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Administration of Different *Lactobacillus* Strains in Fermented Oatmeal Soup: In Vivo Colonization of Human Intestinal Mucosa and Effect on the Indigenous Flora

M.-L. JOHANSSON,[1] G. MOLIN,[1]* B. JEPPSSON,[2] S. NOBAEK,[2] S. AHRNÉ,[1] AND S. BENGMARK[2]

Laboratory of Food Hygiene, Department of Food Technology, Lund University, P.O. Box 124, S-221 00 Lund,[1] and Department of Surgery, Lund University, S-221 85 Lund,[2] Sweden

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In vivo colonization by different *Lactobacillus* strains on human intestinal mucosa of healthy volunteers was studied together with the effect of *Lactobacillus* administration on different groups of indigenous bacteria. A total of 19 test strains were administered in fermented oatmeal soup containing 5×10^6 CFU of each strain per ml by using a dose of 100 ml of soup per day for 10 days. Biopsies were taken from both the upper jejunum and the rectum 1 day before administration was started and 1 and 11 days after administration was terminated. The administration significantly increased the *Lactobacillus* counts on the jejunum mucosa, and high levels remained 11 days after administration was terminated. The levels of streptococci increased by 10- to 100-fold in two persons, and the levels of sulfite-reducing clostridia in the jejunum decreased by 10- to 100-fold in three of the volunteers 1 day after administration was terminated. In recta, the anaerobic bacterium counts and the gram-negative anaerobic bacterium counts decreased significantly by the end of administration. Furthermore, a decrease in the number of members of the *Enterobacteriaceae* by 1,000-fold was observed on the rectal mucosa of two persons. Randomly picked *Lactobacillus* isolates were identified phenotypically by API 50CH tests and genotypically by the plasmid profiles of strains and by restriction endonuclease analysis of chromosomal DNAs. The following five administered *Lactobacillus* strains were reisolated from the mucosa 1 day after the end of administration: *Lactobacillus plantarum* 299 and 299v, *Lactobacillus casei* subsp. *rhamnosus* 271, *Lactobacillus reuteri* 108, and *Lactobacillus agilis* 294. All of these strains were also found 11 days after administration was terminated, although *L. plantarum* 299 and 299v were dominant.

Enteral nutrition has several advantages over total parenteral nutrition. It is simpler to administer and cost effective, and since it maintains intestinal function and structure, it reduces treatment-related morbidity compared with total parenteral nutrition (2, 19, 38). The nutritional formula of an enteral feeding product is crucial, and oats are known to have a favorable nutrient content, comprising high levels of polyunsaturated fatty acids, phospholipids, high-quality protein, and fibers as beta-glucans; oats also contain many minerals and vitamins (12, 37). A new oatmeal-based product for enteral feeding has been developed recently (26). Oatmeal is mixed with water, supplemented with an enzyme mixture, heated, and then cooled and fermented with *Lactobacillus* spp. The product not only has an advantageous nutritional composition but also contains high numbers of viable lactobacilli.

Members of the genus *Lactobacillus* make up an integral part of the healthy human intestinal flora. By producing vitamins and enzymes, *Lactobacillus* spp. can affect the metabolism of a host (8, 16), and by producing antimicrobial compounds, lactobacilli may provide therapeutic benefits by controlling the proliferation of undesired pathogens (4, 7, 11, 13). Antibiotic therapy can disturb the indigenous intestinal flora, resulting in a significant decrease in *Lactobacillus* spp. (3, 20, 21), which is a common problem in treatment of infectious diseases and postoperative septic complications (17). A patient with a suppressed indigenous flora is more susceptible to secondary infections and overgrowth of undesired microorganisms, leading to diarrhea and even pseudomembraneous colitis and development of distant organ failure (5, 17, 22). Administration of *Lactobacillus* spp. to restore the indigenous human intestinal flora in cases of diarrhea has been tried in several studies, mostly with positive results (14, 21, 35, 40).

