

# ERRATUM

## New three-stage *in vitro* model for infant colonic fermentation with immobilized fecal microbiota

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In the paper by Cinquin *et al.* (2006), some footnote symbols were reproduced incorrectly in Tables 2 and 3, and there was also an error in the symbols in the legend to Fig. 2. Tables 2 and 3 and Fig. 2 are reproduced correctly here. The publishers apologize for this error.

**Table 2.** Bacterial populations measured by plate counts and fluorescence *in situ* hybridization in effluent samples from the three reactor stages at the pseudo-steady state and in fecal inocula for fermentation F1 (13 and 10 g L<sup>-1</sup> of carbohydrate concentrations) and F2 (10 g L<sup>-1</sup> of carbohydrate concentrations)

Bacteria/probes	Bacterial counts (Log 10 CFU or cell number per mL medium or g <sup>-1</sup> feces)*,†									
	PCS (R1)		TCS (R2)		DCS (R3)				Feces	
	13 g L <sup>-1</sup>		13 g L <sup>-1</sup>		13 g L <sup>-1</sup>		10 g L <sup>-1</sup>			
	PC	FISH	PC	FISH	PC	FISH	PC	FISH	PC	FISH
Fermentation F1										
DAPI		10.7 <sup>a</sup>		10.7 <sup>a</sup>		10.7 <sup>a</sup>		nd		nd
Total anaerobes/Eub338	9.8 <sub>A</sub>	10.6 <sup>a*</sup>	10.2 <sub>A</sub>	10.6 <sup>a</sup>	10.0 <sub>A</sub>	10.6 <sup>a*</sup>	9.8	nd	10.4 <sub>A</sub>	nd
Facultative anaerobes	7.9 <sub>A</sub>		8.1 <sub>A</sub>		8.0 <sub>A</sub>		8.0	nd	9.2 <sub>B</sub>	
Bifidobacteria/Bif164	9.4 <sub>A</sub>	10.6 <sup>a*</sup>	9.6 <sub>A</sub>	10.4 <sup>a*</sup>	9.3 <sub>A</sub>	10.4 <sup>a**</sup>	9.3	nd	9.5 <sub>A</sub>	nd
Bacteroides/Bac303	7.9 <sub>A</sub>	9.2 <sup>a*</sup>	8.2 <sub>A</sub>	9.7 <sup>a*</sup>	7.8 <sub>A</sub>	9.8 <sup>b*</sup>	8.1	nd	9.6 <sub>B</sub>	nd
Coliforms/EC1531	7.8 <sub>A</sub>	7.5 <sup>a</sup>	8.1 <sub>A</sub>	7.4 <sup>a*</sup>	7.8 <sub>A</sub>	7.2 <sup>b**</sup>	7.0	nd	8.9 <sub>B</sub>	nd
Lactobacilli/Lab164	5.2 <sub>A</sub>	9.1 <sup>a**</sup>	5.6 <sub>A</sub>	9.1 <sup>a**</sup>	5.5 <sub>A</sub>	9.0 <sup>a**</sup>	5.8	nd	< 4 <sub>B</sub>	nd
Clostridia/Erec482	7.5 <sub>A</sub>	8.7 <sup>a**</sup>	7.5 <sub>A</sub>	8.6 <sup>a**</sup>	7.5 <sub>A</sub>	8.8 <sup>a*</sup>	7.6	nd	8.1 <sub>B</sub>	nd
Gram positive cocci	7.9 <sub>A</sub>		8.1 <sub>A</sub>		7.9 <sub>A</sub>		7.8		7.9 <sub>A</sub>	
Staphylococci	7.5 <sub>A</sub>		7.9 <sub>A</sub>		5.9 <sub>B</sub>		6.7		5.0 <sub>C</sub>	
Fermentation F2										
Bacteria/probes	PCS		TCS		DCS				Feces	
	10 g L <sup>-1</sup>		10 g L <sup>-1</sup>		10 g L <sup>-1</sup>					
	PC	FISH	PC	FISH	PC	FISH	PC	FISH	PC	FISH
DAPI		10.6 <sup>a</sup>		10.7 <sup>a</sup>		10.7 <sup>a</sup>				11.0 <sup>b</sup>
Total anaerobes/Eub338	10.0 <sub>A</sub>	10.5 <sup>a*</sup>	10.1 <sub>A</sub>	10.5 <sup>a</sup>	10.0 <sub>A</sub>	10.5 <sup>a**</sup>			10.4 <sub>A</sub>	10.9 <sup>b*</sup>
Facultative anaerobes	8.2 <sub>A</sub>		8.3 <sub>A</sub>		8.1 <sub>A</sub>				9.4 <sub>B</sub>	
Bifidobacteria/Bif164	9.8 <sub>AB</sub>	10.3 <sup>a*</sup>	9.4 <sub>B</sub>	10.4 <sup>a*</sup>	9.3 <sub>B</sub>	10.4 <sup>a**</sup>			10.3 <sub>A</sub>	10.8 <sup>a*</sup>
Bacteroides/Bac303	7.9 <sub>A</sub>	9.1 <sup>a*</sup>	8.7 <sub>B</sub>	9.4 <sup>ab*</sup>	8.8 <sub>B</sub>	9.6 <sup>b**</sup>			8.9 <sub>B</sub>	9.9 <sup>b**</sup>
Coliforms/EC1531	7.7 <sub>A</sub>	9.2 <sup>a**</sup>	8.1 <sub>A</sub>	9.2 <sup>a**</sup>	8.1 <sub>A</sub>	9.2 <sup>a**</sup>			9.3 <sub>B</sub>	9.1 <sup>a</sup>
Lactobacilli/Lab158	6.4 <sub>A</sub>	9.1 <sup>a***</sup>	6.5 <sub>A</sub>	9.2 <sup>a***</sup>	6.6 <sub>A</sub>	9.1 <sup>a***</sup>			8.2 <sub>B</sub>	9.5 <sup>b*</sup>
Clostridia/Erec482	6.6 <sub>A</sub>	ND	6.8 <sub>A</sub>	ND	6.7 <sub>A</sub>	ND			6.7 <sub>A</sub>	ND
Gram positive cocci	8.0 <sub>A</sub>		7.8 <sub>A</sub>		7.9 <sub>A</sub>				9.1 <sub>B</sub>	
Staphylococci	6.6 <sub>A</sub>		6.2 <sub>A</sub>		6.4 <sub>A</sub>				7.5 <sub>B</sub>	

