Publications using GlyCare™ HMOs

DSM
BRIGHT SCIENCE. BRIGHTER LIVING.

Marcobal, A. et al. Bacteroides in the infant gut consume milk oligosaccharides via mucus-utilization pathways. Cell Host Microbe 10, 507–514 (2011).

Ruiz-Moyano, S. et al. Variation in consumption of human milk oligosaccharides by infant gut-associated strains of bifidobacterium breve. Appl. Environ. Microbiol. 79, 6040–6049 (2013).

Crost, E. H. et al. Utilisation of Mucin Glycans by the Human Gut Symbiont Ruminococcus gnavus Is Strain-Dependent. PLoS One 8, (2013).

Weiss, G. A., Chassard, C. & Hennet, T. Selective proliferation of intestinal Barnesiella under fucosyllactose supplementation in mice. Br. J. Nutr. 111, 1602–1610 (2014).

Li, M. et al. Human milk oligosaccharides shorten rotavirus-induced diarrhea and modulate piglet mucosal immunity and colonic microbiota. ISME J. 8, 1609–1620 (2014).

Li, M. et al. Human milk oligosaccharides shorten rotavirus-induced diarrhea and modulate piglet mucosal immunity and colonic microbiota. ISME J. 8, 1609–1620 (2014).

Huang, Y. L., Chassard, C., Hausmann, M., Von Itzstein, M. & Hennet, T. Sialic acid catabolism drives intestinal inflammation and microbial dysbiosis in mice. Nat. Commun. 6, (2015).

Garrido, D. et al. Comparative transcriptomics reveals key differences in the response to milk oligosaccharides of infant gut-associated bifidobacteria. Sci. Rep. 5, (2015).

Dotz, V., Rudloff, S., Meyer, C., Lochnit, G. & Kunz, C. Metabolic fate of neutral human milk oligosaccharides in exclusively breast-fed infants. Mol. Nutr. Food Res. 59, 355–364 (2015).

Balogh, R., Szarka, S. & Béni, S. Determination and quantification of 2'-O-fucosyllactose and 3-O-fucosyllactose in human milk by GC-MS as O-trimethylsilyl-oxime derivatives. J. Pharm. Biomed. Anal. 115, 450–456 (2015).

James, K., Motherway, M. O. C., Bottacini, F. & Van Sinderen, D. Bifidobacterium breve UCC2003 metabolises the human milk oligosaccharides lacto-N-tetraose and lacto-N-neo-tetraose through overlapping, yet distinct pathways. Sci. Rep. 6, (2016).

Garrido, D. et al. A novel gene cluster allows preferential utilization of fucosylated milk oligosaccharides in Bifidobacterium longum subsp. longum SC596. Sci. Rep. 6, (2016).

Elison, E. et al. Oral supplementation of healthy adults with 2'-O-fucosyllactose and lacto-N-neotetraose is well tolerated and shifts the intestinal microbiota. Br. J. Nutr. 116, 1356–1368 (2016).

Crost, E. H. et al. The mucin-degradation strategy of Ruminococcus gnavus: The importance of intramolecular trans-sialidases. Gut Microbes 7, 302–312 (2016).

Bunesova, V., Lacroix, C. & Schwab, C. Fucosyllactose and L-fucose utilization of infant Bifidobacterium longum and Bifidobacterium kashiwanohense. BMC Microbiol. 16, 1–12 (2016).

Yamada, C. et al. Molecular Insight into Evolution of Symbiosis between Breast-Fed Infants and a Member of the Human Gut Microbiome Bifidobacterium longum. Cell Chem. Biol. 24, 515-524. e5 (2017).

Schwab, C. et al. Trophic interactions of infant bifidobacteria and eubacterium hallii during L-fucose and fucosyllactose degradation. Front. Microbiol. 8, (2017).

Rasmussen, S. O. et al. Human milk oligosaccharide effects on intestinal function and inflammation after preterm birth in pigs. J. Nutr. Biochem. 40, 141–154 (2017).

Comstock, S. S. et al. Dietary human milk oligosaccharides but not prebiotic oligosaccharides increase circulating natural killer cell and mesenteric lymph node memory T cell populations in noninfected and rotavirus-infected neonatal piglets. J. Nutr. 147, 1041–1047 (2017).

O'Connell Motherway, M. et al. Carbohydrate Syntrophy enhances the establishment of Bifidobacterium breve UCC2003 in the neonatal gut. Sci. Rep. 8, (2018).

Medina, D. A., Pinto, F., Ortuzar, V. & Garrido, D. Simulation and modeling of dietary changes in the infant gut microbiome. FEMS Microbiol. Ecol. 94, (2018).

James, K., O'connell Motherway, M., Penno, C., Louise O'brien, R. & Van Sinderen, D. Bifidobacterium breve UCC2003 Employs Multiple Transcriptional Regulators To Control Metabolism of Particular Human Milk Oligosaccharides. (2018) doi:10.1128/AEM.

Gotoh, A. et al. Sharing of human milk oligosaccharides degradants within bifidobacterial communities in faecal cultures supplemented with Bifidobacterium bifidum. Sci. Rep. 8, (2018).

Craft, K. M., Thomas, H. C. & Townsend, S. D. Interrogation of Human Milk Oligosaccharide Fucosylation Patterns for Antimicrobial and Antibiofilm Trends in Group B Streptococcus. ACS Infect. Dis. 4, 1755–1765 (2018).

Bunesova, V., Lacroix, C. & Schwab, C. Mucin Cross-Feeding of Infant Bifidobacteria and Eubacterium hallii. Microb. Ecol. 75, 228–238 (2018).

