



KEROUANTON Annaëlle<sup>1,3,\*</sup>, CHIDAINE Bérengère<sup>1,3</sup>, ROSE Valérie<sup>1,3</sup>,  
KEMPF Isabelle<sup>2,3</sup>, et DENIS Martine<sup>1,3</sup>

<sup>1</sup>ANSES, Hygiene and Quality of Poultry and Pig Products Unit, BP53, site des Croix, 22440 Ploufragan, France

<sup>2</sup>ANSES, Mycoplasmaology – bacteriology unit, BP53, site des Croix, 22440 Ploufragan, France

<sup>3</sup>European University of Brittany, France

\*Corresponding author : [Annaelle.KEROUANTON@anses.fr](mailto:Annaelle.KEROUANTON@anses.fr)

## Introduction



Foods of animal origin, like pork meat (1), are one of the most important sources of *Campylobacter* human infections. *C. coli* is the predominant species in pigs (2). The routine use of antimicrobials in conventional production has been attributed to the emergence of antimicrobial-resistant bacterial pathogens (3).

The objectives of this study were to assess the occurrence of *Campylobacter* in organic and conventional pig productions, and to evaluate their antimicrobial resistance and genetic diversity in these two productions.



## Material and Methods

**Sampling:** in one slaughterhouse – On 31 organic pig herds and 31 conventional pig herds (two pigs per herd sampled).

**Detection of *Campylobacter*:** on colon contents for 56 and 58 organic and conventional pigs, respectively, and from swabs of 60 carcasses for each production.

**Minimal Inhibitory Concentration of antimicrobials (MIC):** using the broth dilution method according to Clinical and Laboratory Standards Institute (CLSI) document M31-A3 with Sensititre<sup>®</sup> plates (Biocentric, Bandol, France).

**Antimicrobials tested:** gentamicin (GEN), streptomycin (STR), ciprofloxacin (CIP), nalidixic acid (NAL), tetracycline (TET), erythromycin (ERY) and chloramphenicol (CHL).

**MIC interpretation:** according EUCAST recommendation ([www.eucast.org](http://www.eucast.org)).

**Genetic diversity:** by RFLP-PFGE, according Campynet protocol (4), using *KpnI* enzyme.

**Profile analysis:** using BioNumerics<sup>®</sup> (Applied Maths, Sint-Martens-Latem, Belgium). To assess the genetic diversity of the *Campylobacter* populations, the Simpson's index (D) was determined (5).

## Results

Occurrence in colon content was not significantly different between organic (76.8%) and conventional pigs (74.0%). Among the 120 carcasses, only one conventional carcass was contaminated by *Campylobacter*. All the *Campylobacter* isolates were *C. coli*.

266 *C. coli* isolates were characterized by CMI and PFGE: 138 and 124 from colon content of respectively organic and conventional pigs and 4 from carcass of conventional pigs.

Only 10 isolates were pansusceptible. No isolate was resistant to CHL and only one isolate from conventional pig was resistant to GEN.

The percentage of isolates resistant to STR was high and similar in both productions (Fig. 1). We observed a significant difference between the two productions for resistance to NAL and CIP ( $\chi^2$ ,  $p < 0.05$ ) and for ERY and TET ( $\chi^2$ ,  $p < 0.01$ ) (Fig. 1). For these four antibiotics, resistance was higher for *Campylobacter* isolated from conventional pigs.

The most frequent resistance profile was resistance to streptomycin with tetracycline (Fig. 2) (24.2% for conventional isolates and 33.3% for organic isolates). Isolates from conventional pigs were significantly more frequently resistant to tetracycline and erythromycin, often in association with other resistances: 53.1% of isolates from conventional pigs were resistant to 3 or more antibiotics families compared to 26.8% from organic pigs (Fig. 3).

