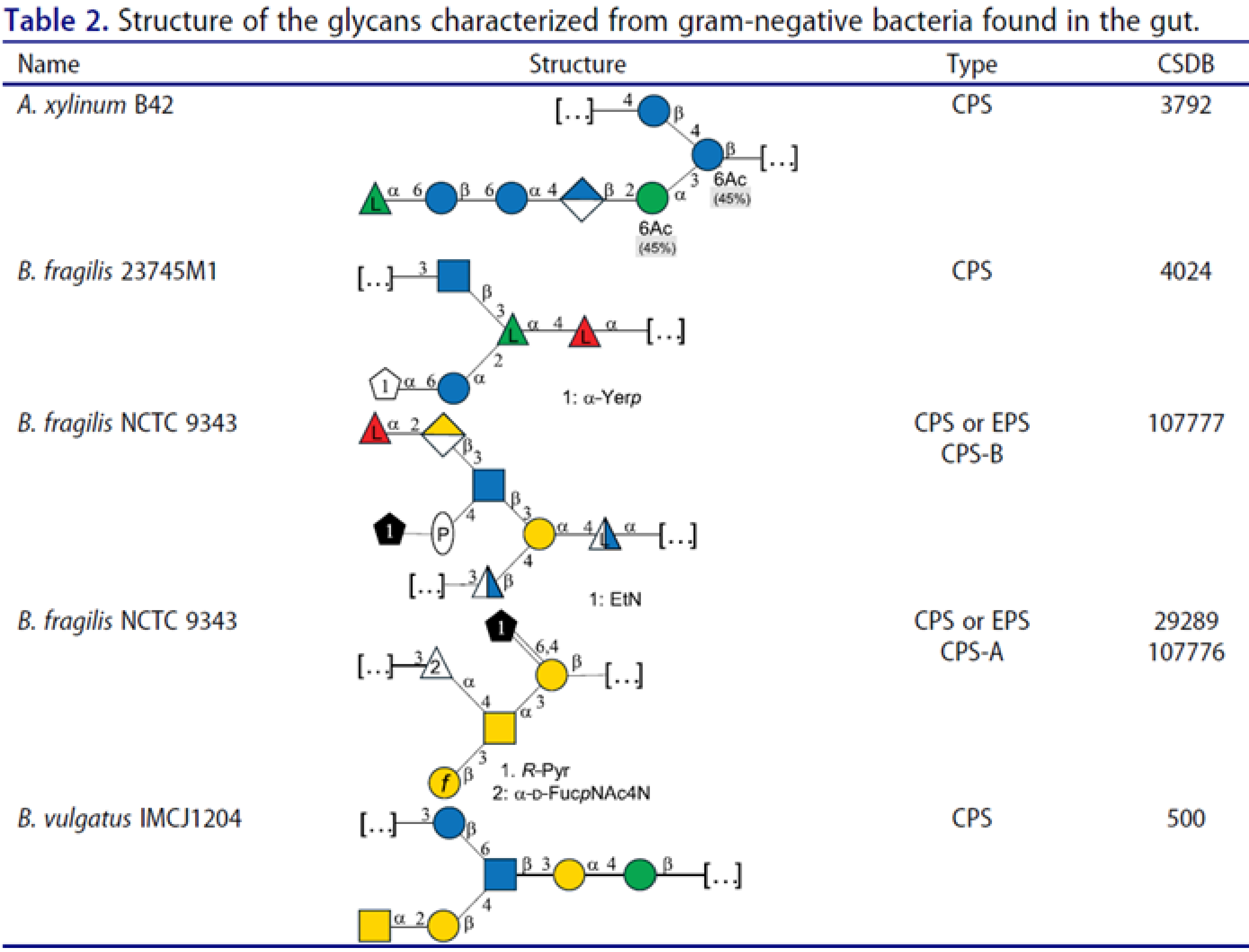
Table 2. Structure of the glycans characterized from gram-negative bacteria found in the gut.

Name	Structure	Type	CSDB
A. xylinum B42	6Ac (45%) 6Ac (45%)	CPS	3792
B. fragilis 23745M1	1: α-Yer*p*	CPS	4024
B. fragilis NCTC 9343	1: EtN	CPS or EPS CPS-B	107777
B. fragilis NCTC 9343	1. *R*-Pyr 2: α-D-Fuc*p*NAc4N	CPS or EPS CPS-A	29289 107776
B. vulgatus IMCJ1204		CPS	500

Cell surface polysaccharides in the gut microbiota: occurrence, structure and role

Description

The gastrointestinal (GI) tract is home to trillions of microorganisms that live in symbiosis with their host. Commensal bacteria in the gut communicate with epithelial and immune cells via effector molecules that are either secreted or attached to the cell surface. Although cell surface polysaccharides have primarily been studied in the context of pathogen-host interactions, they are increasingly being recognized as essential factors in the symbiotic interaction between gut microbiota and host, conferring biological activities and physiological functions. This review focuses on the structure and function of polysaccharides surrounding the bacterial cell wall: capsular polysaccharides (CPS), which are tightly linked to the cell surface; cell wall polysaccharides (CWPS), which are also tightly linked to the cell surface; and exopolysaccharides (EPS), which are loosely attached to the extracellular surface or secreted into the environment. Our focus will be on structurally characterized CPS, CWPS, and EPS from gut commensal and food-derived bacteria. These polysaccharides exhibit significant structural diversity, enabling bacteria to adapt to the GI environment and/or influence the hostâ??s immune response. The combined diversity of microbes in the gut provides a vast array of glycans that could be exploited for the benefit of human health.



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B. vulgatus IMCJ1204		CPS	500

Figure *A*.â?• stands for Acetobacter, and â??*B*.â?• stands for *Bacteroides*, the Carbohydrate Structure Database (CSDB) identification number is given in the corresponding column. The structures are depicted according to the rules given by the Systematic Nomenclature of Glycans. Where not specified, all the residues are in the pyranose form (if furanose, a â??*f*â?• is reported inside the symbol). All residues have the D absolute configuration unless otherwise specified.

Category

1. News