A starter culture suited for fermented oatmeal soup not only should be beneficial for the product per se, but also should be able to colonize the intestinal tract and to compete with the resident flora. Thus, the bacteria should be able to survive the low pH values of the stomach and to tolerate the bile salts in the duodenum. Furthermore, many factors, such as adhering capacity, growth rate, and antimicrobial activity, may be important for establishment on the intestinal mucous membrane (4, 31). Therefore, it may be difficult to identify relevant in vitro tests which can be used for the selection of appropriate strains. An alternative strategy is to use in vivo testing. To our knowledge, all previous in vivo studies on the establishment of *Lactobacillus* spp. in human intestinal tracts have been conducted by sampling feces. However, fecal microorganisms may reflect only part of the flora in the large intestine and are poor indicators of the flora of the upper gastrointestinal tract (32, 34). A more appropriate sampling technique is to take biopsies from the intestinal mucosa.

The aim of this study was to compare the in vivo capacities of different *Lactobacillus* strains to colonize the human intestinal mucosa. A total of 19 strains were administered in fermented oatmeal soup; 17 of these strains were originally isolated from human intestinal mucosa and had phenotypes that occur frequently in *Lactobacillus* spp. obtained from intestinal tracts (24). One strain originated from rat intestinal mucosa (23, 25), and one strain originated from sour dough.

* Corresponding author.

TABLE 1. *Lactobacillus* strains administered in fermented oatmeal soup to healthy volunteers

Designation	Strain[a]	Source of isolation
LS 132	*L. salivarius* 132	Human rectum
LS 280	*L. salivarius* 280	Human colon
LR 108	*L. reuteri* 108	Human jejunum
LR 47	*L. reuteri* 47 (= R2LC)[b]	Rat colon
LCP 136	*L. casei* subsp. *pseudoplantarum* 136	Human rectum
LJG 140	*L. jenseni-L. gasseri* 140	Human colon
LJG 292	*L. jenseni-L. gasseri* 292	Human colon
LAC 308	*L. acidophilus-L. crispatus* 308	Human jejunum
LP 283	*L. plantarum* 283	Human small intestine
LP 299	*L. plantarum* 299	Human colon
LP 299v	*L. plantarum* 299v	Sour dough
LCR 98	*L. casei* subsp. *rhamnosus* 98	Human rectum
LCR 271	*L. casei* subsp. *rhamnosus* 271	Human colon
LA 294	*L. agilis* 294	Human small intestine
LU 96	*Lactobacillus* sp. strain 96	Human colon
LU 99	*Lactobacillus* sp. strain 99	Human rectum
LU 138	*Lactobacillus* sp. strain 138	Human colon
LU 227	*Lactobacillus* sp. strain 227	Human colon
LU 282	*Lactobacillus* sp. strain 282	Human small intestine

[a] See reference 24.
[b] The designation in parentheses is the designation of Molin et al. (25).

The effects of *Lactobacillus* administration on other groups of intestinal bacteria were also determined.

MATERIALS AND METHODS

Strains. The test strains are shown in Table 1. All of the strains were gram positive (15) and catalase negative (9), were able to grow on Rogosa agar (Difco), and were able to produce acid from glucose anaerobically. The ability to ferment different carbohydrates was tested by using the API 50CH system (API, Montalieu Vercieu, France).

Oatmeal soup. Oatmeal soup base was made in a stainless steel tank with continuous stirring. Oatmeal (18.5%, wt/vol) and tapwater were mixed with malted barley flour (5%, wt/wt of oatmeal; Nord Malt AB, Söderhamn, Sweden), which contained amylase, proteinases, and beta-glucanases, and the preparation was heated to 95°C. The oatmeal soup base was transferred to sterile fermentors and cooled to 37°C.

The test strains were cultivated separately in Rogosa broth (Difco) for 12 to 24 h at 37°C and were washed in 0.9% NaCl. The oatmeal soup base was supplemented with malted barley flour (1%, wt/wt of oatmeal), and in individual batches, this preparation was inoculated with the different *Lactobacillus* strains (10^6 to 8×10^7 CFU/ml of soup) and incubated for about 15 h at 37°C (pH, less than 4.0). The fermented oatmeal soup was directly frozen at −80°C and then freeze-dried. The final product administered to volunteers was made by mixing the different freeze-dried batches, each representing a different test strain, with equal numbers of colony-forming units of all of the test strains (about 2.7×10^7 CFU/g of freeze-dried soup). The product was analyzed for the numbers of coliform bacteria, *Bacillus cereus*, *Enterococcus* spp., *Staphylococcus aureus*, *Clostridium perfringens*, *Salmonella* spp., yeasts, and molds, and it satisfied the guidelines of the Swedish food authorities.