Arboleya, S. et al. Gene-trait matching across the Bifidobacterium longum pan-genome reveals considerable diversity in carbohydrate catabolism among human infant strains. BMC Genomics 19, (2018).

Schwab, C., Voney, E., Ramirez Garcia, A., Vischer, M. & Lacroix, C. Characterization of the Cultivable Microbiota in Fresh and Stored Mature Human Breast Milk. Front. Microbiol. 10, (2019).

Publications using GlyCare™ HMOs

../continued

Sakanaka, M. et al. Evolutionary adaptation in fucosyllactose uptake systems supports bifidobacteria-infant symbiosis. Sci. Adv. 5, 7696–7724 (2019).

Rudloff, S. et al. Metabolism of milk oligosaccharides in preterm pigs sensitive to necrotizing enterocolitis. Front. Nutr. 6, (2019).

James, K. et al. Metabolism of the predominant human milk oligosaccharide fucosyllactose by an infant gut commensal. Sci. Rep. 9, (2019).

Duranti, S. et al. Bifidobacterium bifidum and the infant gut microbiota: an intriguing case of microbe-host co-evolution. Environ. Microbiol. 21, 3683–3695 (2019).

Craft, K. M. & Townsend, S. D. Mother Knows Best: Deciphering the Antibacterial Properties of Human Milk Oligosaccharides. Acc. Chem. Res. 52, 760–768 (2019).

Craft, K. M., Thomas, H. C. & Townsend, S. D. Sialylated variants of lacto-: N -tetraose exhibit antimicrobial activity against Group B Streptococcus. Org. Biomol. Chem. 17, 1893–1900 (2019).

Šuligoj, T. et al. Effects of human milk oligosaccharides on the adult gut microbiota and barrier function. Nutrients 12, 1–21 (2020).

Martín, R. et al. The infant-derived bifidobacterium bifidum strain cncm i-4319 strengthens gut functionality. Microorganisms 8, 1–19 (2020).

Lawson, M. A. E. et al. Breast milk-derived human milk oligosaccharides promote Bifidobacterium interactions within a single ecosystem. ISME J. 14, 635–648 (2020).

Kujawska, M. et al. Succession of Bifidobacterium longum Strains in Response to a Changing Early Life Nutritional Environment Reveals Dietary Substrate Adaptations. iScience 23, (2020).

Csernák, O., Rácz, B., Alberti, Á. & Béni, S. Quantitative analysis of 3'- and 6'-sialyllactose in human milk samples by HPLC-MS/MS: A validated method for the comparison of two consecutive lactation periods in the same woman. J. Pharm. Biomed. Anal. 184, (2020).

Chambers, S. A. & Townsend, S. D. Bioorthogonal human milk oligosaccharide probes for antimicrobial target identification within Streptococcus agalactiae. Carbohydr. Res. 488, (2020).

Alcon-Giner, C. et al. Microbiota Supplementation with Bifidobacterium and Lactobacillus Modifies the Preterm Infant Gut Microbiota and Metabolome: An Observational Study. Cell Reports Med. 1, (2020).

Szigeti, M., Meszaros-Matwiejuk, A., Molnar-Gabor, D. & Guttman, A. Rapid capillary gel electrophoresis analysis of human milk oligosaccharides for food additive manufacturing in-process control. Anal. Bioanal. Chem. 1595–1603 (2021) doi:10.1007/s00216-020-03119-0/Published.

Sarkozy, D. et al. Ultrafast high-resolution analysis of human milk oligosaccharides by multicapillary gel electrophoresis. Food Chem. 341, (2021).

Hoedt, E. C. et al. Broad Purpose Vector for Site-Directed Insertional Mutagenesis in Bifidobacterium breve. Front. Microbiol. 12, (2021).

Penno, C. et al. Maximum depth sequencing reveals an ON/OFF replication slippage switch and apparent in vivo selection for bifidobacterial pilus expression. Sci. Rep. 12, (2022).

Miriam N. Ojima et al. Diversification of a fucosyllactose transporter within the genus Bifidobacterium. Appl. Environ. Microbiol. 88, (2022).

Luna, E. et al. Utilization Efficiency of Human Milk Oligosaccharides by Human-Associated Akkermansia Is Strain Dependent. Appl. Environ. Microbiol. 88, (2022).

Li, D., Chen, D., Yu, B., Luo, Y. & He, J. Effect of sialyllactose administration on growth performance and intestinal epithelium development in suckling piglets. Anim. Feed Sci. Technol. 284, (2022).

Kijner, S., Cher, A. & Yassour, M. The Infant Gut Commensal Bacteroides dorei Presents a Generalized Transcriptional Response to Various Human Milk Oligosaccharides. Front. Cell. Infect. Microbiol. 12, (2022).

Giorgetti, A. et al. The effects of 2'-fucosyllactose and lacto-N-neotetraose, galacto-oligosaccharides, and maternal human milk oligosaccharide profile on iron absorption in Kenyan infants. Am. J. Clin. Nutr. (2022) doi:10.1016/j.ajcnut.2022.10.005.

Duan, Q. et al. Effect of sialyllactose on growth performance and intestinal epithelium functions in weaned pigs challenged by enterotoxigenic Escherichia Coli. J. Anim. Sci. Biotechnol. 13, (2022).

Arzamasov, A. A. et al. Human Milk Oligosaccharide Utilization in Intestinal Bifidobacteria is Governed by a Global Transcriptional Regulator NagR. bioRxiv Prepr. (2022) doi:10.1101/2022.04.06.487429.

Garádi, Z., Tóth, A., Gáti, T., Dancsó, A. & Béni, S. Utilizing the 1H-15N NMR Methods for the Characterization of Isomeric Human Milk Oligosaccharides. Int. J. Mol. Sci. 24, 2180 (2023).