of Acacia gum polymers (GA) on both human fecal flora composition and metabolism in vitro.

Methods: GA, together with short chain fructo-oligosaccharides (FOS), were incubated with human fecal bacteria in a continuous fermentor for 10 days. The culture was operated at 0.1 h^{-1} dilution rate, under an anaerobic atmosphere and the pH was controlled at 6.5. After eight bacterial population turn-overs, the short-chain fatty acids (SCFA) concentrations ($n = 5$) and the numbers of bacteria from the main intestinal genera ($n = 3$) were determined from culture effluents. Results were statistically (ANOVA) compared.

Results: SCFA concentration was significantly ($P < 0.05$) increased by both GA and scFOS fermentation (81.2 ± 2.8 and 73.3 ± 3.5 versus 40.1 ± 2.3 mM for GA, scFOS and control, respectively). The molar proportion of butyrate was significantly ($P < 0.05$) higher from GA (17.1 ± 0.1 %) compared to scFOS (12.9 ± 0.9 %) metabolisms. Both GA and scFOS increased *Lactobacillus* sp. members compared to the control (7.8 ± 0.1 and 7.6 ± 0.2 versus 6.1 ± 0.1 log CFU.mL^{-1} for GA, scFOS and control, respectively). Conversely, none of these carbohydrates induced changes in total anaerobes nor in total aerobic bacterial cells.

Conclusion: In vitro, GA and scFOS exhibit similar effects both on SCFA production and bacterial composition of human fecal microbiota. Thus, GA could exert a prebiotic effect similar to that of scFOS.

In vivo enhancing effect of Propionibacteria on the growth of fecal Bifidobacteria. Relationship with colonic transit time. D. Bouglé, N. Roland, F. Lebeurrier, J.L. Maubois, P. Arhan (Laboratoire de physiologie digestive et nutritionnelle, CHU, Avenue Général Clémenceau, 14033 Caen cedex; Standa-Industrie, Caen; Inra, Rennes, France).

While several reports suggest that probiotics are liable to modulate digestive transit, they do not provide details concerning the changes in the digestive flora and their functional consequences.

Colonic transit time was compared with fecal flora during supplementation of healthy subjects ($n = 19$) with Propionibacteria, regularly used for cheese making. Five 10^{10} CFU of two freeze dried strains (equivalent to the ingestion of 100 g Emmental) were ingested daily for 2 weeks. They came from strains known to stimulate in vitro the growth of bifidobacteria.

Segmental colonic transit time was measured by counting radiopaque markers on a plain X-rays of the abdomen before and at the end of the first week of supplementation. Viable Propionibacteria and Bifidobacteria were counted in feces collected weekly, twice before (D–8; D–1), twice during (D7; D14), and twice after the end of supplementation (D21; D28).

Results (*table* below):

Transit time in right and left colons, and rectosigmoid were 17.4 ± 8.1, 7.0 ± 5.0, 12.8 ± 8.5 h before and 17.3 ± 8.3 (NS), 11.9 ± 9.4 ($P = 0.02$), 13.3 ± 10.2 (NS) during supplementation. A significant correlation was found between tran-

	Before 1	Before 2	During 1	During 2	After 1	After 2
Propioni.	< 5*	< 5	5.6 ± 0.6	6.5 ± 0.6	< 5	< 5
Bifido.	7.6 ± 0.7	8.2 ± 0.6	8.3 ± 1.0[a]	8.2 ± 1.2[a]	8.5 ± 1.3[a]	7.7 ± 1.6[b]

* log CFU/mL feces; mean ± 1SD; [a]different from Before 1 ($P < 0.05$); [b]different from After 1 ($P < 0.05$).

sit time in left colon and faecal levels of propionibacteria and bifidobacteria during ingestion period.

Conclusions:

- Part of ingested Propionibacteria survive digestive transit in a large number of subjects. They are not able to colonize the intestine, but promote the growth of colonic Bifidobacteria.
- Digestive motility, assessed by colonic transit time, is directly related to these bacterial changes.

Role of a human digestive strain of *Bacteroides thetaiotaomicron* in the metabolism of food-borne glucosinolates. L. Elfoul[a], S. Rabot[a], A.J. Duncan[b], L. Goddyn[b], N. Khelifa[c], A. Rimbault[c] ([a]Inra UEPSD/MBS 78352 Jouy-en-Josas cedex; [b]MLURI Aberdeen, Faculté des sciences pharmaceutiques et biologiques; [c]Laboratoire de biologie/UMA Paris, France).

Consumption of brassica vegetables (cabbage, broccoli, etc.), which contain thioglucosides named glucosinolates, is associated with a lower risk of cancer. This property has been attributed to the isothiocyanates released by hydrolysis of parent glucosinolates under the action of plant myrosinase (EC 3.2.3.1). When the plant enzyme is inactivated by heating, the digestive microflora is responsible for the glucosinolate degradation into still unknown physiologically active compounds. Our aim was to investigate the ability of a strain of *Bacteroides thetaiotaomicron,* isolated from a human faecal microflora, to convert glucosinolates into isothiocyanates in vivo. Sixteen F344 germ-free rats were inoculated with the *B. thetaiotaomicron* strain and offered a glucosinolate-containing diet to simulate a realistic nutritional situation. They were dosed by stomach tube with 50 µmol of sinigrin, a pure glucosinolate commonly found in many brassica vegetables. Total urine and faeces were thereafter collected separately over 48 h. In the faeces, excretion of intact sinigrin was quantified by HPLC and the release of its specific derivative, allylisothiocyanate, was detected by GC. Conversion of sinigrin into allylisothiocyanate was estimated by quantifying its major final metabolite, a specific urinary mercapturic acid, by HPLC. The *B. thetaiotaomicron* strain was able to degrade sinigrin since only 8 % of the oral dose was excreted intact in the faeces. Trace amounts of allylisothiocyanate were detected in the faeces 18 h after the administration of sinigrin and the mercapturic acids of allylisothiocyanate appeared in the urine as early as the 6th hour. Most mercapturic acid excretion occurred within 30 h following sinigrin administration and the proportion of sinigrin converted into allylisothiocyanate was estimated to be 13 %. This study shows that a strain belonging to the dominant human colonic microflora is able to degrade, in vivo, a glucosinolate commonly found in brassica vegetables, and to convert it into allylisothiocyanate, a compound with potential health benefits.

Butyrate and glutamine metabolism in colonocytes: role of the intestinal microflora. C. Cherbuy[a], C. Andrieux[b], C. Ide[a], C. Tuleu[c], M. Watford[a], P.H. Duée[a], B. Darcy-Vrillon[a] ([a]LNSA, Inra, 78352 Jouy-en-Josas cedex; [b]UEPSD, Inra, 78352 Jouy-en-Josas cedex; [3]Lab. de Pharmacotechnie, Fac. des Sci. Pharm. et Biol. de Paris V, Paris, France).

The principal oxidative substrates of the colonic epithelium are butyrate, produced by bacterial fermentation, and circulating glutamine. We have previously shown that the capacity for ketogenesis from butyrate is lower, while the capacity for glutamine utilization is higher in the germfree rat. The goal of this study was to determine the role of the intestinal