Use of a data-driven algorithm to guide selective dry-cow therapy

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Introduction

Nationally in 2014, 80.3% of dairies applied blanket dry-cow therapy (BDCT) and 93% of cows were treated with dry-cow intramammary (IMM) antimicrobials (NAHMS, 2016). However, surveys indicate that >80% of dry quarters yield negative culture results. Selective dry-cow therapy (SDCT) describes the identification and treatment of only cows/quarters infected or at high risk for infection. The purpose of this study was to determine if a data-driven algorithm, without the use of culture, could identify and selectively treat only "high risk" cows (those likely benefitting from DCT) without adverse effects on animal health and production outcomes.

Materials and Methods

Cows eligible for dry off from Jun 2016 to Jan 2017 at a NY dairy (2000 milking cows; bulk tank SCC 166k cells/mL) were considered for enrollment. A cow was identified as low risk if it met the following criteria outlined by the algorithm: <200k SCC at last test, an average SCC<200k on the last 3 tests, no signs of mastitis at dry-off, and ≤1 clinical mastitis event in the current lactation. Low risk cows were randomly assigned to receive IMM Tomorrow® and external teat sealant (ABXTS) or external teat sealant only (TS). All high risk cows received antibiotics and teat sealant. Samples were collected aseptically from individual quarters at dry off and at 1-7 DIM. Samples were retrieved from a smaller number of high risk cows at the described time points to calculate positive and negative predictive values (PPV, NPV) of the algorithm. Culture was performed according to NMC guidelines. Quarter-level outcomes were bacteriological cure risk and new infection risk. A quarter was defined as a bacteriological cure when an initial pathogen in the dry-quarter sample was absent from the fresh-quarter sample. A new infection was identified as the presence of a different pathogen/result in the fresh-quarter sample from the dry-quarter sample. Only pure or negative cultures were considered for analysis. Cowlevel outcomes included longitudinal milk production over the first 30 DIM, milk production at first test, survival to 30

DIM, and occurrence of clinical mastitis in the first 30 DIM. Analysis of outcomes was completed using PROC MIXED, PROC FREQ (Fisher's exact tests) and PROC TTEST in SAS® 9.4. Results present means and risk ratios (RR) of ABXTS:TS.

Results

Three hundred cows representing 1204 quarters were enrolled in the ABXTS group and 307 cows representing 1183 quarters were enrolled in TS group. Overall, 64% of cows eligible for dry off were allocated to the "low risk" group. Calculated PPV and NPV of the algorithm were 71% and 70%, respectively. Milk production (23.6kg, 23.5kg), DCC (224d, 224d), and DIM (338d, 343d) were similar between TS and ABXTS on dry day. Dry-off cultures returned "negative" results for 90% of quarters and 5.6% of quarters were positive for CNS. Of the positive cultures, 88% of quarters experienced bacteriological cure. This was similar between groups (ABXTS=93%, TS=84%; RR=2.3, 95% CI: 0.9-5.7). Ninety-five percent of the non-cure quarters were contributed by CNS (ABXTS n=6, TS n=13). According to fresh-cow cultures, 6% of quarters experienced a new infection, with groups being similar (ABXTS=5.5%, TS=7.3%; RR=1.3 95%, 95% CI:0.95-1.9). Again, the majority of new infections were described as CNS (57%, 77 quarters). Longitudinal milk production, milk production at first test (kg)(ABXTS=23.6, TS=23.5), culling prior to 30 DIM (n=33; RR=0.8, 95% CI:0.4-1.6), and clinical mastitis events in the first 30 DIM (n=14; RR=0.6, 95% CI:0.2-1.6) were not significantly different between groups.

Significance

Selective antimicrobial use at dry off creates an opportunity to practice good drug stewardship and promote responsible behaviors, protecting animal and human health by reduction of potential drug residues and resistance. Results suggest that on a well-managed dairy farm, IMM use of dry-cow products can be reduced by >60% without unfavorable effects on production or microbiological outcomes.