***Abstract***

In May 2024, the US sold over 63 million kg of organic whole milk, a 20.2% increase from 2023 (USDA-AMS, 2024). Although ranked 19th in overall milk production, dairy farming is an incredibly important part of Vermont’s agricultural sector; dairy comprised 65% of the state’s total farm sales, the highest in the US for 2023 (Progressive Dairy, 2024). In 2021 (the last USDA Certified Organic Survey), Vermont had 147 organic dairy farms, which made over 85 million kg of fluid milk, worth over $59 million (USDA, 2022). In May 2024, the US sold over 63 million kg of organic whole milk.

***Keywords:*** Mastitis, organic dairy cattle, intramammary infection, bedded pack, tiestall

***Introduction, Methods, and Results***

In May 2024, the US sold over 63 million kg of organic whole milk, a 20.2% increase from 2023 (USDA-AMS, 2024). Although ranked 19th in overall milk production, dairy farming is an incredibly important part of Vermont’s agricultural sector; dairy comprised 65% of the state’s total farm sales, the highest in the US for 2023 (Progressive Dairy, 2024). In 2021 (the last USDA Certified Organic Survey), Vermont had 147 organic dairy farms, which made over 85 million kg of fluid milk, worth over $59 million (USDA, 2022).

Differences in both management practices and herd characteristics exist between organic and conventional dairies. Organic farms were found to be smaller, produce less milk, more likely to house cows in tiestalls (TS; vs. freestalls, FS), and exhibited differences in how cows were fed and watered (Zwald et al., 2004). When farms were matched for size, cows on organic farms were older, fed less grain, and produced less milk (Stiglbauer et al., 2013). Perhaps the most significant difference between conventional and organic dairies in the US is that antibiotics are not allowed for use on organic farms (USDA, 2024). Antibiotics are a significant component of mastitis control and treatment on conventional farms, leaving limited available options for organic dairy producers to effectively control mastitis (Ruegg, 2009; NMC, 2019). Although this could potentially result in worse overall udder health on organic farms vs. conventional farms, the differences between the two systems are not clear-cut. At the bulk tank level, organic farms were more likely to be positive for *Staphylococcus aureus,* but less likely to have an increased colony count (Stiglbauer et al., 2013), whereas conflicting findings have been reported for SCC (Cicconi-Hogan et al., 2014; Levison et al., 2016). At the cow level, some work found SCC was higher on organic farms (Zwald et al., 2004), while others found no difference (Hardeng and Edge, 2001; Mullen et al., 2013). A lower level of clinical mastitis has been reported for organic dairies (Hamilton et al., 2006; Richert et al., 2013; Levison et al., 2016), although this difference disappeared in Valle et al. (2007) when controlling for lower milk yield in organic cows. While some research found no difference (Mullen et al., 2013), a large US study by Pol and Ruegg (2007) found that the prevalence of most mastitis pathogens (except *Staph. aureus*) differed between organic and conventional farms. Overall, research suggests that differences in mastitis epidemiology may exist between conventional and organic dairy farms.

Organic dairy producers with small-midsize farms in the Northeastern US have expressed interest in bedded pack systems (BP) as an option to house cows during the non-grazing season, as these facilities integrate well with pasture-based farm systems (Thurgood, 2009; Andrews et al., 2021). Additionally, state and federal agencies in the U.S. are providing financial incentives to build these structures as part of manure management practices which improve water quality and contribute to soil conservation (USDA-NRCS). Currently, most organic dairies in Vermont use a TS to house their animals while not on pasture (Andrews et al., 2021). As interest in BP grow among organic farmers, it is important to understand udder health for farms using this facility type. Given the importance of organic dairies to Vermont and the continued increase in demand for organic dairy products, a longitudinal study was undertaken to describe the diversity of species causing IMI on organic dairy farms in the state. The specific objectives of the project were to characterize the prevalence of IMI caused by different microorganisms in lactating dairy cattle on 10 small-midsize organic farms in Vermont, both for farms using TS (the most common type of housing for organic dairies in the state) and farms using BP.

