Screening the prebiotic effects of human milk oligosaccharides on 330 bacterial strains derived from the infant gut microbiota

Simone Renwick (University of Guelph, Guelph, ON, Canada), Annalee Furst (University of California, San Diego, CA, USA), Lars Bode (University of California, San Diego, CA, USA), Emma Allen-Vercoe (University of Guelph, Guelph, ON, Canada).

Introduction: Human milk oligosaccharides (HMOs) perform several functions critical to infant development, including acting as prebiotic stimulants for gut microbes. Several species of Bifidobacterium have demonstrated an ability to directly metabolize HMO structures in vitro, but data on the capacity of other species is limited. The aim of this study was to evaluate the ability of infant gut-associated bacterial strains to metabolize HMOs in monocultures.

Methods: A total of 330 bacterial strains, spanning 160 species, were isolated from infant fecal cultures, using a variety of selective and non-selective media types under aerobic and anaerobic conditions. Strains were treated with 15 g/L pHMOs (or a no-treatment control) in biological triplicate under anaerobic conditions. Growth responses were monitored over 48 h, and the degradation of 19 HMO structures were evaluated by HPLC-glycoprofiling to determine microbial HMO structure preferences.

Results: A wide variety of taxa were capable of degrading HMOs in vitro. Some strains demonstrated the ability to metabolize numerous HMO structures while others displayed structure-based specificity. In most cases, strains of the same species exhibited similar HMO metabolism capabilities, but exceptions included strains of [*Ruminococcus*] *gnavus* and *Alistipes finegoldii*. HMOs also suppressed the growth of several strains of species from the *Sellimonas* and *Sutterella* genera.

Discussion: HMOs interacted with a wide range of species, including those reported to be beneficial to human health as well as potential pathogens. Previously, direct HMO metabolism has only been reported in 17 species not including Bifidobacterium members. This study has greatly increased this figure through the discovery of HMO use in 60 previously untested species. Overall, this study has considerably expanded our knowledge of HMO–gut microbiota interactions.