Volunteers and administration. A total of 13 healthy volunteers (9 women and 4 men), who were between 31 and 56 years old, participated. No antibiotic had been taken by any volunteer during a 2-month period prior to the study, and no antibiotics were allowed during the investigation period. Also, the volunteers were not permitted to eat any lactic acid-fermented products before the test (for 2 weeks before administration) and during the test period (11 days plus 2 weeks after the end of administration). An 18.4-g portion of freeze-dried fermented oatmeal soup was mixed with cold water to make a final volume of 100 ml, and this preparation was ingested once a day for 10 days. The daily intake was about 5×10^8 CFU of each test strain.

This study was approved by the Ethics Committee for Human Studies at Lund University.

Sampling. Samples were taken as biopsies at the following times: (i) before the administration of fermented oat meal soup, (ii) 1 day after the end of administration, and (iii) 11 days after the end of administration. The samples were removed from the rectum by rectoscopy and from the upper jejunum just distal to the ligament of Treitz by using a Watson intestinal biopsy capsule (Ferraris Development and Engineering Co., Ltd., Edmonton, London, England). The biopsy samples were gently washed with a sterile 0.9% NaCl solution, immediately put into transport medium (0.9% NaCl, 0.1% peptone, 0.1% Tween 80, 0.02% cysteine), kept cold, and delivered to the laboratory for microbiological examination. They were then weighed (average weight, 0.05 ± 0.005 g), treated in an ultrasonic bath for 5 min, and vortexed for 2 min before dilution and inoculation onto selective media.

Viable counts were obtained from brain heart infusion agar (Difco) that was incubated aerobically and anaerobically at 37°C for 3 days (aerobic and anaerobic bacterial counts, respectively), from Rogosa agar (Difco) that was incubated anaerobically at 37°C for 5 days (*Lactobacillus* counts), from MRS agar at pH 5.5 (Oxoid) that was incubated anaerobically at 37°C for 5 days (lactic acid bacterial counts), from phenylethanol agar (Difco) that was incubated aerobically and anaerobically at 37°C for 3 days (gram-positive bacterial counts), from azide blood agar (Oxoid) that was incubated aerobically and anaerobically at 37°C for 3 days (mainly streptococcal counts), from Slanetz-Bartley agar (Oxoid) that was incubated aerobically at 37°C for 2 days (*Enterococcus* counts), from tryptose-sulfite-cycloserine agar (perfringens agar base [Oxoid] containing 4% cycloserine [Sigma]) that was incubated anaerobically at 37°C for 3 days (sulfite-reducing clostridial counts), from violet red-bile-glucose agar (Oxoid) that was incubated aerobically at 37°C for 1 day (*Enterobacteriaceae* counts), and from brain heart infusion agar containing a gram-negative anaerobic supplement (Oxoid) that was incubated anaerobically at 37°C for 3 days (gram-negative anaerobic bacterial counts). The Gaspak system (BBL Microbiology Systems, Cockeysville, Md.) was used for the anaerobic incubations.

Statistical evaluation. A statistical evaluation of the significance of the differences in the numbers of bacteria obtained at the three sampling times was performed by using the Kruskal-Wallis test and the Wilcoxon signed rank test.

Isolation and identification. For each biopsy, 10 *Lactobacillus* colonies were isolated randomly from the countable Rogosa plates. Each isolate was purified on Rogosa agar, suspended in freezing buffer (1), and stored at −80°C. The isolates were tentatively identified by using the API 50CH system. These identifications were confirmed by analyzing the plasmid profiles (6) and by restriction endonuclease analysis of chromosomal DNAs (36). The positions of the bands on the restriction endonuclease patterns differed more

