

Table 1. Interactions with the relative abundance of bacterial taxa at genus level (abundance in percent. of the total number of sequences). Genus mean relative abundances are greater than 0.1% of the total relative abundance in all the fecal samples.

Interactions on genera	D0	D2	D7	D14	D21	D28	D56	Mean	SD	P-Value
	HF	HS	HF	HF	HF	HF	HF			
Group C										
<i>Ruminiclostridium</i>	0.28ab	0.23b	0.45a	0.30b	0.20b	0.35b	0.58a	0.32	0.22	0.0147
<i>Ruminococcaceae</i> UCG-013	0.21b	0.15b	0.17b	0.22b	0.15b	0.19b	0.27a	0.24	0.15	0.0064
<i>Streptococcus</i>	2.81b	5.84a	2.22b	1.63b	1.83b	2.34b	1.70b	2.16	2.31	0.0245
Group S										
<i>[Eubacterium] coprostanoligenes</i> group	2.44bc	3.24a	2.48bc	2.32b	2.06c	2.33c	2.64bc	2.52	0.78	0.0058
<i>Alloprevotella</i>	0.73bc	0.95a	0.62b	0.79b	0.47b	0.63b	0.58b	0.56	0.34	0.0479
<i>Candidatus Soleaferrea</i>	0.33b	0.46a	0.36b	0.23b	0.24b	0.35b	0.35b	0.35	0.24	0.0276
<i>Lachnospiraceae</i> UCG-004	0.21b	0.12c	0.29b	0.25bc	0.28b	0.23ab	0.32a	0.27	0.16	0.0238
<i>Rikenellaceae</i> RC9 gut group	4.7b	5.46a	5.05a	4.08b	4.24b	4.71b	4.80b	5.18	1.55	0.0233
<i>Ruminococcaceae</i> NK4A214 group	2.87bc	3.61a	3.35b	2.51bc	2.59bc	2.64bc	2.81c	3.21	1.37	0.0032
<i>Ruminococcaceae</i> UCG-002	1.23b	2.6a	1.36b	1.03b	1.08b	1.05b	1.04b	1.43	0.87	0.0054
<i>Ruminococcaceae</i> UCG-010	2.24abc	2.83a	2.38abc	1.97b	1.87c	2.12bc	2.78bc	2.45	0.94	0.0261

For each line, means with different superscripts differ at $P < 0.05$.

Table 2. Effect time on the relative abundance of bacterial taxa at (A) phylum, (B) family and (C) genus levels (abundance in percent of the total number of sequences). Genus mean relative abundances are greater than 0.1% of the total relative abundance in all the fecal samples.

Effect of Days	D0	D2	D7	D14	D21	D28	D56	Mean	S.D.	P-Value
	HF	HS	HF	HF	HF	HF	HF			
(A) Phylum										
Firmicutes	52.43bc	55.21a	54.54ab	52.54bc	52.28bc	53.32abc	51.26c	53.08	3.81	0.0254
Proteobacteria	0.83b	1.91a	0.86b	0.81b	0.70b	0.68b	0.85b	0.95	0.83	0.0030
Spirochaetes	5.44ab	3.46c	4.65b	5.54ab	5.64ab	5.98a	4.88b	5.07	2.09	0.0003
(B) Family										
BacteroidalesRF16group	0.83bc	0.78c	1.04b	0.72c	0.88bc	0.83bc	1.30a	0.91	0.36	0.0002
Christensenellaceae	3.33abc	3.77a	3.72ab	3.10c	3.25bc	3.31abc	2.97c	3.35	0.82	0.0145
CoriobacterialesIncertaeSedis	0.11ab	0.10abc	0.12a	0.11ab	0.07c	0.10bc	0.10abc	0.10	0.05	0.0276
Lachnospiraceae	24.63b	20.86c	27.13a	26.59ab	27.25a	25.51abc	24.96ab	25.27	4.06	<0.0001
Muribaculaceae	0.52b	1.09a	0.42b	0.47b	0.41b	0.47b	0.63b	0.57	0.51	0.0035
Spirochaetaceae	5.28ab	3.34c	4.49b	5.45ab	5.48ab	5.95a	4.71b	4.94	2.11	0.0002
Succinivibrionaceae	0.08b	1.71a	0.06b	0.08b	0.14b	0.05b	0.09b	0.28	0.77	0.0001
(C) Genus										
[Eubacterium]nodatumgroup	0.13ab	0.13ab	0.10abc	0.10abc	0.07c	0.14a	0.09bc	0.23	0.06	0.0244
[Eubacterium]ruminantiumgroup	0.41bc	0.25d	0.35bcd	0.32cd	0.57a	0.48ab	0.44abc	0.40	0.23	0.0017
Agathobacter	1.02b	0.77c	1.17ab	1.24a	1.05b	1.07b	0.99b	1.04	0.30	0.0003
Blautia	0.46bc	0.36c	0.60a	0.50ab	0.47ab	0.48bc	0.39bc	0.46	0.22	0.0061