\*FISH counts significantly different from plate counts at the significance level: \* $P < 0.05$ , \*\* $P < 0.005$ , \*\*\* $P < 0.0005$ .

†Effects of fermentation section (PCS, TCS and DCS) on bacterial populations: values with different letters (capital for plate counts and small letters for FISH) are significantly different by Tukey-Kramer HSD test ( $P < 0.05$ ).

Data are mean values calculated for the last 4 and 2 days for each fermentation period for plate counts and FISH, respectively.

PCS, proximal colon simulation; TCS, transverse colon simulation; DCS, distal colon simulation; PC, plate counts; nd, not determined; ND, not detected, value below the detection threshold of the FISH method which was 6.8 Log 10 cell number per mL for effluent samples and 7.5 Log 10 cell number per g for wet feces.

**Table 3.** Metabolite concentrations and ratios in effluent samples from the three reactor stages at the pseudo-steady state and fecal inocula for fermentation F1 (13 and 10 g L<sup>-1</sup> of carbohydrates) and F2 (10 g L<sup>-1</sup> of carbohydrates)

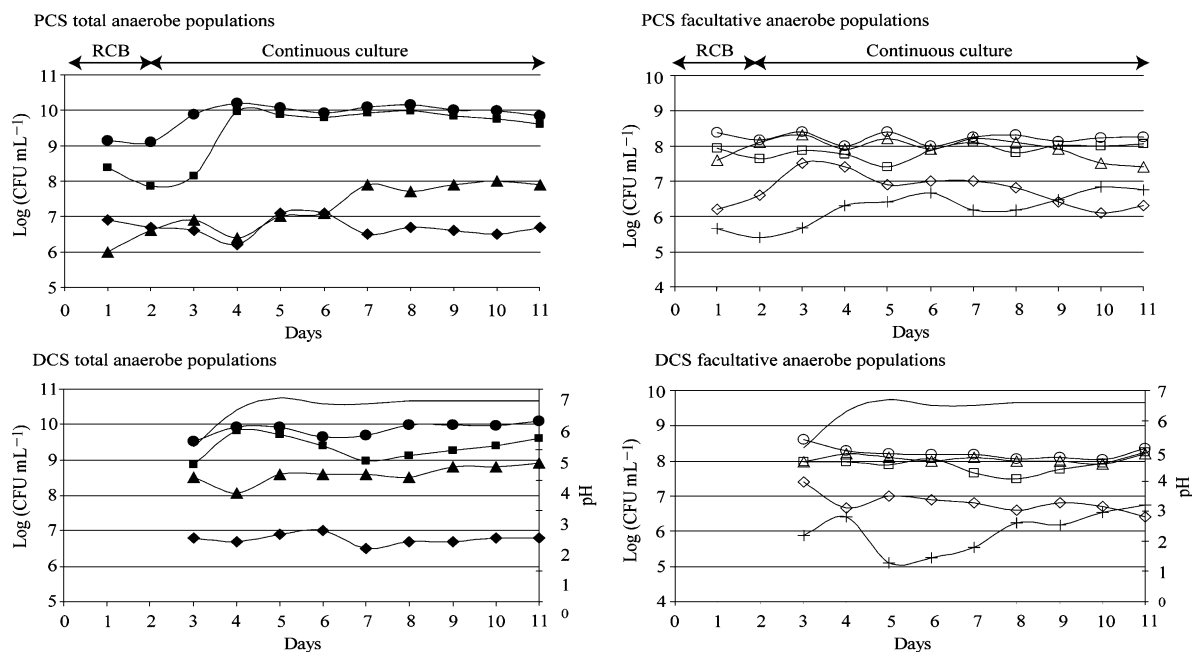
	PCS (R1)		TCS (R2)		DCS (R3)		Fecal samples		
Fermentation metabolites <sup>*,†</sup>	mM	%	mM	%	mM	%	mmol kg <sup>-1</sup> wet weight feces	%	Pooled SEM <sup>‡</sup>
Fermentation F1									
13 g L <sup>-1</sup>									
Total SCFA	136.2 <sup>a</sup>	100	167.4 <sup>a</sup>	100	187.6 <sup>b</sup>	100	nd		7.3
Acetic acid	94.3 <sup>a</sup>	69	107.4 <sup>ab</sup>	64	118.7 <sup>b</sup>	63	nd		5.0
Propionic acid	23.9 <sup>a</sup>	18	35.0 <sup>b</sup>	21	42.2 <sup>b</sup>	23	nd		2.4
Butyric acid	18.0 <sup>a</sup>	13	25.0 <sup>a</sup>	15	26.7 <sup>a</sup>	14	nd		2.5