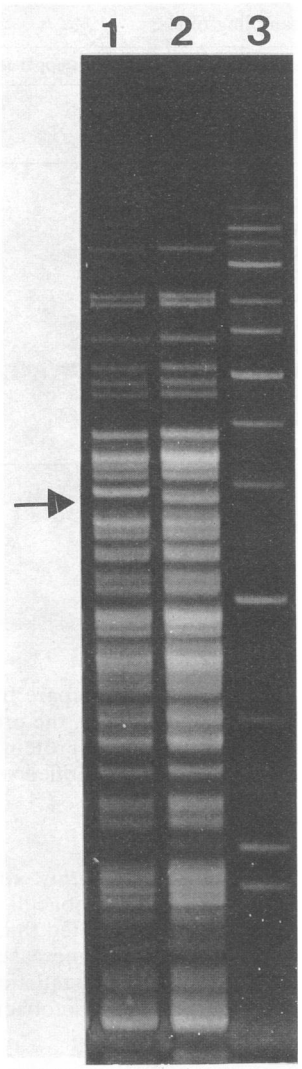

FIG. 1. Agarose gel electrophoresis of chromosomal DNAs from *L. plantarum* 299v (lane 1) and *L. plantarum* 299 (lane 2) digested with *Eco*RI. Lane 3 contained high-molecular-weight DNA markers (Bethesda Research Laboratories, Inc., Gaithersburg, Md.). The arrow indicates the difference in band patterns.

than 30% among the test strains except for strains LP 299 and LP 299v, which differed in only one band (Fig. 1).

It was extremely difficult to prepare DNA from some isolates, and therefore, the soluble protein contents of these organisms were studied as described below. A 0.1-g portion of cells from an overnight culture was mixed with 0.9 ml of sample buffer (0.05 M Tris-acetate [pH 7.5], 0.005 M DL-dithiothreitol, 0.01% [wt/vol] bromophenol blue). After sonication for eight cycles (30 s each) with a Soniprep apparatus (MSE Scientific Instruments, Sussex, England), 0.1 ml of a 10% sodium dodecyl sulfate solution was added, and the samples were steamed for 3 min. Approximately 20 μl of each sample was then applied to a 0.5-mm-thick 8 to 18% polyacrylamide gradient gel for horizontal electrophoresis of the sodium dodecyl sulfate-denatured proteins (ExcelGel SDS; Pharmacia LKB Biotechnology, Uppsala, Sweden). During the run, the gel was supplied with buffer ions through precast anode and cathode ExcelGel SDS buffer strips (Pharmacia LKB Biotechnology), and the gel was run at a constant voltage of 500 V for about 1 h at 11°C. The gel was then immersed in a fixing solution containing 40% (vol/vol) ethanol and 10% (vol/vol) acetic acid for 30 min and stained for 10 min in a Coomassie brilliant blue solution (25% [vol/vol] ethanol, 8% [vol/vol] acetic acid, 0.1% [wt/vol] Coomassie brilliant blue R250) that had been preheated to 65°C. The gel was washed several times with a destaining solution containing 25% (vol/vol) ethanol and 8% (vol/vol) acetic acid and was finally preserved in preserving solution containing 25% (vol/vol) ethanol, 8% (vol/vol) acetic acid, and 10% (vol/vol) glycerol for 30 min. The resulting protein profiles were compared visually.

RESULTS

Intestinal microflora. The effects of the administration of 19 different *Lactobacillus* strains in fermented oatmeal soup on the intestinal microflora are shown in Tables 2 and 3. In the upper jejunum the number of *Lactobacillus* counts increased significantly during administration; the high levels remained 11 days after the end of administration.

No other significant changes were observed in the jejunum. However, during the period of administration, the levels of aerobic streptococci increased in the jejuna of two persons by at least 10- to 100-fold, while the levels of sulfite-reducing clostridia in jejuna decreased by 10- to 100-fold in three persons. These changes were observed 11 days after the end of administration (Table 2 and data not shown).

On the rectal mucosa a slight, but not significant increase in the number of lactobacilli was observed both 1 and 11 days after administration ended. Significant decreases in anaerobic bacterial counts and in gram-negative anaerobic bacterial counts were detected both 1 and 11 days after administration ended.

In two persons, the levels of members of the *Enterobacteriaceae* on the rectal mucosa decreased by at least 1,000-fold during the period of administration. The levels then increased slightly 11 days after the end of administration (Table 3 and data not shown).

Colonization. (i) Phenotypic identification. The ability of the 19 administered *Lactobacillus* strains to colonize the intestinal mucosa of healthy volunteers was evaluated phenotypically (Table 4). Before administration, two of the volunteers were colonized with strains having the same phenotype (identical API 50CH patterns) as strain LCR 271, and three volunteers harbored strains identical to strain LA 294. None of these phenotypes was observed in these persons 11 days after the end of administration (Table 4).

