

cases were distributed as gram-negative (60%), no bacterial growth (19%), and gram-positive (21%). Many gram-negative cases suggest that few cases would benefit from antimicrobial therapy. Overall, 60% of cows were culled (Table 1), but farm 1 was 12 times more likely to cull cases compared with other farms ($P < 0.001$). Monthly price of cull cows (\$4.13/kg \pm 0.04) was associated with monthly culling rate ($R^2 = 0.31$; $P = 0.07$). After CM, the M305 was reduced by 547 kg ($P = 0.04$), resulting in a loss of about \$270 of milk income/cow per lactation. High beef prices have been shown to drive culling decisions, and based on etiology, few cases would benefit from antibiotic treatment. Future studies will compare the economic impact of this approach with that of treated cows.

Key Words: culling, mastitis, milk yield

1350 Associations between mastitis incidence and risk factors in US organic-certified dairy farms. C. Nino De Guzman¹, L. Prada², S. Bellinconi², P. Muñoz³, C. Hernandez³, C. Ibarguren³, R. Weng³, Q. Kolar⁴, V. E. Cabrera⁵, B. J. Heins⁶, R. Lynch⁴, E. K. Miller-Cushon¹, G. M. Schuenemann², P. Pinedo³, and A. De Vries¹, ¹University of Florida, Gainesville, FL, ²The Ohio State University, Columbus, OH, ³Colorado State University, Fort Collins, CO, ⁴Cornell University, Ithaca, NY, ⁵University of Wisconsin, Madison, WI, ⁶University of Minnesota, Morris, MN.

The objective of this study was to assess the association between mastitis incidence and self-reported risk factors in organic dairy farms in the United States. Through farm visits and questionnaires, we surveyed 48 organic farms: 25 in Ohio, 10 in New York, 5 in California, 4 in Colorado, 3 in Texas, and 1 in Georgia. The average reported annual mastitis incidence was $13\% \pm 9$. The median milking herd size was 74 cows (range: 22–4081). The average daily milk yield was 22 ± 6 kg/cow. Farms were categorized by region as West (19%), Central (6%), and East (75%). The proportions of cows by region relative to the number of cows in total were 56% for the West, 31% for the Central, and 13% for the East. Farms were categorized as small (<100 cows, 62%), medium (100–1,000 cows, 21%), and large (>1,000 cows, 17%). Explanatory variables were analyzed using the “lm” function of R Studio. Region and farm size were included in all statistical models as control variables. Tested individually, variables with a $P \leq 0.20$ were added to the final model. The final model included the variables milk yield, the importance of vaccines to control mastitis, the concern threshold for bulk tank SCC, the concern threshold for mastitis cases in a single day, the number of towels used to clean udder before attachment, cluster removal method, and use of vaccines. An increase in annual mastitis incidence was associated with milk yield ($+0.5\% \pm 0.2$ /kg) and perception of the importance of vaccination (very important: $+18\% \pm 9$), possibly due to a greater use of vaccines in farms where mastitis is a problem. A decrease in annual mastitis incidence was associated with the concern threshold for bulk tank SCC ($-5\% \pm 2$ /100,000 cells/mL). In conclusion, only 3 explanatory variables were associated with annual mastitis incidence. Further research will include associations of mastitis with milking procedures, cow hygiene, management, and facilities.

Key Words: mastitis, milk quality, organic

1351 Microbiome dynamics associated with mastitis-causing bacteria in different hotspots within organic and conventional dairy farms. B. Shrestha*, R. Neupane, S. Chitlapilly Dass, K. Mani, V. Palanisamy, Z. Vice, and S. Paudyal, Texas A&M University, Department of Animal Science, College Station, TX.