<i>Celulosilyticum</i>	0.12 ^{bc}	0.18 ^{ab}	0.13 ^{bc}	0.16 ^b	0.13 ^{bc}	0.09 ^c	0.23 ^a	0.15	0.10	0.0016
<i>Christensenellaceae</i> R-7group	3.30 ^{abc}	3.73 ^a	3.68 ^{ab}	3.06 ^c	3.22 ^{bc}	3.25 ^{abc}	2.94 ^c	3.32	0.82	0.0145
FamilyXIIIAD3011group	0.27 ^{bcd}	0.34 ^{ab}	0.31 ^{abc}	0.26 ^{cd}	0.22 ^d	0.37 ^a	0.26 ^{cd}	0.29	0.10	0.0029
<i>Lachnospiraceae</i> ND3007group	0.37 ^a	0.24 ^c	0.27 ^{bc}	0.27 ^{bc}	0.26 ^{bc}	0.35 ^{ab}	0.28 ^{bc}	0.29	0.14	0.0237
<i>Lachnospiraceae</i> NK4A136group	3.98 ^a	2.98 ^b	3.73 ^a	4.26 ^a	4.17 ^a	3.66 ^{ab}	4.03 ^a	3.85	1.23	0.0202
<i>Lachnospiraceae</i> UCG-002	0.11 ^{abc}	0.10 ^{bc}	0.14 ^a	0.12 ^{ab}	0.12 ^{ab}	0.09 ^c	0.11 ^{bc}	0.11	0.05	0.0345
<i>Lachnospiraceae</i> UCG-008	0.52 ^a	0.40 ^b	0.58 ^a	0.54 ^a	0.53 ^a	0.60 ^a	0.52 ^a	0.53	0.16	0.0220
<i>Lachnospiraceae</i> UCG-009	2.52 ^{abcd}	2.07 ^d	2.75 ^{ab}	2.84 ^a	2.57 ^{abc}	2.23 ^{cd}	2.30 ^{bcd}	2.48	0.72	0.0278
<i>Prevotellaceae</i> UCG-004	1.49 ^{bc}	1.91 ^a	1.45 ^c	1.54 ^{bc}	1.48 ^{bc}	1.80 ^{ab}	1.52 ^{bc}	1.59	0.48	0.0447
<i>Roseburia</i>	0.24 ^{ab}	0.12 ^c	0.22 ^b	0.23 ^{ab}	0.30 ^a	0.28 ^{ab}	0.25 ^{ab}	0.23	0.13	0.0017
<i>Ruminococcaceae</i> UCG-005	2.22 ^b	2.77 ^a	2.21 ^b	2.36 ^b	1.82 ^c	2.23 ^b	2.18 ^b	2.25	0.65	0.0002
<i>Ruminococcaceae</i> UCG-014	0.44 ^b	0.76 ^a	0.36 ^b	0.42 ^b	0.38 ^b	0.50 ^b	0.45 ^b	0.48	0.26	0.0003
<i>Succinivibrio</i>	0.10 ^b	1.35 ^a	0.06 ^b	0.11 ^b	0.12 ^b	0.07 ^b	0.12 ^b	0.28	0.78	0.0001
<i>Treponema</i> 2	5.24 ^{ab}	3.31 ^c	4.46 ^b	5.41 ^{ab}	5.45 ^{ab}	5.91 ^a	4.65 ^b	4.89	2.12	0.0002

For each line, means with different superscripts differ at $P < 0.05$.