At 1 day after the end of administration, 5 of the 19 test strains were identified phenotypically from mucosal samples (strains LP 299, LP 299v, LCR 271, LR 108 and LA 294). Strains having the same phenotypes were also isolated from the intestinal mucosa 11 days after the end of administration; However, strains LP 299 and LP 299v were now dominating (Table 4).

(ii) Genotypic identification. The phenotypic identification of isolates sampled 11 days after the end of administration was checked by plasmid analysis and restriction endonuclease analysis of chromosomal DNAs.

Of 11 persons harboring bacteria having the phenotype of strains LP 299 and LP 299v, 8 were colonized with strain LP 299v (originating from sour dough), whereas the remaining 3 persons were colonized with strain LP 299 (originating from human intestinal mucosa). In previous studies, strains LP

TABLE 2. Bacterial counts in upper jejuna at the three sampling times.

Group	Median bacterial counts (log CFU/g of mucosa) in upper jejuna		
	Before administration (n = 12)[a]	1 day after administration ended (n = 12)	11 days after administration ended (n = 10)
Anaerobic bacteria	4.1 (3.1–5.9)[b]	4.6 (3.4–5.9)	4.6 (3.9–5.5)
Aerobic bacteria	3.9 (3.4–5.4)	4.3 (3.4–5.7)	4.5 (3.1–5.7)
Gram-negative anaerobic bacteria	3.8 (3.1–5.3)[6][c,d]	3.4 (3.1–4.4)[5][d]	3.1 (3.1–4.6)[7][d]
Gram-positive anaerobic bacteria	3.8 (3.4–5.2)[3][d]	4.1 (3.1–5.4)[1][d]	4.2 (3.6–5.1)[3][d]
Gram-positive aerobic bacteria	4.1 (3.4–4.6)[3][d]	3.9 (3.1–5.4)	3.8 (3.1–4.7)
Lactobacillus spp.	3.0 (2.1–4.1)[3][e]	3.9 (3.1–5.6)[f]	4.0 (3.2–5.0)[f]
Lactic acid bacteria	3.8 (3.1–4.6)	4.3 (3.4–5.7)	4.4 (3.1–5.4)
Anaerobic bacteria on azide blood agar	3.4 (3.1–4.8)[5][d]	4.2 (3.1–5.7)[3][d]	4.4 (3.1–5.3)[3][d]
Aerobic bacteria on azide blood agar	3.6 (3.1–4.0)[6][d]	4.0 (3.6–5.7)[2][d]	4.0 (3.6–5.4)[2][d]
Sulfite-reducing clostridia	3.1 (3.1–5.2)[4][d]	3.5 (3.1–3.9)[7][d]	—[g]
Enterococcus spp.	3.8 (3.1–4.0)[8][d]	4.2 (3.7–5.6)[2][d]	4.4 (3.6–5.3)[1][d]
Enterobacteriaceae	—	—	—

[a] n is the number of volunteers.
[b] The values in parentheses are ranges.
[c] The values in brackets are the numbers of volunteers for whom the bacterial counts were below the limit of detection.
[d] Limit of detection, 1,000 CFU/g of mucosa.
[e] Limit of detection, 100 CFU/g of mucosa.
[f] $P < 0.01$ compared with the value before administration.
[g] —, all values were below the limit of detection (1,000 CFU/g of mucosa).

299 and LP 299v exhibited the same plasmid profile containing four plasmids (4.2, 9.1, 20, and 35 MDa). The cleavage patterns of chromosomal DNAs obtained by digestion with *Eco*RI differed only in one band (Fig. 1).

Three volunteers harbored isolates having a phenotype identical to that of strain LCR 271. However, the presence of strain LCR 271 was confirmed genetically in only one of the volunteers. Both the plasmid profiles and the restriction endonuclease patterns of the isolates from the other two persons differed slightly from those of strain LCR 271. (Strain LCR 271 contained two plasmids [2.7 and 4.7 MDa].)

