|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| 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* | | | | | | | | | | | | | | | |

***Results***

Participating 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. The mean time elapsed between farm visits was 33.6 days (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 dry, fine wood 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 1 remaining farm fell somewhere between these 2 types of BP; this farm bedded with straw and woodchips and cultivated every 48 hrs., adding chopped hay and woodchips every time the pack was cultivated. The depth of the 5 packs ranged from 0.9-1.7 m of organic material (measured at visit when management questionnaire was administered).

*Prevalence of intramammary infections*

In total, 1,536 quarters belonging to 384 cows were enrolled for at least one visit throughout the study, for a total of 4,212 quarter-observations collected. Of these, 880 quarter-observations were excluded from further analyses: 34 quarter-observations did not meet definition of either having an IMI or being healthy; 88 quarter-observations were from enrolled quarters that were non-lactating mammary glands (blind); 224 quarter-observations were excluded due to a sampling error (e.g., missing cow ID, colony not selected from quartermilk culture, duplicate quartermilk sample missing); and 534 quarter-observations were excluded because ≥ 1 of the 2 duplicate quartermilk samples collected was classified as contaminated (12.7% of total quarter-observations collected).

The final data set for describing quarter-level prevalence of all pathogens causing IMI on these 10 certified organic dairy farms consisted of 3,332 quarter-observations where the IMI status of the quarter could be determined at that visit (Table1). There were 2,290 quarter-observations from healthy quarters. Observations included in the final data set came from 1,456 quarters of 382 cows across all 10 herds included in the field study. The mean (median; range) number of cows included per herd was 38.2 (38; 35-41), whereas the number of quarters included per cow was 3.8 (4; 1-4). The mean number of observations per quarter included 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 *Staphylococcus aureus* (3.6%) and *Corynebacterium* species (3.1%). *Streptococcus uberis* and *Streptococcus dysgalactiae* were the next most commonly found pathogens (3.1% and 0.9%, respectively). Twenty-one different NASM were identified to be causing IMI, with *S. chromogenes* as the dominant species (13.6%). The next most frequently isolated NASM were *S. haemolyticus* (1.5%), *S. simulans* (1.3%), *S. warneri* (0.6%), and *S. equorum/S. devriesei* (both 0.6%).

* + Not a ton of work describing overall prevalence of IMI on organic farms
    - Pena-Mosca
      * The objective of this study was to describe the IMI dynamics of primiparous cows on certified organic farms during early lactation. Longitudinal study enrolled 503 primiparous cows from 5 organic dairy farms around the US
      * Although the epidemiology of mastitis on organic farms has not been extensively studied,
* Previous work describing mastitis risk and cow hygiene on BP systems includes descriptive studies of CBP (Barberg et al., 2007b; Black et al., 2013; Fávero et al., 2015; Eckelkamp et al., 2016b; Albino et al., 2018; Heins et al., 2019). However, research comparing milk quality and cow hygiene between BP and more traditional housing types has so far been limited to freestalls with sand, which is an uncommon housing type for organic farms in Vermont (Andrews et al. 2021). These include a study comparing CBP and sand-bedded freestalls for farms with a history of low bulk tank somatic cell counts (Eckelkamp et al., 2016a), work describing hygiene and bulk tank milk somatic cell count (BTSCC) for sand-bedded freestalls and CBP (Adkins et al., 2022), and a comparison of CBP and 2 types of freestall barns (Lobeck et al., 2011). It is unclear whether the herds included in these prior studies were conventionally-managed or organic dairies
  + Not a ton of work speciating subclinical IMI from bedded pack farms
    - Pamela’s paper
    - Condas? Don’t give too much detail about what kind of BP
    - Check 40 herd notes for quarter-level
  + BP systems have a number of advantages for producers considering updating their facilities, including a smaller initial investment when compared to a new FS or TS barn (Barberg et al., 2007a; Janni et al., 2007; Black et al., 2013), although the cost year-over-year for bedding is substantial (Shane et al., 2010). Bedded packs are designed for cow comfort (Barberg et al., 2007b; Bewley et al., 2012), and prevalence of lameness, foot, and leg injuries in these systems has been found to be less than TS and FS barns (Barberg et al., 2007b; Lobeck et al., 2011; Burgstaller et al., 2016). Lastly, manure management and environmental stewardship is a top concern for both dairy producers and the general public (Holly et al., 2018). Anecdotally, the BP producers enrolled in the study were pleased with their systems of manure management, viewing their used bedding material and manure as a valuable soil amendment and an integral part of their nutrient management plan. Bedded pack systems decrease the amount of liquid manure waste when compared to conventional barns, and the used bedding with manure is more easily composted before use as a soil amendment. As aged pack material is drier before it is spread on fields, it poses less of a risk for run-off into waterways, increases soil infiltration of nutrients, and creates flexibility around timing of manure application to fields (Rushmann, 2023). Bedded packs may be a good housing option for small, pasture-based farms in the Northeastern U.S. when properly managed on farms with excellent milking hygiene practices already in place.

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