

Differential patterns of glycerol metabolism by the human colon microbiota

Daily, significant amounts of glycerol may reach the colon microbiota upon ingestion and/or by *in situ* microbial formation or liberation from sloughed mucus and dead epithelial cells. A small group of microorganisms may anaerobically reduce glycerol to 1,3-propanediol (1,3-PDO), with 3-hydroxypropanal (3-HPA) as intermediate. The latter is part of the HPA-system, also known as reuterin. Reuterin is reported to have a significant antimicrobial activity and may furthermore cause (geno)toxic effects by binding to sulfhydryl groups as such or after dehydration to acrolein. Of all glycerol-reducing species, lactobacilli and enterococci are most efficient in accumulating the intermediate 3-HPA. So far, glycerol metabolism has barely been studied in mixed cultures of the human colon microbiota. In this study, we examined the colonic glycerol metabolism by incubation of faecal samples from 10 different donors. We have found that addition of 140 mM resulted in a clear effect on the microbial metabolism and community composition. Although all samples exhibited clear changes in their total bacterial community, a remarkable metabolic variation was observed. About a third of the samples exhibited rapid glycerol conversion, yielding relatively higher levels of acetate and 1,3-propanediol. The slower conversions tended to give higher levels of propionate and butyrate. Rapid glycerol conversion furthermore related with shifts in the lactobacilli-enterococci community, indicating a possible stimulation of glycerol-degrading and thus reuterin-accumulating lactobacilli and/or enterococci. Overall, the results indicate that glycerol may act as an effective hydrogen acceptor and hence might be a tool to modulate fermentation kinetics and patterns in the gastro-intestinal tract.

Keywords: glycerol; gut microbiota; colon; 1,3-propanediol; reuterin; *Lactobacillus reuteri*; lactobacilli; enterococci