Enrolled farms were a non-probability subsample of certified organic dairies which had participated in previous studies and milked 35-120 cows. The study was carried out Winter 2019-2020, with 5 herds enrolled using a TS bedded with shavings/sawdust to house lactating dairy cows, and 5 herds using a BP. The inclusive term “bedded pack” encompasses both aerobically composting bedded packs and deep bedded packs, and was defined as an enclosed loose housing facility deeply bedded with organic material (Jeffrey et al., 2024). Approximately 35 cows in early- to mid-lactation were enrolled from each herd. For 8 herds with DHIA data, cows were stratified by SCC, parity, and DIM, then randomly selected across these variables. All cows were sampled in 1 herd with ~35 lactating cows, and for the remaining herd the producer generated a list of 35 cows in early lactation. Cows unable to be sampled at a follow-up visit were replaced with another lactating cow dictated by convenience. At each farm visit, duplicate quarter-milk samples were aseptically collected from each lactating quarter immediately before milking for all enrolled cows according to NMC guidelines (NMC, 2017).

Standard aerobic bacteriological culture of quarter-milk was performed in duplicate to identify bacterial species present in the sample according to NMC guidelines (NMC, 2017). Aerobic culture results of both samples were then used together to determine the overall bacteriological status of each quarter-milk sample into the following categories: 1) “no significant growth,” when there was no growth on both plates, or ≤ 200 CFU/mL on one plate and no growth on the other plate, or ≤ 200 CFU/mL on both plates and morphology of isolates on each plate was different; 2) “pure culture,” when there was ≥ 100 CFU/mL of a particular isolate identified with the same morphology on both plates; 3) “mixed culture,” when there was ≥ 100 CFU/mL of two phenotypically-distinct isolates identified, each growing on both plates; 4) “contaminated,” when ≥ 1 of the 2 samples had more than 2 morphologically distinct isolates growing on a plate; 5) and “indeterminate,” when the set of quarter-milk samples did not meet the criteria for any of the previous categories (e.g., missing duplicate). Quarter-day observations were included in this study when the bacteriological status of a quarter on a given day could be determined.

Isolates from both pure and mixed culture quarter-milk samples were then identified to species or genus using MALDI-TOF mass spectrometry (Microflex, Bruker Daltonics). The protocol for identifying bacterial isolates with MALDI-TOF mass spectrometry has been described previously in Haw et al. (2024). For isolates unable to be identified with MALDI-TOF, other identification methods were used [colony morphology, catalase reaction, Gram stain, PCR-based amplicon sequencing for16S rRNA gene (Weisburg et al., 1991) or *rpob* gene (Drancourt et al., 2004)]. Using the bacteriological status and speciation information, a quarter-day IMI status was assigned to each quarter observation: 1) “healthy,” when there was no significant growth; 2) “single pathogen infection,” when ≥ 100 CFU/mL of a particular pathogen was identified in pure culture on both plates (interpretation in series; Dohoo et al., 2011); 3) “mixed infection,” when ≥ 100 CFU/mL of 2 different pathogens were identified in mixed culture on both plates; and 4) “unknown” if the sample status had been identified as contaminated or indeterminate as previously described. A quarter-day observation was included in the final data set if the IMI status was classified as healthy, single pathogen infection, or mixed infection.

Quarter-day IMI status, cow information, visit, and herd data were organized into a spreadsheet and imported into the R Statistical Programming Environment (R Development Core Team, 2023) for analysis. The quarter-level prevalence for each farm visit was calculated by dividing the number of quarters infected with a particular pathogen (or grouping of similar pathogens) by the total number of sampled quarters at risk where IMI status could be determined for that farm visit. Median and range of quarter-level prevalence for each herd was then calculated using all consecutive visits to a particular farm. Median and range of quarter-level prevalence for tiestalls and bedded packs were calculated over all 15 visits to each facility type, respectively. Overall median and range of quarter-level prevalence were calculated using all 30 visits to the 10 farms.