Strain LR 108-like isolates, which occurred in three volunteers, were all identified as strain LR 108. (Strain LR 108 contained five plasmids [2.6, 4.8, 5.1, 20.9, and 30 MDa].)

DNA was extremely difficult to prepare from the isolates identified as strain LA 294. However, the protein profiles of these organisms were identical to the protein profile of strain LA 294, and they were therefore identified as strain LA 294.

DISCUSSION

Oral administration of *Lactobacillus* strains has been shown to increase the levels of lactobacilli in human feces (22, 33). In this study, we demonstrated that administration of *Lactobacillus* strains can also increase the levels of lactobacilli on the mucosa of jejuna (statistically significant) and can slightly affect the levels of lactobacilli in recta (not statistically significant).

TABLE 3. Bacterial counts in recta at the three sampling times

Group	Median bacterial counts (log CFU/g of mucosa) in recta		
	Before administration (n = 13)[a]	1 day after administration ended (n = 12)	11 days after administration ended (n = 11)
Anaerobic bacteria	6.6 (5.9–7.7)[b]	6.4 (5.1–7.0)	6.0 (4.4–7.6)[c]
Aerobic bacteria	6.4 (4.1–7.4)	5.6 (4.6–6.8)	5.6 (4.7–7.1)
Gram-negative anaerobic bacteria	6.0 (4.0–7.1)	5.7 (4.3–6.9)	4.9 (4.0–6.4)[2][d,e,f]
Gram-positive anaerobic bacteria	6.3 (4.1–7.4)	6.1 (4.1–6.9)	5.8 (4.7–7.2)
Gram-positive aerobic bacteria	6.5 (4.2–7.6)	5.4 (4.1–6.8)	5.8 (4.3–7.1)[1][g]
Lactobacillus spp.	4.6 (2.1–6.6)[1][h]	5.2 (3.6–6.4)	5.3 (3.2–7.5)
Lactic acid bacteria	4.9 (3.9–6.8)	4.7 (3.4–6.6)	4.9 (3.1–6.5)
Anaerobic bacteria on azide blood agar	5.3 (3.1–6.7)	4.5 (3.1–6.7)[1][f]	4.7 (3.1–5.1)[2][f]
Aerobic bacteria on azide blood agar	4.0 (3.4–6.5)[1][f]	4.4 (3.4–6.5)[2][f]	3.6 (3.1–4.7)[4][f]
Sulfite-reducing clostridia	4.9 (3.1–6.3)	4.2 (3.1–6.2)[1][f]	5.0 (3.4–5.5)
Enterococcus spp.	3.6 (3.0–7.4)[4][f]	4.0 (3.1–6.0)[1][f]	3.4 (3.1–5.1)[4][f]
Enterobacteriaceae	6.1 (3.4–7.2)[1][f]	5.3 (4.0–6.9)[3][f]	5.4 (4.0–6.5)[1][f]

[a] n is the number of volunteers.
[b] The values in parentheses are ranges.
[c] $P < 0.01$ compared with the value before administration.
[d] The values in brackets are the numbers of volunteers for whom the bacterial counts were below the limit of detection.
[e] $P < 0.05$ compared with the value before administration.
[f] Limit of detection, 1,000 CFU/g of mucosa.
[g] Limit of detection, 10,000 CFU/g of mucosa.
[h] Limit of detection, 100 CFU/g of mucosa.

TABLE 4. Distribution in the volunteers of *Lactobacillus* isolates with phenotypes identical to those of test strains (as determined by API 50CH tests) at the three sampling times

Volunteer	% of total no. of lactobacilli[a]									
	Before administration		1 day after administration ended				11 days after administration ended			
	Strain LCR 271	Strain LA 294	Strain LR 108	Strains LP 299 and LP 299v	Strain LCR 271	Strain LA 294	Strain LR 108	Strains LP 299 and LP 299v	Strain LCR 271	Strain LA 294
1					20 (J)			10 (R)	10 (J), 10 (R)	
2		10 (J)		10 (J)				10 (J)	20 (R)	
3				10 (R)		60 (R)		20 (R)		
4						10 (J), 40 (R)		80 (R)		
5				10 (R)	10 (R)			10 (R)		
6	70 (R)		10 (R)		20 (R)		10 (R)	30 (R)		
7					10 (R)	10 (J)		30 (J)	10 (R)	40 (J)
8							10 (R)	40 (R)		
9				10 (R)		10 (R)		40 (J)		
10							20 (J),10 (R)	40 (J)		20 (J), 20 (R)
11	10 (R)		10 (J)	30 (J), 10 (R)		10 (J), 10 (R)				
12		10 (J)		10 (J)						
13		10 (R)		30 (J)	30 (R)			20 (J)		

[a] J, jejunum; R, rectum.

