

ERRATA

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Page 52, 1º Column, Line 22

Replace: Quintanilha et al ^{20,21} for Quintanilha et al ²¹⁻²²

Page 52, Tables 4 e 5

Table 4 - Mean Concentration and Prevalence (%) of Microorganisms in each Site of the LDT

Microorganisms	ÍLEUM		CECUM		COLON								RECTUM	
	MC	%	MC	%	Ascending		Transverse		Descending		Sigmoid		MC	%
	MC	%	MC	%	MC	%	MC	%	MC	%	MC	%	MC	%
<i>Bacillus</i> sp	1	9.5	2	4.2	5	4.2	3	4.2			1	4.3	3	5.0
<i>Bacteroides</i> sp (pig.)	5	4.8									5	4.3	1	5.0
<i>Bacteroides</i> sp (npg)	3	47.6	5	29.2	4	37.5	5	12.5	5	12.5	5	47.8	5	65.0
<i>Bacteroides</i> sp	2	4.8					2	4.2					3	5.0
<i>Bifidobacterium</i> sp	2	9.5			3	4.2	4	4.2	4	8.3	4	8.7	3	5.0
<i>Candida</i> sp	3.5	9.5	2	20.8	3	20.8	2	29.2	4	16.7	3	34.8	3	35.0
<i>Clostridium ramosum</i>	1	4.8							3	4.2				
<i>Clostridium</i> sp (gel -)	4	66.7	4	45.8	5	50.0	4.5	58.3	5	54.2	5	69.6	7	60.0
<i>Clostridium</i> sp (gel+)			2	4.2	4	4.2							3	5.0
<i>Clostridium</i> sp	1	4.8	4	45.8	7	4.2							5	5.0
<i>Corynebacterium</i> sp	3	57.1	3	54.2	3.5	50.0	4	41.7	4	45.8	5	60.9	5	65.0
<i>E.coli</i>	5	47.6	5	37.5	5	45.8	4.5	50.0	5	37.5	5	69.6	7	80.0
<i>Enterobacter cloacae</i>			4	4.2	1	4.2								
<i>Enterobacter</i> sp	4	28.6	4	20.8	7	37.5	4	29.2	5	45.8	5	52.2	7	35.0
<i>Enterococcus faecalis</i>	4.5	9.5	3	4.2	4	4.2	3	4.2	1	4.2	4	8.7		
<i>Enterococcus faecium</i>							5	4.2						
<i>Enterococcus</i> sp	4	38.1	2.5	33.3	3.5	33.3	3	58.3	5	58.3	5	34.8	5	60.0
<i>Eubacterium lentum</i>	4	4.8												
<i>Eubacterium</i> sp	3.5	9.5												
<i>Fusobacterium fusiformes</i>	3	4.8												
<i>Fusobacterium</i> sp	3.5	19.0	2.5	25.0	3	20.8	4	16.7	4	8.3	3	21.7	4	55.0
<i>Klebsiella pneumoniae</i>									5	4.2				
<i>Klebsiella</i> sp	5	76.2	4	54.2	6	62.5	5	54.2	5	41.7	7	69.6	7	65.0
<i>Lactobacillus acidophilus</i>	4	4.8	3	4.2										
<i>Lactobacillus</i> sp	4	33.3	2	29.2	2.5	33.3	3	37.5	3	25.0	2	43.5	4	70.0
<i>Leptotrichia</i> sp					1	4.2					1	4.3		
<i>Peptococcus anaerobius</i>	2	4.8	4	4.2	2	4.2					1	4.3		
<i>Peptococcus assachalyticus</i>	2	4.8												
<i>Peptococcus</i> sp	2	28.6	2.5	33.3	3	25.0	3	33.3	3	25.0	3	56.5	3	35.0
<i>Peptostreptococcus</i> sp	3	9.5			2	8.3			1	4.2	5	13.0		
<i>Propionibacterium</i> sp	3	52.4	3	20.8	4	33.3	3	50.0	3	29.2	5	26.1	5	30.0
<i>Proteus</i> sp	3.5	19.0	4	12.5	5	33.3	5	37.5	5	25.0	7	34.8	7	30.0
<i>Pseudomonas</i> sp	3	9.5					1	4.2						
<i>Rodothorula</i> sp	4	14.3	2	20.8	1	4.2	1	12.5	3	16.7	1	4.3	3.5	20.0
<i>Selenomonas</i> sp													2	5.0
<i>Staphylococcus</i> sp	5	4.8	2	4.2										
<i>Staphylococcus</i> sp coag -	2	33.3	2	20.8	1.5	8.3	2	20.8	2	8.3	3	21.7	3	45.0
<i>Staphylococcus</i> sp (coag+)													3	5.0
<i>Streptococcus</i> gama hem									2	8.3				
<i>Streptococcus</i> sp/alfa hemolítico grupo Viridans	4	14.3	4	16.7	2	8.3	3.5	8.3			2	13.0	3	5.0
<i>Veillonella</i> sp (Gel -)							3	8.3						
<i>Veillonella</i> sp	4	90.5	2.5	83.3	4	70.8	4	62.5	5	75.0	5	95.7	5	90.0

MC = Mean concentration (UFC / Log₁₀), % = prevalence**Table 5 - Association between microorganisms/sites of the lower digestive tract**

Microbiota	Lower Digestive Tract site
<i>Klebsiella</i> sp, <i>Clostridium</i> sp (gel-), <i>Veillonella</i> sp	All sites
<i>Enterobacter</i> sp	Sigmoid*
<i>Cândida</i> sp	Sigmoid and Rectum*
<i>Enterococcus</i> sp e <i>Lactobacillus</i> sp	Rectum*

sp = species, *p < 0,05 or < 5%