Diffusion of antimicrobial resistance across management niches on dairy farms

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INTRODUCTION

A major challenge to develop strategies that mitigate the global impact of farm origin antibiotic resistance is a failure to describe dissemination patterns of resistance within the farm via animals or environmental flow. This study focuses on the presence and diversity of phenotypic antibiotic resistance within niches on the whole dairy enterprise. The goals are:

- Identify niches where diversity is generated and maintained
- Identify niches connected by phenotype similarity suggesting dissemination, and
- Identify niches that narrow diversity.

The premise is: diversity is generated in niches with high antibiotic use and disseminate through the dairy system with animal movement or environmental flow.

METHODS

- We sampled from commercial dairy herds that maintain a milking herd and rear replacement animals.
- Farm niches were defined by housing and function. Housing niches are areas with pre-weaned heifers, weaned and bred heifers, early lactation cows, lactating cows, pregnant non-lactating cows, antibiotic treated cows, and cows leaving the herd. Function niches include milk, waste, water, and feeds.
- For each sampling, 72 animal fecal samples, 8 water, 8 feed samples, 1 milk filter, samples from the waste stream, and soil samples are collected.
- We used Escherichia coli (EC) as our model bacterium and antimicrobial susceptibility tested 4 isolates from each sample against 13 antimicrobials.
- Latent class analysis (LCA) was used to organize isolate-based resistance patterns.

RESULTS

Twelve farms were enrolled and each visited 3 times. More than 14,000 EC isolates were tested for antimicrobial susceptibility patterns. Based on LCA, 26 different susceptible patterns were observed. The most common pattern was pan-susceptible (68%) followed by a pattern with tetracycline resistance only (7%). The greatest resistance diversity was observed in pre-weaned and weaned calves followed by treated animals. EC from adult cows were pan-susceptible (approaching 90% of isolates). EC from soil samples were pan-susceptible except for samples in pre-weaned housing areas. There were farm-specific patterns and between farm differences in diversity.

Figures:
26 Resistant Classes by tested antibiotic
Distribution of classes by production animal niche
Distribution of classes by sampled farm

CONCLUSIONS

There are niche specific patterns of resistance that suggest there is little to no dissemination across niches. Diversity is generated in areas where antibiotic use is greatest, hospital pens and pre-weaned calf areas. Weaned calves also have a high level of diversity which may be a result of transitioning across age groups. The between-farm patterns also suggest that resistance traits are farm-specific and driven more by local features rather than shared across spatially distinct farms.