It has also been shown by other workers that *Lactobacillus* administration can decrease the numbers of fecal *Escherichia coli* and anaerobic cocci (22). In our study, the levels of members of the *Enterobacteriaceae* on the rectal mucosa were decreased in some volunteers, but not in all volunteers. However, the anaerobic bacterial counts and the counts of gram-negative anaerobic bacteria were significantly decreased on the mucosa of recta, and this was especially pronounced 11 days after the end of administration. This suggests that after a period of establishment, the lactobacilli, exercise an antagonistic effect against the anaerobic flora. From a medical perspective, this must be regarded as advantageous. Several studies have shown that gram-negative anaerobic bacteria are frequently isolated from infected sites in patients with postoperative intraabdominal septic complications (28, 30, 39).

Previous administration studies have been performed with *Lactobacillus acidophilus* NCDO 1748 (22) and *Lactobacillus casei* GG (33). In the former study, volunteers were given about 3×10^{11} CFU per day for 7 days, but increases in the numbers of *L. acidophilus* were observed only as long as the participants were consuming the preparation. In the latter study, it was shown that *L. casei* GG must be given in doses of about 10^9 to 10^{10} CFU per day to be detectable in feces during the administration period. The volunteers in our study were given about 5×10^8 CFU of each test strain per day, although we were able to show that five of the strains colonized the intestinal mucosa and remained there for at least 11 days after administration ended.

L. acidophilus is often referred to as the most typical *Lactobacillus* species in gastrointestinal tracts (18, 27). However, in our study, none of the *L. acidophilus*-like test strains was reisolated from the mucosa. Instead, the two *Lactobacillus plantarum* strains seemed to be superior. Strain LP 299v, which originated from sour dough, was surprisingly dominant. The other strain, strain LP 299, which was of human intestinal origin, would be expected to be the strain that is best adapted to the intestinal environment. However, we do not know the reason for the colonization, and the two strains were closely related. Phenotypically, they were identical, and only minor differences were observed in their chromosomal DNAs in the restriction endonuclease analysis (Fig. 1).

The *L. casei* subsp. *rhamnosus* test strain, strain LCR 271, was observed in one person 11 days after the end of administration. In addition, phenotypically identical isolates were found in two other volunteers. However, these organisms differed genetically from strain LCR 271. This demonstrates why it is necessary to use genetic identification methods in colonization studies.

The following two *Lactobacillus reuteri* strains were administered in this study: strain LR 108, which was of human intestinal origin, and strain LR 47, which originated from rat intestinal mucosa. Strain LR 108 was reisolated from the intestinal mucosa of three volunteers 11 days after the end of administration, while strain LR 47 was never found. However, in a previous study (23), it was shown that strain LR 47 had an outstanding colonization capacity in rat intestines, while strain LR 108 could not colonize at all. This clearly shows that a certain *Lactobacillus* strain with an excellent colonization capacity in one species is not necessarily a good colonizer in another species.

Our results show that the genus *Lactobacillus* is one of the dominant genera in the jejunum. It could be argued that the bacterial concentrations in the mucosa of jejuna are relatively low and that the bacteria present are only temporary contaminants from the upper respiratory tract. However, more permanent establishment is indicated by the facts that (i) the test organisms were detected 11 days after the end of administration, and (ii) test strains found on the mucosa of jejuna were also found in recta.

In conclusion, we proved that certain *Lactobacillus* strains have a general ability to colonize human intestinal mucosa, independent of dietary and physiological differences among individuals. There is still a question to be answered: do these colonizing lactobacilli have any beneficial effects on the host? It has been shown recently that strain LR 47, which exhibits a pronounced colonizing ability in rats, also has the ability to reduce the incidence of bacteremia in rats after experimental intraabdominal infection (29) and the ability to hinder acetic acid-induced colitis (10).

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