Herds milked an average of 69.5 cows (median: 70; range: 44-105) of various breeds, with a mean rolling herd average of 13,995 lbs. (median: 13,250 lbs.; range: 10,675-21,204 lbs.). Three visits were completed at 8 farms, 1 herd was sampled twice, and 1 was sampled 4 times before interruption by the COVID-19 pandemic. Mean days elapsed between farm visits was 33.6 (median: 34; range: 27-43). Of the 5 enrolled BP farms, 2 were compost bedded-packs, utilizing aerobic decomposition to break down a bedding material of sawdust or shavings (The Dairyland Initiative, 2024; Bewley et al., 2017; Endres, 2021). These 2 farms bedded solely with shavings/sawdust, adding new bedding only as needed, and cultivated the pack twice a day. Two other farms used a “traditional” or “deep bedded pack” system, where large volumes of fresh, dry straw (or poor-quality hay) sufficient to keep cows clean and dry was added daily to a mass of bedding that accumulates over the 6-8 months cows are housed indoors (The Dairyland Initiative, 2024; Thurgood, 2009; Benson, 2012; Bewley et al., 2017). The remaining BP bedded with straw and woodchips and cultivated every 48 hrs., adding chopped hay and woodchips every time the pack was cultivated.

In total, 4,212 quarter-observations were collected from 1,536 quarters belonging to 384 cows were enrolled for at least 1 visit. Of these, 880 quarter-observations were excluded from further analyses: 34 did not meet definition of either having an IMI or being healthy; 88 were from non-functional mammary glands; 224 were excluded due to a sampling error; and 534 were excluded because ≥ 1 of the 2 duplicate quartermilk samples was contaminated. The final data set consisted of 3,332 quarter-observations (from 1,456 quarters of 382 cows) where the IMI status of the quarter could be determined (Table 1). There were 2,290 quarter-observations from healthy quarters. The mean (median; range) number of cows included per herd was 38.2 (38; 35-41), quarters per cow was 3.8 (4; 1-4) and observations per quarter was 2.3 (2; 1-4).

There were 1,042 quarter-observations from quarters with an IMI at time of sampling: 953 with an IMI due to a single pathogen (28.6% of all quarter-observations), and 89 with a mixed infection (2.7% of all quarter-observations). Overall, the majority of IMI were caused by NASM species (19.9%), followed by *Staph. aureus* (3.6%) and *Corynebacterium* spp. (3.1%). *Streptococcus uberis* and *Strep. dysgalactiae* were the next most commonly found pathogens (3.1% and 0.9%, respectively). Twenty-one different NASM were identified, with *Staph. chromogenes* as the dominant species (13.6%). The next most frequently isolated NASM were *Staph. haemolyticus* (1.5%), *Staph. simulans* (1.3%), *Staph. warneri* (0.6%), and *Staph. equorum/Staph. devriesei* (both 0.6%).