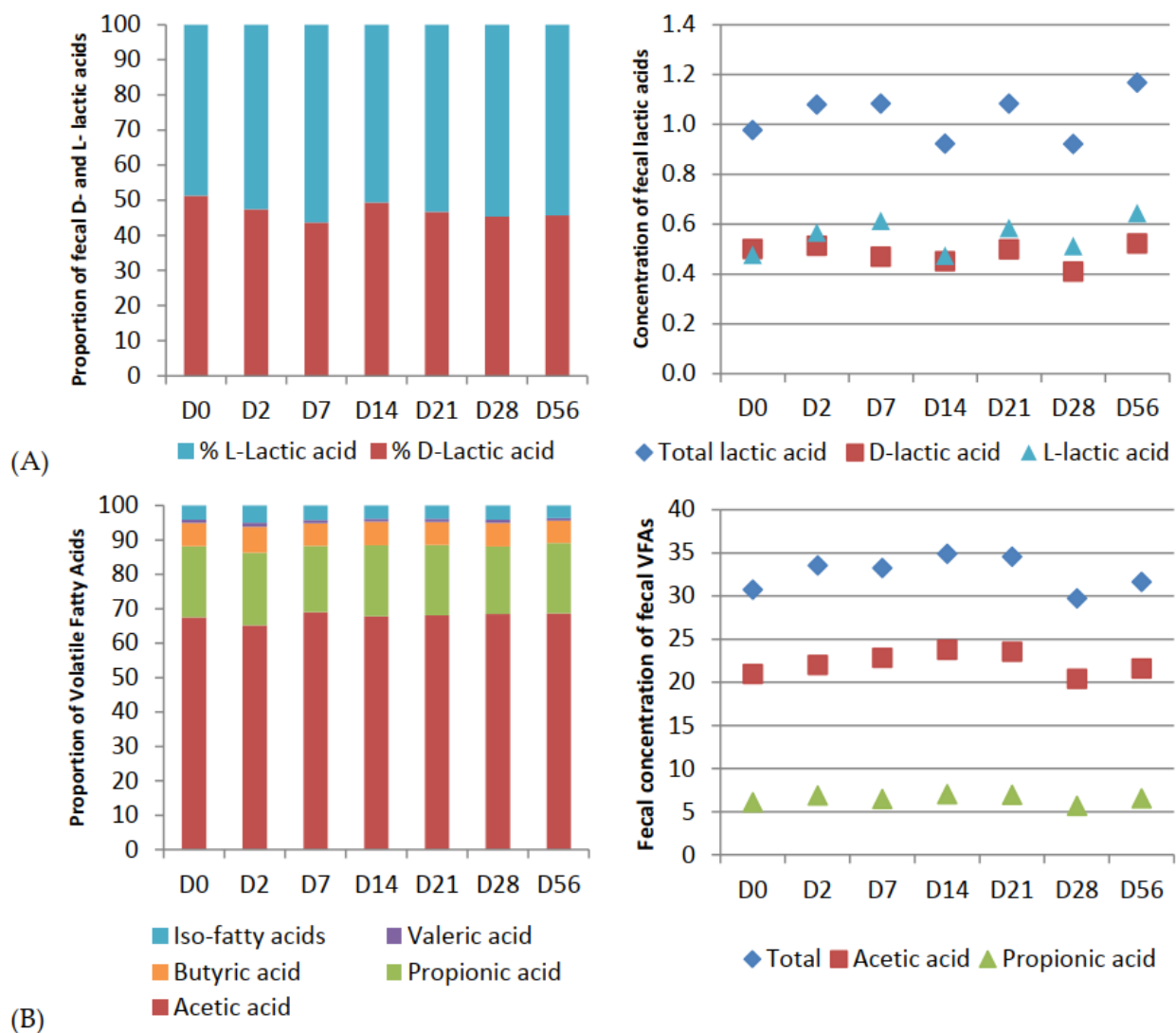


Figure 1. Days-related modifications of the proportions (%) and concentrations (mmol/L) of (A) 16 lactic acids and (B) volatile fatty acids.