The objective was to characterize diversity and relative abundance (RA) of microbiomes associated with mastitis-causing bacteria in different pathogen hotspots within organic (ORG) and conventional dairy farms (CON). Representative CON and ORG dairy farms in Texas were selected and cross-sectional samples from bedding (SAN, n = 24), water (WAT, 26), feed area (FED, 18), milking parlor floor (MAT, 12), teats before predip (TBP, 22), teats after predip (TAP, 22), milking unit before milking (BML, 4) and after milking (AML, 22), cow milk samples (MLK, 22), and bulk milk tank (BMT, 4) were collected. The genomic DNA extraction for all swab samples were performed using DNeasy PowerSoil Pro Kit and milk samples were performed using DNeasy Blood & Tissue Kit (Qiagen, Germany). The extracted DNA was quantified, followed by library preparation and sequencing on the DNBSEQ platform. The obtained raw shotgun metagenomic sequences were quality-filtered and taxonomically annotated for mastitis-causing bacteria using the Kraken2v2.1.2 tool. Nonparametric ANOVA in SAS 9.4 was used for statistical analysis of bacterial abundance. The phyla *Proteobacteria*, *Firmicutes*, *Actinobacteria*, and *Tenericutes* were observed with RA of 61%, 34%, 4%, and 0.02% in ORG compared with 88%, 5.8%, 6%, and 0.03%, respectively, in CON. Overall, RA of *Staphylococcus aureus*, *Streptococcus agalactiae*, and *Streptococcus uberis* were not statistically different ($P > 0.05$) between farms, indicating minimal variation in the major contagious mastitis pathogens. However, RA for *Streptococcus dysgalactiae* ($0.015\% \pm 0.002\%$ vs. $0.012\% \pm 0.004\%$, $P < 0.05$), *Corynebacterium sp* ($14.8\% \pm 2.18\%$ vs. $10.8\% \pm 2.03\%$, $P < 0.05$), *Staphylococcus chromogenes* ($0.13\% \pm 0.03\%$ vs. $0.05\% \pm 0.02\%$, $P < 0.0001$), and *Escherichia coli* ($1.1\% \pm 0.41\%$ vs. $0.45\% \pm 0.18\%$, $P < 0.0001$) were higher in CON compared with ORG. The RA of *Proteobacteria* in ORG was highest in WAT ($97.3\% \pm 0.51\%$) than FED ($72.7\% \pm 7.74\%$, $P < 0.01$), MAT ($75.4\% \pm 10.77\%$, $P < 0.05$), BML ($67.9\% \pm 8.46\%$, $P < 0.05$), SAN ($29.4\% \pm 3.46\%$, $P < 0.001$), TBP ($33.8\% \pm 7.70\%$, $P < 0.001$), and MLK ($4.9\% \pm 0.55\%$, $P < 0.001$). In CON, the RA of *Proteobacteria* was higher in LIN ($98.4\% \pm 0.67\%$) than SAN ($75.1\% \pm 2.32\%$, $P < 0.05$), TAP ($73.9\% \pm 5.53\%$, $P < 0.05$), WAT ($65.7\% \pm 2.48\%$, $P < 0.05$), MAT ($32.7\% \pm 4.7\%$, $P < 0.05$), FED ($10.9\% \pm 1.99\%$, $P < 0.05$), and MLK ($6.02\% \pm 0.96\%$, $P < 0.05$). These results suggest a difference in mastitis-causing pathogens microbiome in different hotspots in the organic and conventional dairy farming systems with opportunities for targeted intervention.

Key Words: microbiome, mastitis, dairy farm

1352 Dynamics of culling risk in organic dairy herds in the United States. B. Shrestha¹, R. Neupane¹, P. Pinedo², J. Piñeiro¹, and S. Paudyal¹, ¹Department of Animal Science, Texas A&M University, College Station, TX, ²Department of Animal Sciences, Colorado State University, Fort Collins, CO.

The objective was to understand the culling dynamics with reported disposal reason for the cows in organic dairy herds. A total of 160,667 lactation records were obtained from DHIA records for cows calving between 2018 and 2022 in 483 certified organic dairy herds from 38 states in the United States. Nine disposal codes including feet and legs, low production, injury or other, mastitis, disease, udder problems, died, and reason not reported were considered as codes of interest. The distribution of culled cows by disposal code was estimated by parity (1, 2, 3, and ≥ 4), cow-relative 305-d mature equivalent milk yield (low, intermediate, and high), herd-relative 305-d mature equivalent milk yield (low: $<$ mean $- SD$; medium: mean $- SD$ to mean $+ SD$; high: $>$ mean $+ SD$), herd size (small: 0–99, medium: 100–999, and large: >999). Annualized live culling rate and death rate were 25% and 4.7%, respectively. The primary disposal codes were reproduction problem