***Discussion***

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Table 1. Quarter-level prevalence of pathogens (or grouping of similar pathogens) causing intramammary infections [median (range)] by farm, stratified by facility type. 3,332 quarter-level observations were collected from 1,456 quarters belonging to 382 cows during a longitudinal, cross-sectional observational study of 10 certified organic dairy farms in Vermont (US). The quarter-level prevalence represents the percent of sampled quarters infected with a particular pathogen over all sampled quarters at risk where IMI status could be determined for that farm visit. Median and range of quarter-level prevalence for each herd were calculated using all consecutive visits to a particular farm. Median and range of quarter-level prevalence for tiestalls (TS) and bedded packs (BP) were calculated over all visits to TS (n = 15) and BP (n = 15), respectively. Overall median and range of quarter-level prevalence were calculated using all visits to all 10 farms (n = 30). | | | | | | | | | | | | | | | |
|  | | | TS-1 | TS-2 | TS-3 | TS-4 | TS-5 | TS avg. | BP-1 | BP-2 | BP-3 | BP-4 | BP-5 | BP avg. | Overall |
| Num. farm visits | | | 3 | 3 | 3 | 3 | 3 | 15 | 3 | 4 | 3 | 2 | 3 | 15 | 30 |
| Pathogen (group) | | |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | *Staphylococcus aureus* | | 3.5 (3.1-4) | 1.9 (1.7-2.4) | 4 (3.4-4.1) | 3.5 (3.2-3.9) | 0.9 (0.9-1) | 3.2 (0.9-4.1) | 4.8 (4.7-8.4) | 13.1 (11.7-14.1) | 0.8 (0-2.6) | 1.3 (0.9-1.7) | 0.8 (0-0.8) | 2.6 (0-14.1) | 3.2 (0-14.1) |
|  | Non-*aureus* staphylococci and mammaliicocci | | 10 (9.7-10.4) | 19.6 (16.7-23.2) | 24 (22.3-25.6) | 15.8 (14.2-18.5) | 20.4 (19-24.5) | 19 (9.7-25.6) | 24.8 (21.9-39.8) | 14.1 (12.8-18.2) | 23.6 (21.9-25.5) | 19.4 (17.6-21.1) | 20.6 (19.4-22.4) | 21.1 (12.8-39.8) | 20 (9.7-39.8) |
|  | | *Staphylococcus agnetis* | 2 (1.8-2.1) | 0 (0-0) | 0 (0-0.8) | 0 (0-0) | 0 (0-0.9) | 0 (0-2.1) | 2.4 (0.8-3.6) | 1.1 (0-2) | 0 (0-0) | 0.9 (0.8-0.9) | 0.8 (0.8-0.9) | 0.8 (0-3.6) | 0.8 (0-3.6) |
|  | | *Staphylococcus auricularis* | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0.8) | 0 (0-0) | 0 (0-0.8) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0.8) |
|  | | *Staphylococcus capitis* | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0.8 (0-0.8) | 0 (0-0) | 0 (0-0.8) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0.8) |
|  | | *Staphylococcus chromogenes* | 6 (5.3-6.3) | 13.1 (11.7-15.9) | 16.2 (14.9-16.8) | 8.8 (7.1-8.9) | 15.5 (13.8-15.5) | 13.1 (5.3-16.8) | 15.2 (13.3-21.7) | 7.8 (6.5-10.1) | 19.5 (17.5-21.8) | 15.9 (14.3-17.4) | 16.8 (16.1-17.6) | 16.1 (6.5-21.8) | 14.6 (5.3-21.8) |
|  | | *Staphylococcus cohnii* | 0 (0-0) | 0.9 (0.8-1.2) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1.2) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1.2) |
