COMPLEMENTARY DEGRADATION MECHANISMS OF INULIN-TYPE FRUCTANS AND ARABINOXYLAN-OLIGOSACCHARIDES AMONG BIFIDOBACTERIAL STRAINS ISOLATED FROM THE SIMULATOR OF THE HUMAN INTESTINAL MICROBIAL ECOSYSTEM

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Introduction and objectives. Inulin-type fructans (ITF) and arabinoxylan-oligosaccharides (AXOS) are broken down to different extents by various bifidobacterial strains. To date, phenotypic heterogeneity in the consumption of complex oligosaccharides on strain level in the human colon remains poorly studied. To examine mechanistic variations in ITF and AXOS constituent preferences present in one individual, ITF and AXOS consumption by strains isolated from the simulator of the human intestinal microbial ecosystem (SHIME®), inoculated with feces from one healthy individual, was investigated.

Materials and Methods. Bifidobacterial strains were isolated from different selective media and classified and identified through $(GTG)_5$-PCR fingerprinting of their genomic DNA and sequencing of the partial 16S rRNA gene. All strains were analyzed as to their AXOS and ITF degradation capacity. The data were analyzed statistically to cluster the strains. Laboratory fermentations with a strain representing each of the four clusters were performed to monitor bacterial growth, arabinose, fructose, oligofructose, inulin, xylose, xylo-oligosaccharide, and AXOS consumption as well as metabolite production as a function of time.

Results and Discussion. Among the 19 strains identified, four species-independent clusters displaying different ITF and AXOS degradation mechanisms and preferences were found. *B. bifidum* B46 showed limited growth on all substrates, while *B. longum* B24 and *B. longum* B18 could grow better on short oligofructose fractions than on fructose. *B. longum* B24 could cleave arabinose substituents of AXOS extracellularly without using the AXOS-derived xylose backbones, while *B. longum* B18 was able to take up short oligosaccharides (up to xylotetraose) preferentially, and consume AXOS to a limited extent. *B. adolescentis* B72 degraded all chain length fractions of oligofructose simultaneously, partially degraded inulin, and could use xylose backbones longer than xylotetraose extracellularly. The strain-specific degradation mechanisms suggested to be complementary and indicated resource partitioning, *i.e.,* bifidobacteria with different degradation mechanisms can co-exist in the human colon. Specialization in degradation of complex carbohydrates by bifidobacteria present on the individual level could have *in vivo* implications for the successful implementation of ITF and AXOS aiming at a bifidogenic and/or butyrogenic effect. Finally, this work shows once more the importance of taking strain-level differences into account in gut microbiota research.