

# *Salmonella and Other Enterobacteriaceae in Dairy Cow Feed Ingredients and Their Antimicrobial Resistance*

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## **Introduction:**

Antimicrobial resistant Enterobacteriaceae might be introduced into dairy cows through the consumption of feeds, and the microbes may eventually enter the human food supply.

Members of the Enterobacteriaceae family are becoming more important in food safety and medicine. Estimates of medical and lost productivity costs associated with *Salmonella* species and *Escherichia coli* O157 ranged from \$0.2 to 3.5 billion in 1996. Additionally, *Escherichia*, *Klebsiella*, *Enterobacter*, *Serratia*, and *Citrobacter* are responsible for almost one-third of nosocomial infections in the United States (1990-92 data).

Several studies have suggested an association between antimicrobial use in animal feeds and the possible risk of humans contracting resistant bacterial strains such as *Salmonella* spp., *E. coli*, and other enteric infections from food-producing animals. Other studies have isolated different types of *Salmonella* spp. from animal feeds and other feed products. Veldman and others, for example, tested poultry feeds and feed components (fish meal, meat/bone meal, tapioca, maize grits) from 57 feed mills. Among the isolated bacteria, the most frequent serotype was *Salmonella hadar*. Harris and others tested swine feed and feed ingredients (grain, soybean meal, milk/whey, fats/oils, and protein products). The most frequent serotype isolated was *Salmonella worthington*.

Because of sparse data on antimicrobial resistant *Salmonella* spp. and other enteric bacteria in animal feeds and from dairy farms, the objectives of this study include the following:

1. Identify *Salmonella* spp. and other Enterobacteriaceae in dairy cow-feed-ingredient piles on the farms and their antimicrobial-resistance patterns.
2. Determine the prevalence of *Salmonella* spp. in the piles.
3. Determine whether the prevalence of *Salmonella* increases in individual piles over time.

## **Methods and Materials:**

Thirty-two farms were selected at random from 43 commodity dairy feeding farms. Of the 32 farms selected, 12 farms agreed to participate in the study. In the prevalence survey, 50 feed-ingredient piles were sampled for the presence of bacteria. In the repeated samples survey, 10 of the original 50 piles were sampled over time. Presumptive *Salmonella* positives (Assurance EIA *Salmonella* kit) were evaluated further using cultural methods and the Enterobacteriaceae Micro-ID system. A disk-diffusion method was used to identify ampicillin, chloramphenicol, ciprofloxacin, streptomycin, and tetracycline resistance.

## **Results:**

In the prevalence study, 42.0 % (21/50) of the 50 feed-ingredient piles were presumptive positive for *Salmonella*. By the culture method and Enterobacteriaceae Micro-ID system, 2.0 % (1/50) was confirmed as *Salmonella enteritidis* and serogrouped as poly Group B, Group C<sub>1</sub>. In the repeated samples study, 60.0 % (6/10) of the piles were presumptive positive for *Salmonella*. By the culture method and the Enterobacteriaceae Micro-ID system, 20.0 % (2/10) were confirmed as *Salmonella enteritidis* and serogrouped as poly Group B, Group C<sub>1</sub>. Fifty bacterial isolates were tested for antimicrobial resistance. Sixty-two percent (31/50) of the isolates demonstrated ampicillin resistance while 10.0 % (5/50) displayed tetracycline resistance.

## **Conclusions:**

The presence of antimicrobial resistant Enterobacteriaceae in feed ingredients raises concerns about health risks to food-producing animals such as dairy cows and subsequently to the consumer.

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