|  | | *Staphylococcus devriesei* | 0 (0-0) | 0.9 (0.8-1.2) | 0 (0-0) | 0 (0-0) | 1.9 (1.7-2.7) | 0 (0-2.7) | 0.8 (0.8-2.4) | 1 (0-1.1) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-2.4) | 0 (0-2.7) |
|  | | *Staphylococcus epidermidis* | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1) | 0 (0-1) |
|  | | *Staphylococcus equorum* | 0 (0-0) | 3.7 (1.7-3.7) | 0 (0-0) | 0 (0-0) | 1 (0.9-1.7) | 0 (0-3.7) | 0 (0-1.2) | 0 (0-1.1) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1.2) | 0 (0-3.7) |
|  | | *Staphylococcus gallinarum* | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0.8 (0-1.2) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1.2) | 0 (0-1.2) |
|  | | *Staphylococcus haemolyticus* | 1 (0.9-1) | 0 (0-0) | 0.8 (0.8-1.7) | 1.6 (1.6-1.8) | 0 (0-0.9) | 0.9 (0-1.8) | 3.1 (2.4-4.8) | 3 (2.1-3.3) | 3.3 (2.7-3.5) | 0.9 (0.8-0.9) | 0.8 (0-1.9) | 2.7 (0-4.8) | 1.3 (0-4.8) |
|  | | *Staphylococcus hominis* | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0.8) | 0 (0-0) | 0 (0-0.8) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0.8) |
|  | | *Staphylococcus hyicus* | 0 (0-0) | 0 (0-0) | 0.8 (0.8-0.9) | 0 (0-0) | 0 (0-0) | 0 (0-0.9) | 0 (0-0) | 1 (0-1.1) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1.1) | 0 (0-1.1) |
|  | | *Staphylococcus pseudintermedius* | 0 (0-0) | 0.9 (0.8-1.2) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1.2) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1.2) |
|  | | *Staphylococcus saprophyticus* | 0 (0-0) | 0 (0-0.8) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0.8) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0.8) |
|  | | *Staphylococcus simulans* | 1 (0.9-1) | 0 (0-0) | 3.2 (2.5-4.3) | 3.2 (3.1-3.5) | 0 (0-0) | 1 (0-4.3) | 2.4 (2.3-2.4) | 0 (0-0) | 0.9 (0.8-0.9) | 0.9 (0.8-0.9) | 1.5 (0.8-1.9) | 0.9 (0-2.4) | 0.9 (0-4.3) |
|  | | *Staphylococcus succinus* | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1) | 0 (0-1) |
|  | | *Staphylococcus warneri* | 0 (0-0) | 0 (0-0) | 2.5 (2.4-2.6) | 1.6 (1.6-1.8) | 0 (0-0) | 0 (0-2.6) | 1.6 (0.8-2.4) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-2.4) | 0 (0-2.6) |
|  | | *Staphylococcus xylosus* | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 1 (0.9-1.8) | 0 (0-1.8) | 0 (0-0) | 0.5 (0-1.1) | 0 (0-0) | 0.9 (0.8-0.9) | 0.8 (0.8-0.9) | 0 (0-1.1) | 0 (0-1.8) |
|  | | *Mammaliicoccus fleurettii* | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 1 (0-1.8) | 0 (0-1.8) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1.8) |
|  | | *Mammaliicoccus sciuri* | 0 (0-0.9) | 0 (0-0) | 0 (0-0) | 0 (0-0.8) | 0 (0-0) | 0 (0-0.9) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0.9) |
|  | | *Mammaliicoccus vitilinus* | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0.9) | 0 (0-0.9) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0.9) |