Isoacids	9.9 <sup>a</sup>	100	18.2 <sup>b</sup>	100	21.7 <sup>c</sup>	100	nd		1.7
Isobutyric acid	7.7 <sup>a</sup>	78	14.2 <sup>b</sup>	78	17.3 <sup>c</sup>	80	nd		1.7
Isovaleric acid	2.2 <sup>a</sup>	22	4.0 <sup>b</sup>	22	4.4 <sup>b</sup>	20	nd		2.2
Ammonia	7.7 <sup>a</sup>		24.6 <sup>b</sup>		26.3 <sup>b</sup>		nd		1.6
10 g L <sup>-1</sup>									
Total SCFA	108.8 <sup>a*</sup>	100	136.4 <sup>a</sup>	100	146.1 <sup>a**</sup>	100			
Acetic acid	77.7 <sup>a*</sup>	72	84.4 <sup>a*</sup>	62	94.0 <sup>a*</sup>	65			4.3
Propionic acid	16.4 <sup>a*</sup>	15	26.0 <sup>b*</sup>	19	25.2 <sup>b**</sup>	17			2.8
Butyric acid	14.7 <sup>a</sup>	13	26.0 <sup>b</sup>	19	26.9 <sup>b</sup>	18			2.8
Isoacids	10.3 <sup>a</sup>	100	17.5 <sup>a</sup>	100	15.8 <sup>a**</sup>	100			6.7
Isobutyric acid	7.8 <sup>a</sup>	76	11.1 <sup>a</sup>	63	10.6 <sup>a**</sup>	67			2.5
Isovaleric acid	2.5 <sup>a</sup>	24	6.4 <sup>a*</sup>	37	5.2 <sup>a</sup>	33			2.0
Ammonia	10.2 <sup>a</sup>		24.5 <sup>b*</sup>		29.1 <sup>c*</sup>				1.6
Fermentation F2									
10 g L <sup>-1</sup>									
Total SCFA	118.6 <sup>a</sup>	100	141.4 <sup>b</sup>	100	157.3 <sup>c</sup>	100	71.5 <sup>d</sup>	100	1.9
Acetic acid	92.7 <sup>a</sup>	78	104.4 <sup>ab</sup>	74	115.3 <sup>b</sup>	73	54.0 <sup>c</sup>	75	2.3
Propionic acid	20.4 <sup>a</sup>	17	25.5 <sup>ab</sup>	18	29.0 <sup>b</sup>	19	13.5 <sup>a</sup>	19	1.8
Butyric acid	5.5 <sup>a</sup>	5	11.5 <sup>b</sup>	8	13.0 <sup>b</sup>	8	4.0 <sup>a</sup>	6	1.3
Isoacids	3.6 <sup>a</sup>		10.2 <sup>b</sup>		12.6 <sup>b</sup>		ND		0.9
Isobutyric acid	3.6 <sup>a</sup>		10.2 <sup>b</sup>		12.6 <sup>b</sup>		ND		0.9
Isovaleric acid	ND		ND		ND		ND		
Ammonia	9.1 <sup>a</sup>		29.4 <sup>b</sup>		33.5 <sup>c</sup>		29.1 <sup>b</sup>		1.4

