## PREVALENCE AND ANTIMICROBIAL RESISTANCE OF CAMPYLOBACTER COLI ISOLATED FROM FATTENING PIGS IN FRANCE

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## Introduction

*Campylobacter* are a leading cause of human diarrhea<sup>1</sup>. The usual source of infection is contaminated food, particularly poultry but pork has also been described<sup>2</sup>. Increasing resistance to antimicrobial drugs has been documented in human and animal strains of this zoonotic pathogen<sup>3</sup> and the veterinary use of antimicrobial drugs has been suggested to be largely responsible for this resistance. A study was carried out to investigate the occurrence and antimicrobial resistance of *Campylobacter* isolated from French fattening pigs.

### Materials and methods

Thermophilic *Campylobacter* were isolated from stomach samples obtained at slaughter from 240 fattening pigs originating from 24 different farms in the period March 1998-June 1999. The isolates were characterised at the species level by multiplex PCR. The agar dilution method was used for MIC determinations<sup>4</sup>. GyrA mutations were detected by MAMA-PCR and CmeB expression analysed by Western Blot as described previously<sup>4</sup>.

### Results

Half of the pigs (121 out of 240 animals) were found to be positive for *Campylobacter* but considerable variation was observed between farms (4 farms free of *Campylobacter*, and for the other farms 2 to 9 positive pigs among the 10 animals sampled). Isolates all belong to the C. coli species. Resistance to tetracycline and erythromycin was high (79 and 55 % respectively) and for nalidixic acid, enrofloxacin and ampicillin, resistance was observed in 34, 15 and 20 % of the isolates respectively (Table 1). More than one third of the strains was resistant to at least three antimicrobial drugs. A biphasic distribution was observed for tetracycline resistant isolates (MIC of 32 µg/ml and 256 µg/ml)(Table 1). Two groups of erythromycin-resistant strains could also be distinguished according to their level of resistance (MIC of 8-16  $\mu$ g/ml or MIC $\geq$ 256  $\mu$ g/ml for 10% of the isolates) (Table 1). One-third of the pigs whose isolates were included in the MIC determinations were found to harbour more than one isolate (exhibiting different susceptibility patterns). A Thr86Ile modification in GyrA was observed in the 16 enrofloxacin-resistant strains analysed. These isolates were also resistant to erythromycin, the other therapeutic molecule used to treat human campylobacteriosis. The multiresistant strains analysed expressed the multidrug transporter CmeB at a high level.

<u>Table 1.</u> Distribution of MICs and resistance (%R) for five antimicrobial drugs (Ap, ampicillin; Nal, nalidixic acid; Enr, enrofloxacin; Ery, erythromycin; tet, tetracycline) of the C. coli strains (n=131) isolated from pigs at slaughter. Vertical lines indicate the breakpoints used.

	No. of isolates with a MIC ( $\mu g/ml$ ) of								%R
	≤	0.5-	4	8	16	32	64	≥128	-
	0.25	2							
Ap		9	17	60	19	24	2		20
Nal		1	9	44	32	9	18	17	34
Enr	96	15	1	7	12				15
Ery	1	40	18	15	50			7	55
Tet	10	15	1	1	5	74	2	23	79

### Discussion

Results indicated a high prevalence of *C. coli* in the stomach of the French pigs examined. A high prevalence of *Campylobacter* in pigs was also described in other european studies, going from 63 to 100%. The predominance of *C. coli* is also in accordance with previous reports. In addition, a high proportion of the strains was resistant to antimicrobial drugs, particularly to tetracycline and erythromycin, or were multiresistant. Tetracycline is extensively used in pig production and macrolides (especially tylosin) were permitted as growth promoters for pigs in Europe until 1999. This could explain the high rates of resistance observed. Increasing quinolone resistance is compromising the use of this criteria for routine clinical laboratory identification of thermophilic *Campylobacter*.

## Conclusion

Increasing antimicrobial resistance in *Campylobacter* is raising concern not only for human therapy but also for horizontal transmission of this resistance in the natural ecosystem of this bacterium.

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