A snapshot into the metabolism of isomalto-oligosaccharides in probiotic bacteria

In vitro and in vivo studies have demonstrated the prebiotic potential of isomalto-oligosaccharides (IMO), comprising α-(1,6)-gluco-oligosaccharides and panose, which selectively stimulate the growth of probiotic bifidobacteria and lactobacilli. The protein machinery conferring the utilization of IMO by probiotics, however, remains vaguely described. We have used genomic, transcriptomic, enzymatic, and biophysical analyses to explore IMO utilization routes in probiotic lactobacilli and bifidobacteria as represented by Lactobacillus acidophilus NCFM and Bifidobacterium animalis subsp. lactis BI-04, respectively. Utilization of IMO and malto-oligosaccharide (α-(1,4)-glucosides) appears to be linked both at the genetic and transcriptomic level in the acidophilus group lactobacilli as suggested by reverse transcriptase PCR (RT-PCR) and gene landscape analysis. Canonical intracellular GH13_31 glucan 1,6-α-glucosidases active on IMO longer than isomaltose occur widely in acidophilus group lactobacilli. Interestingly, however, isomaltose, isomaltulose and panose seem to be internalized through a phosphoenolpyruvate transferase system (PTS) and subsequently hydrolyzed by a GH4 6-phosphate-α-glucosidases based on whole genome microarray analysis. This sub-specificity within GH4 seems to be unique for lactobacilli mainly from the gut niche, as the sequences from this group segregate from characterized GH4 maltose-6-phosphate-α-glucosidases in other organisms. By comparison, IMO utilization in bifidobacteria is linked to soybean oligosaccharide utilization loci harboring GH36 galactosidases, GH13_31 oligo 1,6-α-glucosidases and a dual specificity ATP-binding cassette (ABC) transport system active in the uptake of both classes of α-(1,6)-glycosides. These data bring novel insight to advance our understanding of the basis of selectivity of IMO metabolism by important gut microbiome members.