|  | *Streptococcus dysgalactiae* | | 0 (0-0) | 3.3 (2.8-7.3) | 1.7 (0.8-1.7) | 0.8 (0.8-0.9) | 0 (0-0) | 0.8 (0-7.3) | 0 (0-0) | 1.6 (1.1-2) | 0.9 (0-1.8) | 0 (0-0) | 0 (0-0) | 0 (0-2) | 0.4 (0-7.3) |
|  | *Streptococcus uberis* | | 1 (0.9-1) | 5.6 (5-6.1) | 5 (4-5.1) | 2.4 (2.4-2.6) | 0.9 (0.9-1) | 2.4 (0.9-6.1) | 3.6 (3.2-5.5) | 4.2 (1.1-6.1) | 2.4 (1.8-3.5) | 0.4 (0-0.8) | 5.3 (4-5.6) | 3.6 (0-6.1) | 3.4 (0-6.1) |
|  | *Aerococcus* spp.1 | | 1 (0-1.8) | 0 (0-1.7) | 0 (0-1.7) | 0 (0-1.6) | 0 (0-0.9) | 0 (0-1.8) | 0 (0-4.8) | 0.5 (0-4) | 0 (0-0.9) | 0 (0-0) | 1.6 (0-3.7) | 0 (0-4.8) | 0 (0-4.8) |
|  | Other streptococcal and streptococcal-like organisms2 | | 0 (0-0) | 0 (0-0.8) | 0 (0-0.8) | 0 (0-0) | 0 (0-0) | 0 (0-0.8) | 0 (0-1.2) | 0.5 (0-1.1) | 0 (0-1.6) | 0 (0-0) | 0.8 (0-1.6) | 0 (0-1.6) | 0 (0-1.6) |
|  | *Corynebacterium* spp.3 | | 4 (0.9-6.3) | 7.5 (6.7-11) | 2.4 (0.8-2.6) | 1.6 (0-1.6) | 0 (0-0.9) | 1.6 (0-11) | 0.8 (0-8.4) | 11.5 (5.3-20.2) | 0 (0-0) | 0.4 (0-0.8) | 0 (0-0) | 0 (0-20.2) | 0.9 (0-20.2) |
|  | *Kocuria* spp.4 | | 1 (0-3.5) | 0 (0-0.8) | 1.6 (0-2.6) | 0 (0-1.6) | 0 (0-0.9) | 0 (0-3.5) | 0 (0-1.6) | 0 (0-0) | 0 (0-2.6) | 0 (0-0) | 0 (0-0) | 0 (0-2.6) | 0 (0-3.5) |
|  | Other gram-positive bacteria | | 1 (0.9-1) | 0 (0-1.2) | 0.8 (0-0.8) | 0.8 (0-1.6) | 0 (0-1.8) | 0.8 (0-1.8) | 0.8 (0-0.8) | 2.1 (1-4.3) | 0 (0-0) | 1.3 (0.8-1.8) | 0.8 (0-0.8) | 0.8 (0-4.3) | 0.8 (0-4.3) |
|  | Coliforms5 | | 0 (0-0) | 0 (0-0.9) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0.9) | 0 (0-0) | 1.1 (1-2) | 1.8 (0-2.4) | 0.5 (0-0.9) | 0 (0-0) | 0 (0-2.4) | 0 (0-2.4) |
|  | Other gram-negative bacteria | | 0.9 (0-2) | 0.9 (0.8-1.2) | 0 (0-0) | 0.8 (0-0.8) | 0.9 (0-0.9) | 0.8 (0-2) | 0 (0-0) | 0.5 (0-2) | 0 (0-0.9) | 0.8 (0-1.7) | 0 (0-0.9) | 0 (0-2) | 0 (0-2) |
|  | *Candida rugosa* | | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1.2) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1.2) | 0 (0-1.2) |
|  | Unable to be identified | | 0 (0-0) | 0 (0-0) | 0 (0-0.8) | 0 (0-0) | 0 (0-0) | 0 (0-0.8) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0.8) |
| 1 *Aerococcus* sp. (genus-level identification only), *Aerococcus viridans* | | | | | | | | | | | | | | | |
| 2Other streptococcal and streptococcal-like organisms not listed separately: *Streptococcus* sp*.* (genus-level identification only)*, Streptococcus canis, Enterococcus saccharolyticus* | | | | | | | | | | | | | | | |
| 3 *Corynebacterium* sp. (genus-level identification only), *C. amycolatum, C. callunae, C. casei, C. confusum, C. glutamicum, C. stationis, C. ulcerans, C. variabile, C. xerosis* | | | | | | | | | | | | | | | |
| 4 *Kocuria* sp. (genus-level identification only), *Kocuria* *carniphila, Kocuria* *palustris* | | | | | | | | | | | | | | | |
| 5 *Enterobacter* sp. (genus-level identification only), *Escherichia coli, Klebsiella aerogenes, Klebsiella pneumoniae, Klebsiella variicola, Serratia marcescens* | | | | | | | | | | | | | | | |

