

PREVALENCE OF MULTIDRUG-RESISTANT (MDR) SALMONELLA ON BOVINE DAIRY HERDS IN FRANCE

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Introduction

Multidrug resistant (MDR) salmonellae have been isolated from bovine herds since the 80's, then from other species, and finally have been found to cause human food-borne disease in numerous developed countries. Among MDR salmonellae, one particular serotype -namely *Salmonella* Typhimurium (STm) DT (definitive type) 104- was the most prevalent (1,2). The chromosomal structure responsible for the resistance to at least five antibiotics simultaneously has been found in strains belonging to other serotypes (3). Therefore, the study of MDR salmonellae can not be focused on STm DT104 only. Moreover, no precise epidemiological study has been realised in France in order to appreciate the prevalence of such strains in bovine dairy herds. In the global frame of Quantitative Risk Analysis (QRA) on food-borne diseases due to MDR *Salmonella*, a 2 year-study was conducted in order to appreciate, in first intention, the prevalence of these bacteria on bovine dairy herds located in Western France. These data are essential for risk assessment of human infection by MDR *Salmonella* of bovine origin.

Material and Methods

Hypothesis :

- prevalence of contaminated herds = 10%
- overall precision expected = 3% Dairy herds
- 489 bovine dairy herds (>20 cattle).
- from 3 "départements" in Western France.
- simple random sampling (5%) from exhaustive database.
- all producers were voluntary.
- 2 sampling periods in 2001-2003. (November to April)

Sample collection

- first visit (V1) : manure or dung sample (60 ml).
- second visit (V2) for V1 positive herds : bulk milk, water and environmental swabs sampling.
- pools of individual fecal sampling (1-6/pool) according to calving status and birth date. Sample testing
- Rappaport-Vassiliadis culture following enrichment in EPT (dilution 1/5).
- XLT4 agar isolation plates, biochemical confirmation.
- serotyping and antimicrobial susceptibility testing.

MDR = resistant or intermediate to, at least, two antimicrobials belonging to different families, according to the CASFM recommendations. Epidemiological data

- herd structure and animal husbandry questionnaire at V1 (herd level exposure).
- animal level prevalence estimated by Bayesian approach (WinBUGS).

Results

Sample description

- Herd sampling representative of the dairy herds density.
- Predominant breed : Prim'Hostein (60,5%), Normande (32,2%).
- median annual milk production / cow = 6991 litres (range : 2100 – 10300).

- Average number of dairy cows sampled / herd : 42 (CI95% : 29-56, range : 21-87).

Herd prevalence - 35/489 bovine dairy herds contaminated by *Salmonella* in manure or dung, - 9 contaminated herds showed MDR strains.

- weighted prevalence for the 3 "départements": p*Salmonella*=8.1% and pMDR=1.9%.

- 11 *Salmonella* serotypes identified : *S. Montevideo* (26%), *S. Typhimurium* (14%)....

- *Salmonella* have been isolated in V2 sampling in 14/35 herds contaminated at V1. Strains isolated at V2 belonged to the serotype initially recovered in the herd, and exhibited the same antibiotic resistance phenotype. - Data analysis stratified by month of sampling date and "département" revealed more MDR strains isolation at the end of winter (*Fisher test*, $p=0.04$).

salmonellosis history was a predictive risk factor for detection of MDR *Salmonella* contamination in manure or dung

Discussion

These results are in agreement with the initial hypothesis. Prevalences are probably underestimated because there were probable false negatives for manure or dung contamination (sensitivity not 100%) and shedding without faecal excretion of *Salmonella* is possible. The end of winter is a risky period for herd contamination by MDR *Salmonella*. This observation suggested that a selection pressure linked to antimicrobial use during winter could lead to MDR strains emergence. Further works are needed to confirm the impact of antimicrobial use on MDR *Salmonella* herd contamination.

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