

**Table 1 Composition of the microflora in the contents from different parts of the chicken alimentary tract, determined by microflora count (Smith, 1965)<sup>1</sup> .**

Organisms	Viable count ( $\log_{10}$ CFU <sup>2</sup> /g contents)						
	Crop	Gizzard	Intestine 1 <sup>3</sup>	Intestine 3	Intestine 5	Intestine 7	Caeca
<i>Lactobacilli</i>	8.7	7.3	8.0	8.2	8.2	8.6	8.7
<i>Streptococci</i>	4.0	3.7	4.0	4.0	3.7	4.2	6.7
<i>Escherichia coli</i>	1.7	n	2.0	1.7	1.7	2.7	5.6
Yeasts	2.7	n	1.7	n	1.7	n	2.0
<i>Clostridium welchii</i>	n <sup>4</sup>	n	n	n	n	n	1.7
<i>Bacteroides</i>	n	n	n	n	n	n	8.7

<sup>1</sup> Birds (6 individuals) originated from a flock whose diet was composed of ground cereals and fish meal (10-15%), without antibiotics.

<sup>2</sup> CFU: colony-forming units.

<sup>3</sup> The intestine was divided in 7 portions; four of them were studied (the first, third, fifth, and seventh).

<sup>4</sup> n: no viable organisms found in 0.02 g chyme, i.e.  $\log_{10}$  viable count per g <1.7

**Table 2 Diversity and prevalence of bacterial 16S rDNA sequences isolated from the intestinal and caecal flora of broiler chickens (Lu *et al.*, 2003) <sup>1</sup>.**

Group	Class	% of class <sup>2,3</sup>	
		Jejunum + Ileum	Caeca
Gram +, low G+C Intestine: 94.2%; Caeca 76.9%	<i>Lactobacillaceae</i>	68.7	8.2
	<i>Clostridiaceae</i> <sup>6</sup>	10.8	65.6
	<i>Bacillaceae</i>	0.7	1.4
	<i>Staphylococcaceae</i>	1.0	0
	<i>Streptococcaceae</i>	6.6	0.7
	<i>Enterococcaceae</i>	6.4	1.0
Gram +, high G+C Intestine: 0.9%; Caeca 13.9%	<i>Fusobacteriaceae</i>	0.7	13.9
	<i>Bifidobacteriaceae</i>	0.2	0
Gram -, proteobacteria <sup>4</sup> Intestine: 2.3%; Caeca 2.8 %		2.3	2.8
Gram - <sup>5</sup> Intestine: 0.6%; Caeca 5.2%	<i>Flavobacteriaceae</i>	0	0.2
	<i>Bacteroidaceae</i>	0.6	5.0

<sup>1</sup> Broiler chickens reared under standard management practices, fed a commercial corn-soy diet, without antibiotics.

<sup>2</sup> Mean values for animals between 3 and 49 d.

<sup>3</sup> 614 and 616 sequences for the intestine and the caeca, respectively.

<sup>4</sup> *Ochrobacterium*, *Alcaligenes*, *Escherichia*, *Campylobacter*

<sup>5</sup> *Cytophaga*, *Flexibacter*, *Bacteroides*

<sup>6</sup> *Clostridium*, *Ruminococcus*, *Eubacterium*