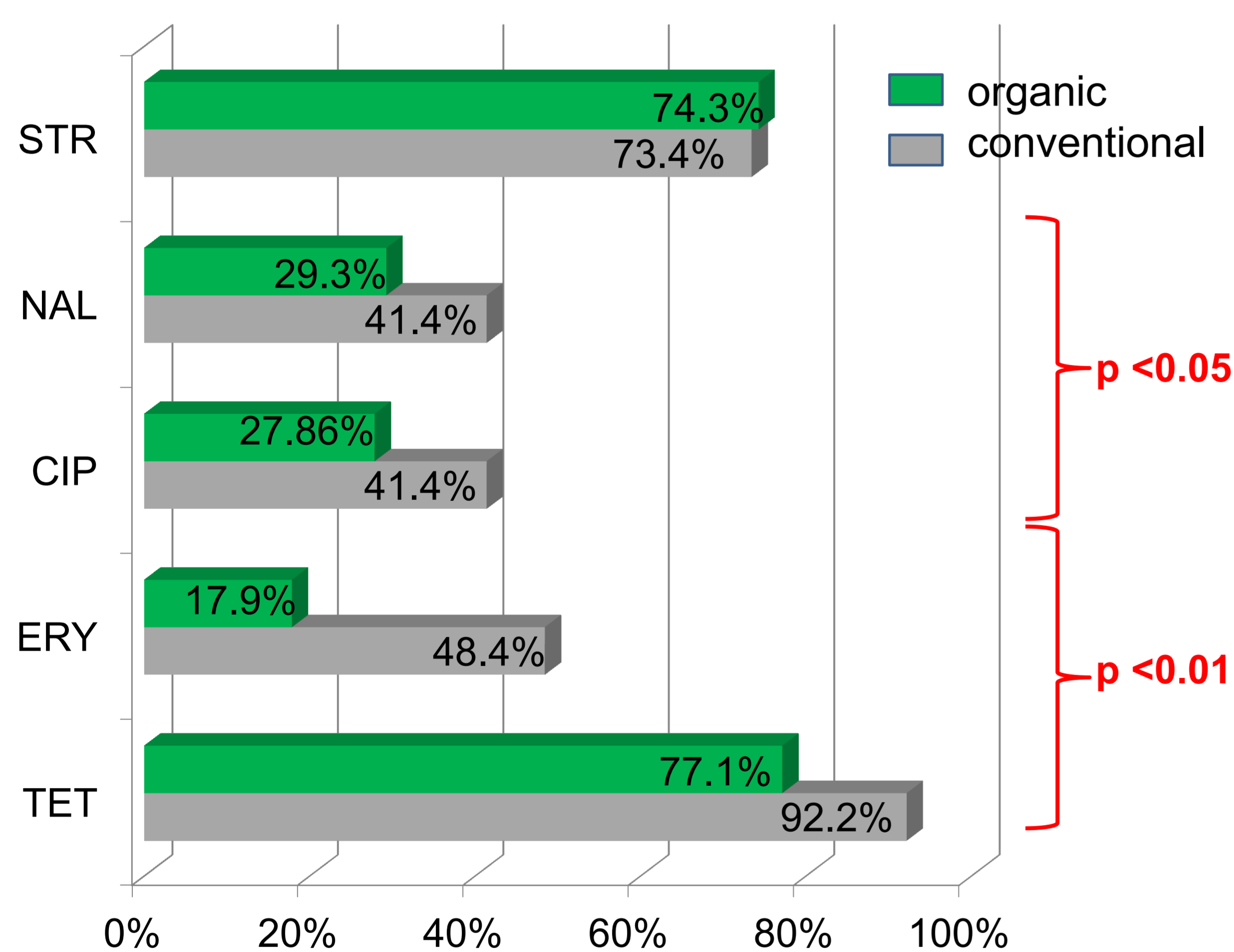


Figure 1 : percentage of isolates resistant to antimicrobials in each production

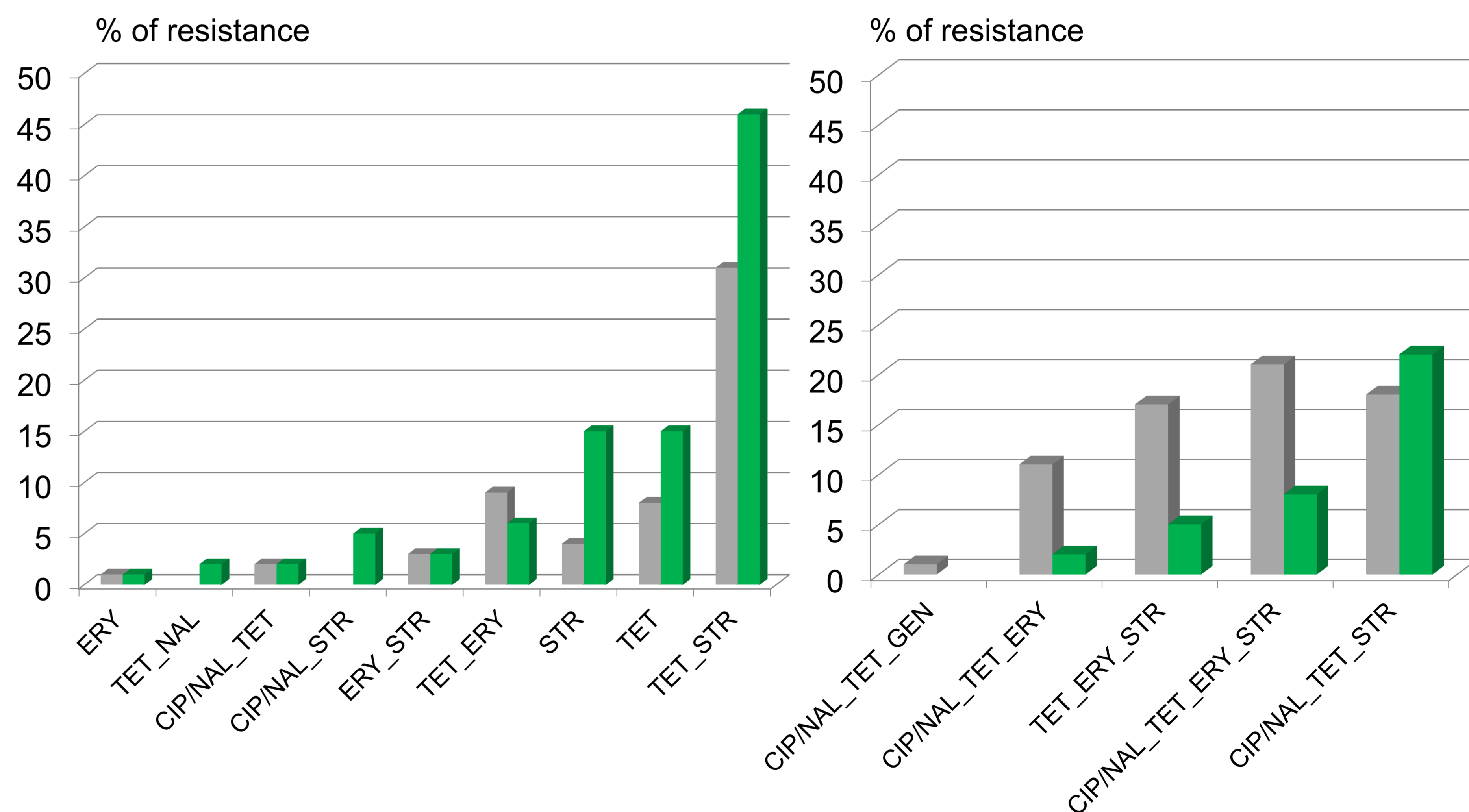


Figure 2 : percentage of isolates resistant to 1 or 2 antimicrobial family in each production

Figure 3 : percentage of isolates resistant to 3 antimicrobial families or more in each production

The 240 typable isolates were distributed in 122 *KpnI* profiles. No evidence of genetic clusters specific to a production was shown and only one *KpnI* profile was common between organic and conventional isolates, for one isolate in each production. Likewise, no link was observed between *KpnI* profiles and resistance profiles. Index of diversity was very high ( $D > 0.98$ ) in both productions.

## Discussion/Conclusion

This study showed that occurrence and diversity of *Campylobacter* in organic and conventional pigs was similar. High genetic diversity in *C. coli* in pigs was previously described (6).

Resistance and multi resistance observed for conventional pigs isolates are commonly identified (2,7). The lower level of antibiotic resistance for organic pigs have also been previously described (2) and may be related to the restricted use of antibiotics in this production and / or to the colonization of organic pigs with susceptible environmental strains.

## Acknowledgment

This study was conducted in the frame of ERA NET CORE organic II project "Safeorganic". The authors thank the persons in charge of the slaughterhouse and M. Even, E. Eveno and E. Boilletot from Anses for sampling help.

## References

- (1) Friedman *et al.* (2004) Clin Infect Dis 38 Suppl 3: S285-296
- (2) Thakur and Gebreyes (2005) J Clin Microbiol 2005;43:5705-14
- (3) Aarestrup *et al.* (2008) Anim. Health Res. Rev. 9 : 135-148
- (4) Rivoal *et al.* (2005) Appl Environ Microbiol 71:6216-27
- (5) Hunter and Gaston (1988) J Clin Microbiol 26, 2465-2466
- (6) Denis *et al.* (2011) Vet Microbiol 154: 163-170
- (7) Mattheus *et al.* (2012) Foodborne Pathog Dis 9(5): p. 465-72.