

Prevalence of multidrug resistant (MDR) *Salmonella* in bovine dairy herds in western France

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Abstract

As a part of our effort in quantitative risk analysis of food-borne diseases, we carried out an epidemiologic study to estimate the prevalence of multidrug resistant (MDR) *Salmonella* in dairy herds situated in western France. The study population consisted of 489 farms in the region and manure or slurry was sampled from these operations and tested for the *Salmonella* spp. All strains isolated during the study were serotyped and tested for their antimicrobial susceptibility. *Salmonella* spp. was isolated from 8.1% (95% confidence interval (CI 95%): 4.5–13.3%) of the sampled herds. The herd prevalence of MDR *Salmonella* among the sampled herds was 1.9% (CI 95%: 0.5–5.4%). Spatial statistics were used to check for sampling representativeness and to determine if infected herds were clustered spatially.

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1. Introduction

During the last decades, *Salmonella* has been the principle cause of outbreaks of food-borne disease in France and in many countries (Haeghebaert et al., 2002; Herikstad et al., 2002). The transmission of these bacteria from foods of animal origin to humans has been largely demonstrated (Swartz, 2002; Haeghebaert et al., 2003; O'Brien and De Valk, 2003). Non-typhoidal *Salmonella enterica* strains with multidrug resistance (MDR) have been encountered widely in many European countries, with a variety of food products being implicated in their spread (Threlfall et al., 2000, 2003; Alban et al., 2002). In the 1990's, the high incidence of MDR strains in Europe was due to a clonal and international spread of *Salmonella enterica* subsp. *enterica* serovar Typhimurium phage type DT104, initially linked to bovine farms (Akkina et al., 1999; Chaslus-Dancla et al., 2000; Threlfall et al., 2000; Cloeckeaert and Schwarz, 2001). Other MDR *Salmonella* was isolated from bovine products that did not belong to DT104 phage type (Gupta et al., 2003; Threlfall et al., 2003).

The few epidemiological studies conducted in Europe focused on clinical cases (Martel et al., 1996). However, it is difficult to predict a herd's *Salmonella* shedding status when using only clinical data (Giles et al., 1989; Huston et al., 2002). A case/control study was conducted in France to determine risk factors associated with contamination of milk with *Salmonella* (Heuchel et al., 2000) and incriminated manure or slurry in the process. *Salmonella* spp. has been reported in convenience samples of manure or slurry from dairy herds in France and other places around the world (Heuchel et al., 2000; Warnick et al., 2001, 2003a).

To shed light on the potential risk of the spread of multidrug resistant *Salmonella* from animals to humans, we conducted an epidemiological study to assess the prevalence of resistant pathogen shedding in dairy farms and to determine if infected herds with *Salmonella* are associated spatially.

2. Materials and methods

2.1. Study population

With the help of an extended partnership, 489 dairy herds were included in this study over two sampling periods: November 2001–April 2002 and November 2002–April 2003. Three geographic administrative areas (“départements”) in western France (Mayenne, Orne and Sarthe) were targeted in this study. The minimum number of dairy cows per herd was 20. We assumed that approximately 10% of dairy herds were contaminated by *Salmonella* and we expected an allowable error of 3%. Then the required sample size was 385 herds.

For logistical reasons, an equal number from approximately 80 dairy herds was investigated per year and per “département”. Herds were randomly selected from a sampling frame managed by each “local animal health organism” (GDS). In the areas studies, more than 95% of all the dairy herds are listed in the GDS database.

2.2. Sample and data collection

A single sample of manure or slurry was taken from the principal storage area of each farm. The sample of 60 mL was taken by the GDS technician, under the dried surface of the

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