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Ecology of Salmonella and antimicrobial resistance in a pig slaughterhouse

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Introduction

Salmonella is responsible for a large number of food associated infections. To guarantee food safety, a better understanding of *Salmonella* ecology and adaptation strategies on the food production chain constitutes a prerequisite. In a *One Health* perspective, data on *Salmonella* antibiotic resistance in food environments are also crucial to decipher transmission routes of resistant foodborne pathogens as well as resistance genetic determinants involved, and the role of process and selection pressures underwent in food industries (as cleaning and disinfection) in bacterial adaptation and antimicrobial resistance emergence.

Methods

Occurrence of *Salmonella* was investigated at six different areas along a pig slaughter chain and through 4 sampling campaigns, each time before and after cleaning and disinfection (C&D) procedures. A total of 48 surface samples were collected. *Salmonella* strains were characterized using serotyping and pulsotyping to trace persistent strains in the slaughterhouse. Minimal inhibiting concentrations (MIC) were also determined for various relevant antibiotics and for biocides used in the slaughterhouse. In addition, associated indigenous bacterial communities were characterized using 16S rRNA amplicon sequencing.

Results

Salmonella was present at nearly all sampling areas but was not isolated from the neck clipper. Thirty eight strains were isolated and five serotypes were identified: S.4,5,12:i:- (50%), Rissen (16%), Typhimurium (16%), Infantis (10%) and Derby (8%). We observed a high prevalence of the monophasic variant of the serotype Typhimurium in the slaughterhouse. Sixteen PFGE types were identified among the 38 strains (Table 1). Some strains were found at different dates and potentially at the same sampling area suggesting that they persisted in the slaughterhouse despite of C&D procédures (data not shown).

Approximately 70% of isolated *Salmonella* strains exhibited resistance to ampicillin and sulfamethoxazole, 80% to tetracycline and 10% to chloramphenicol. There was statistically no significant evolution of CMI comparing strains before and after C&D procedures concerning both biocides and antibiotics (Figure 1).

Bacterial diversity analyses showed that populations in the slaughterhouse were highly dominated by γ-proteobacteria and especially by the Moraxellaceae family (genus *Psychrobacter*, *Moraxella*, *Enhydrobacter* and *Acinetobacter*) at the different sampling areas (data not shown).

Population compositions were overall stable in time at a given sampling area suggesting that the surface populations were resident populations within the slaughterhouse, rather than populations introduced each week by the new swine bands. C&D procedures tended to reduce bacterial diversity by eliminating the minority species but did not greatly impact the composition of dominant species.

Conclusions

Cleaning and disinfection procedures applied in this slaughterhouse did not appear to affect the biocides and antibiotics resistance of isolated *Salmonella* strains. Microbial flora diversity analyses showed that populations were resident with persistent *Salmonella* strains isolated at the same sites over time.

Together, such data participate to the construction of a comprehensive view of *Salmonella* ecology in food environments integrating associated resident microbial flora and the distribution of antimicrobial resistance in relation to processing conditions.

Table 1: Serotype and PFGE-types diversity among the 38 isolated Salmonella strains

Serotype (%)	4,5,12:i:- (58%)	Typhimurium (13%)	Rissen (10,5%)	Infantis (10,5%)	Derby (8%)
PFGE-type	B01, B02, B03, B04, B05, B06, B09, B15, B16	B09	B10, B11	B12	B08, B13, B14

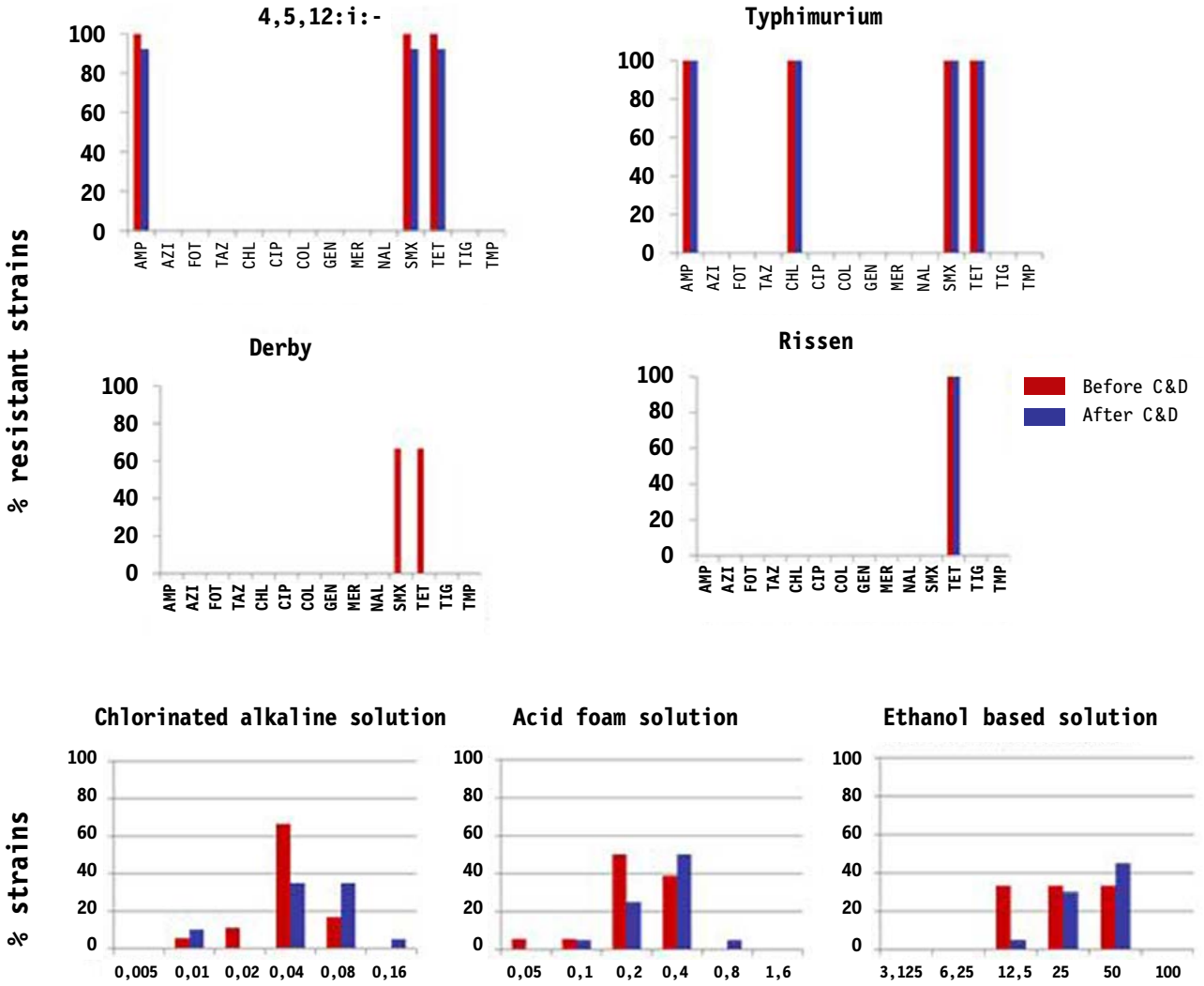

Figure 1: Salmonella resistance to biocides and antibiotics before and after C&D