\*SCFA concentrations in F1 (10 g L<sup>-1</sup> total carbohydrate) significantly different from SCFA concentrations in F1 (13 g L<sup>-1</sup> total carbohydrate) at the significance level: \* $P < 0.05$ , \*\* $P < 0.005$ , \*\*\* $P < 0.0005$ .

†Effects of fermentation section (PCS, TCS and DCS) on metabolites concentrations: values with different letters are significantly different by Tukey-Kramer HSD test ( $P < 0.05$ ).

‡Pooled SEM, pooled standard errors of the mean.

Data are mean values calculated for the last 4 days of each period. PCS, proximal colon simulation; TCS, transverse colon simulation; DCS, distal colon simulation; PC, plate counts; nd, not determined; ND, not detected, value below the detection threshold of the HPLC method (2 mM).



**Fig. 2.** Viable bacterial counts of total and facultative anaerobe populations in proximal (PCS) and distal (DCS) effluent from fermentation F2 with total carbohydrate concentration of 10 g L<sup>-1</sup>: total anaerobes (●), bifidobacteria (■), bacteroides (▲), clostridia (◆), facultative anaerobes (○), Gram+ cocci (□), staphylococci (+), coliforms (△), lactobacilli (◇), pH (—). RCB (repeated batch cultures) corresponding to beads precolonization.

## Reference

Cinquin C, Le Blay G, Fliss I & Lacroix C (2006) New three-stage *in vitro* model for infant colonic fermentation with

immobilized fecal microbiota. *FEMS Microbiol Ecol* **57**: 324–336.