

Table 2.1. Description of the numerically predominant anaerobes that occur in the large intestine

Bacteria	Description	Numbers reported in faeces Log ₁₀ (g dry wt.) ⁻¹		Nutrition	Principal metabolic products
		Mean	Range		
Bacteroides	Gram negative rods	11.3	9.2 - 13.5	Saccharolytic	A, P, S
Eubacteria	Gram positive rods	10.7	5.0 - 13.3	Saccharolytic, some amino acid fermenting species	A, B, l
Bifidobacteria	Gram positive rods	10.2	4.9 - 13.4	Saccharolytic	A, l, f, e
Clostridia	Gram positive rods	9.8	3.3 - 13.1	Saccharolytic and amino acid fermenting species	A, P, B, L, e
Lactobacilli	Gram positive rods	9.6	3.6 - 12.5	Saccharolytic	L
Ruminococci	Gram positive cocci	10.2	4.6 - 12.8	Saccharolytic	A
Peptostreptococci	Gram positive cocci	10.1	3.8 - 12.6	As for the clostridia	A, L
Peptococci	Gram positive cocci	10.0	5.1 - 12.9	Amino acid fermenters	A, B, L
Anaerobic streptococci	Gram positive cocci	10.3	7.0 - 12.3	Saccharolytic	L, a
Methanobrevibacters	Gram positive coccobacilli	8.8	7.0 - 10.5	Chemolithotrophic	CH ₄
Desulfovibrios	Gram negative rods	8.4	5.2 - 10.9	Various ^a	A

^a These bacteria can grow chemolithotrophically on H₂ and CO₂ fermentatively, or oxidatively on some organic acids using SO₄²⁻ as a terminal electron acceptor.

^b With the exception of the methanogenic bacteria (Miller and Wolin 1982; Jones *et al* 1987) and the sulphate-reducing bacteria (Gibson *et al* 1988a; Gibson 1990), the cell count results are taken from Finegold *et al* (1983), and the fermentation product information from Holdeman *et al* (1977).

^c A = acetate, P = propionate, B = butyrate, L = lactate, f = formate, e = ethanol

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