The effects of fructo-oligosaccharides or whole wheat on the digestive bacterial community of broiler chickens using fingerprint methods

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OBJECTIVES

January 2006 : in the European Union, ban of antibiotic growth promoters (AGP) from animal feed

→ Search for **alternatives** to AGP to control the balance of the digestive microflora

METHODS

Experimental diets

(1) a negative control (ground wheat based) with no additives
(2) a positive control containing an AGP (0.01 g/kg avilamycin)
(3) a diet containing 0.6 g/kg of short chain **fructo-oligosaccharides (FOS)**
(4) as the Nc diet, but with **whole wheat** (40%)

Broiler chickens

- 6 replicate pens / dietary treatment
- 3 weeks of age : sampling of ileal, cloacal and caecal contents (pools of 6 birds / pen)

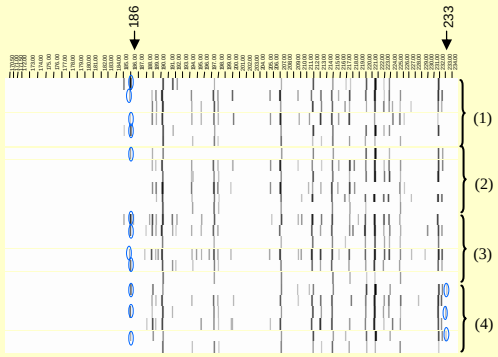
Analysis of predominant digestive microflora

by two fingerprint methods (universal primers)
Temporal Temperature Gradient gel Electrophoresis (TTGE)
Capillary Electrophoresis Single-Strand Conformation Polymorphism (CE-SSCP) (6-Fam and Hex labelling)

RESULTS

Dietary treatments → **Specific bands** (Figures 1 to 4)

Avilamycin →	CE-SSCP	Disappearance of several bands in the three digestive contents / Appearance of a band in the caeca
	TTGE	Presence of a band corresponding to long segmented filamentous micro organism in the cloaca
FOS →	CE-SSCP	Appearance of bands in the cloaca and in the caeca
	TTGE	Appearance of a band corresponding to segmented filamentous bacterium in the ileum
Whole wheat →	CE-SSCP	Appearance of a band in the ileum
	TTGE	Appearance of 2 bands corresponding to segmented filamentous bacterium and *Lactobacillus salivarius* in the ileum Disappearance of a band corresponding to *Escherichia coli* in the cloaca



(1) Negative control
(2) Avilamycin
(3) FOS
(4) Whole wheat

Figure 1. Fingerprints of CE-SSCP (6-Fam labelling) from pools of ileal contents (6 individuals)

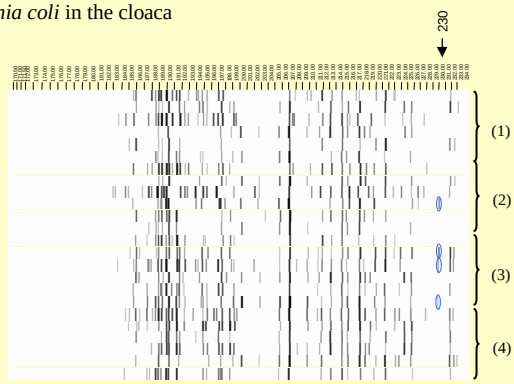


Figure 2. Fingerprints of CE-SSCP (6-Fam labelling) from pools of cloacal contents (6 individuals)

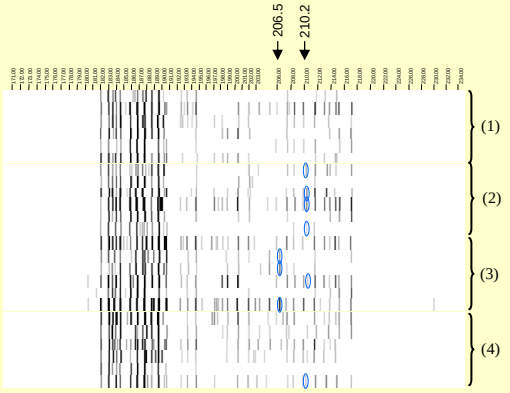
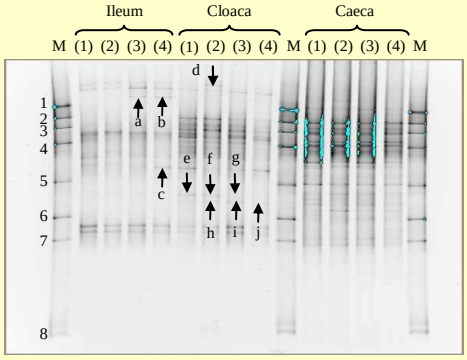


Figure 3. Fingerprints of CE-SSCP (Hex labelling) from pools of caecal contents (6 individuals)



(a,b) Segmented filamentous bacterium
(c) *Lactobacillus salivarius*
(d) Long segmented filamentous organism
(e,f,g) *Escherichia coli*
(h,i,j) Belonging to Order Clostridiales

Figure 4. Fingerprints of TTGE from pools of digestive contents (36 individuals)

AGP and two potential alternatives to AGP, FOS and whole wheat, lead to digestive microflora modifications

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