***Declarations***

*Ethics approval and consent to participate*

STROBE-VET (Strengthening the Reporting of Observational Studies in Epidemiology–Veterinary Extension) statement guidelines were followed in the reporting of this study (O'Connor et al., 2016). Animal use for this project was approved by the University of Vermont Institutional Animal Care and Use Committee (IACUC; protocol #19-001).

*Consent for publication*

Not applicable

*Availability of data and materials*

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

*Competing interests*

The authors have not stated any conflicts of interest.

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*Authors' contributions*

Caitlin Jeffrey conceptualized the study, acquired funding, coordinated farm recruitment and sampling, conducted on-farm sample collection, managed and curated the data, conducted the data analysis, prepared data visualizations and presentation, wrote the original and final drafts. Pamela Adkins, conducted isolate species identification by MALDI-TOF. John Barlow conceptualized the study, acquired funding, supervised the research, conducted on-farm sample collection, reviewed and edited the manuscript.

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Not applicable

***References***

Andrews, T., C. E. Jeffrey, R. E. Gilker, D. A. Neher, and J. W. Barlow. 2021. Design and implementation of a survey quantifying winter housing and bedding types used on Vermont organic dairy farms. J. Dairy Sci. 104(7):8326-8337.

Benson, A. F. 2012. Consider deep pack barns for cow comfort and manure management. Accessed March 18, 2024. Cornell University, Ithaca, NY. <https://smallfarms.cornell.edu/2012/04/consider-deep-pack-barns-for-cow-comfort-and-manure-management/>.

Bewley, J. M., L. M. Robertson, and E. A. Eckelkamp. 2017. A 100-Year Review: Lactating dairy cattle housing management. J. Dairy Sci. 100(12):10418-10431.

Cicconi-Hogan, K. M., N. Belomestnykh, M. Gamroth, P. L. Ruegg, L. Tikofsky, and Y. H. Schukken. 2014. Short communication: Prevalence of methicillin resistance in coagulase-negative staphylococci and Staphylococcus aureus isolated from bulk milk on organic and conventional dairy farms in the United States. J Dairy Sci 97(5):2959-2964.

The Dairyland Initiative: School of Veterinary Medicine, Univeristy of Wisconsin-Madison. Housing Module: Adult Cow Housing, Bedded Packs. University of Wisconsin-Madison. Accessed March 18, 2024. <https://thedairylandinitiative.vetmed.wisc.edu/home/housing-module/adult-cow-housing/bedded-pack/>.

Dohoo, I., S. Andersen, R. Dingwell, K. Hand, D. Kelton, K. Leslie, Y. Schukken, and S. Godden. 2011. Diagnosing intramammary infections: Comparison of multiple versus single quarter milk samples for the identification of intramammary infections in lactating dairy cows. J. Dairy Sci. 94(11):5515-5522.

Drancourt, M., V. Roux, P.-E. Fournier, and D. Raoult. 2004. rpoB Gene Sequence-Based Identification of Aerobic Gram-Positive Cocci of the Genera Streptococcus, Enterococcus, Gemella, Abiotrophia, and Granulicatella. Journal of Clinical Microbiology 42(2):497-504.

Endres, M., K. Janni. 2021. Compost-bedded pack barns for dairy cows. University of Minnesota Extension. Minneapolis, MN. Accessed March 18, 2024. <https://extension.umn.edu/dairy-milking-cows/compost-bedded-pack-barns-dairy-cows#a-wall-borders-the-pack-727910>.

Hamilton, C., U. Emanuelson, K. Forslund, I. Hansson, and T. Ekman. 2006. Mastitis and related management factors in certified organic dairy herds in Sweden. Acta Vet Scand 48(1):11.

Hardeng, F. and V. L. Edge. 2001. Mastitis, Ketosis, and Milk Fever in 31 Organic and 93 Conventional Norwegian Dairy Herds. J. Dairy Sci. 84(12):2673-2679.

Haw, S. R., P. R. F. Adkins, V. Bernier Gosselin, S. E. Poock, and J. R. Middleton. 2024. Intramammary infections in lactating Jersey cows: Prevalence of microbial organisms and association with milk somatic cell count and persistence of infection. J. Dairy Sci. 107(5):3157-3167.

Jeffrey, C. E., T. Andrews, S. M. Godden, D. A. Neher, and J. W. Barlow. 2024. Relationship Between Facility Type and Bulk Tank Milk Bacteriology, Udder Health, Udder Hygiene, and Milk Production on Vermont Organic Dairy Farms. J. Dairy Sci.

