

Occurrence and genetic diversity of *Salmonella* in organic and conventional pig productions in France

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The objectives of this study were 1) to assess the occurrence of *Salmonella* in organic pig production, in comparison with conventional pig production, 2) to evaluate the genetic diversity of strains isolated from these two productions and 3) to estimate the cross-contamination on slaughter line between conventional pig and organic pig.

In one slaughterhouse, 26 organic herds and 31 conventional herds (2 pigs per herd) were sampled for *Salmonella* detection. Analyses were realized on colon content and swabs of carcass for each pig. Two isolates by positive samples were serotyped and typed by PFGE using *Xba*I enzyme. All *S. Typhimurium* and monophasic variant of serovar Typhimurium were subtyped by MLVA.

Prevalence of *Salmonella* in colon content was higher for organic pigs, 37.9% _{IC95} than for conventional pigs, 32.7% but difference was not significant ($p=0.563$). *Salmonella* prevalence was lowest on carcasses and very close between the two productions: 10.7% for organic and 10.3% for conventional.

The 104 isolates were distributed in 7 serovars: Derby (46 isolates), Brandenburg (18), Typhimurium (13), monophasic variant of Typhimurium 4,12:i:- (11) and 4,5,12:i:- (10), Infantis (2) and Mbandaka (2). Sixteen PFGE profiles were obtained: 1 per serovar for serovars Mbandaka, Infantis, and Brandenbrug, 3 for Derby, 4 for Typhimurium and 4 for monophasic variant 4,12:i:-.

Seven PFGE profiles, representing 84% of the isolates, were common between organic and conventional pigs. A major profile gathered 79% of the *S. Derby* strains. *S. Brandenburg* strains were also very clonal, all presented the same PFGE profiles whereas they came from 5 different herds. With 20 isolates from 12 carcasses, it has not been possible to show with certainty *Salmonella* cross-contamination between organic and conventional pigs during the process.

For *S. Typhimurium*, MLVA gave a better discrimination than PFGE, 8 patterns against 4; particularly for 6 isolates with the same PFGE pattern which was subdivided into 5 MLVA patterns. While on the 21 monophasic isolates, MLVA and PFGE gave similar discrimination (7 patterns with MLVA and 6 with PFGE).