Levison, L. J., E. K. Miller-Cushon, A. L. Tucker, R. Bergeron, K. E. Leslie, H. W. Barkema, and T. J. DeVries. 2016. Incidence rate of pathogen-specific clinical mastitis on conventional and organic Canadian dairy farms. J Dairy Sci 99(2):1341-1350.

Mullen, K. A. E., L. G. Sparks, R. L. Lyman, S. P. Washburn, and K. L. Anderson. 2013. Comparisons of milk quality on North Carolina organic and conventional dairies. J. Dairy Sci. 96(10):6753-6762.

National Mastitis Council. 2019. Mastitis Control on Organic Dairies in the United States

Fact Sheet. Accessed July 19, 2024. <https://www.nmconline.org/wp-content/uploads/2019/02/final-mastitis-control-on-organic-dairies-in-the-us-for-nmc-posted-Feb.-2019.pdf>.

NMC (National Mastitis Council). 2017. Laboratory Handbook on Bovine Mastitis. Third ed. National Mastitis Council, Inc., New Prague, MI.

Pol, M. and P. L. Ruegg. 2007. Relationship between antimicrobial drug usage and antimicrobial susceptibility of gram-positive mastitis pathogens. J Dairy Sci 90(1):262-273.

Progressive Dairy. 2023. U.S. Dairy Statistics. Accessed July 19, 2024. <https://www.progressivepublish.com/downloads/2024/general/2023-pd-stats-lowres.pdf>.

R Development Core Team. 2023. R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria.

Richert, R. M., K. M. Cicconi, M. J. Gamroth, Y. H. Schukken, K. E. Stiglbauer, and P. L. Ruegg. 2013. Risk factors for clinical mastitis, ketosis, and pneumonia in dairy cattle on organic and small conventional farms in the United States. J Dairy Sci 96(7):4269-4285.

Ruegg, P. L. 2009. Management of mastitis on organic and conventional dairy farms. J Anim Sci 87(13 Suppl):43-55.

Stiglbauer, K. E., K. M. Cicconi-Hogan, R. Richert, Y. H. Schukken, P. L. Ruegg, and M. Gamroth. 2013. Assessment of herd management on organic and conventional dairy farms in the United States. J. Dairy Sci. 96(2):1290-1300.

Thurgood, J. M., C. M. Comer, D. J. Flaherty, and M. Kiraly. 2009. Bedded pack management system case study. Pages 184–188 in Proc. Proc. 5th National Small Farm Conference, Springfield, IL. Accessed March 18, 2024. <https://conferences.illinois.edu/resources/20033/Proceedings_8-12-13.pdf>.

USDA-AMS. 2024. Agricultural Marketing Service, Dairy Market News: U.S. Organic Dairy Fluid Overview. Accessed July 19, 2024. <https://www.ams.usda.gov/mnreports/ams_1594.pdf>.

USDA-NRCS. (U.S. Department of Agriculture: Natural Resources Conservation Service). NRCS Climate-Smart Mitigation Activities. Accessed Dec. 14, 2023. <https://www.nrcs.usda.gov/conservation-basics/natural-resource-concerns/climate/climate-smart-mitigation-activities>.

USDA. 2022. Certified Organic Survey, 2021 Summary. Accessed Nov. 10, 2023. <https://downloads.usda.library.cornell.edu/usda-esmis/files/zg64tk92g/2z10z137s/bn99bh97r/cenorg22.pdf>.

Valle, P. S., G. Lien, O. Flaten, M. Koesling, and M. Ebbesvik. 2007. Herd health and health management in organic versus conventional dairy herds in Norway. Livestock Science 112(1):123-132.

Weisburg, W. G., S. M. Barns, D. A. Pelletier, and D. J. Lane. 1991. 16S ribosomal DNA amplification for phylogenetic study. J Bacteriol 173(2):697-703.

Zwald, A. G., P. L. Ruegg, J. B. Kaneene, L. D. Warnick, S. J. Wells, C. Fossler, and L. W. Halbert. 2004. Management Practices and Reported Antimicrobial Usage on Conventional and Organic Dairy Farms. J. Dairy Sci. 87(1):191-201.