|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Table 1. Quarter-level prevalence of pathogens causing intramammary infections [mean (SD)] 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). A quarter-level prevalence for each pathogen causing IMI was calculated for each farm by visit, and 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 visit. Mean quarter-level prevalence for each farm was then calculated by averaging the quarter-level prevalence over all visits to a particular farm. Mean quarter-level prevalences for pathogens causing IMI in tiestalls (TS) and bedded packs (BP) were calculated by averaging the values for each of the five TS and BP farms, respectively. The overall quarter-level prevalence for each pathogen causing IMI was calculated by averaging the values of all 10 farms. | | | | | | | | | | | | | | |
|  | | 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 |  | 3 | 4 | 3 | 2 | 3 |  |  |
| Pathogen causing IMI | |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | *Staphylococcus aureus* | 3.6 (0.4) | 2 (0.4) | 3.9 (0.4) | 3.6 (0.4) | 0.9 (0.1) | 2.8 (1.3) | 6 (2.1) | 13 (1.3) | 1.1 (1.3) | 1.3 (0.5) | 0.5 (0.5) | 4.4 (5.3) | 3.6 (3.7) |
|  | |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | Non-aureus staphylococci and mammaliicocci | 10.1 (0.3) | 19.8 (3.3) | 24 (1.7) | 16.2 (2.2) | 21.3 (2.9) | 18.3 (5.4) | 28.8 (9.6) | 14.8 (2.3) | 23.7 (1.8) | 19.4 (2.4) | 20.8 (1.5) | 21.5 (5.2) | 19.9 (5.3) |
|  | *Staphylococcus agnetis* | 2 (0.2) | 0 | 0.3 (0.5) | 0 | 0.3 (0.5) | 0.5 (0.8) | 2.3 (1.4) | 1 (0.8) | 0 | 0.9 (0.1) | 0.8 (0.1) | 1 (0.8) | 0.8 (0.8) |
|  | *Staphylococcus auricularis* | 0 | 0 | 0 | 0.3 (0.5) | 0 | 0.1 (0.1) | 0 | 0 | 0 | 0 | 0 | 0 | 0.03 (0.1) |
|  | *Staphylococcus capitis* | 0 | 0 | 0 | 0.5 (0.5) | 0 | 0.1 (0.2) | 0 | 0 | 0 | 0 | 0 | 0 | 0.1 (0.2) |
|  | *Staphylococcus chromogenes* | 5.9 (0.5) | 13.5 (2.1) | 16 (1) | 8.2 (1) | 14.9 (1) | 11.7 (4.4) | 16.7 (4.4) | 8.1 (1.6) | 19.6 (2.1) | 15.9 (2.2) | 16.8 (0.7) | 15.4 (4.4) | 13.6 (4.6) |
|  | *Staphylococcus cohnii* | 0 | 1 (0.2) | 0 | 0 | 0 | 0.2 (0.4) | 0 | 0 | 0 | 0 | 0 | 0 | 0.1 (0.3) |
|  | *Staphylococcus devriesei* | 0 | 1 (0.2) | 0 | 0 | 2.1 (0.5) | 0.6 (0.9) | 1.3 (0.9) | 0.8 (0.5) | 0 | 0 | 0 | 0.4 (0.6) | 0.5 (0.8) |
|  | *Staphylococcus epidermidis* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.3 (0.5) | 0 | 0 | 0 | 0.1 (0.1) | 0.03 (0.1) |
|  | *Staphylococcus equorum* | 0 | 3 (1.2) | 0 | 0 | 1.2 (0.5) | 0.8 (1.3) | 0.4 (0.7) | 0.3 (0.5) | 0 | 0 | 0 | 0.1 (0.2) | 0.5 (1) |
|  | *Staphylococcus gallinarum* | 0 | 0 | 0 | 0 | 0 | 0 | 0.7 (0.6) | 0 | 0 | 0 | 0 | 0.1 (0.3) | 0.1 (0.2) |
|  | *Staphylococcus haemolyticus* | 1 (0.1) | 0 | 1.1 (0.5) | 1.6 (0.1) | 0.3 (0.5) | 0.8 (0.7) | 3.4 (1.2) | 2.9 (0.5) | 3.2 (0.4) | 0.9 (0.1) | 0.9 (0.9) | 2.2 (1.3) | 1.5 (1.2) |
|  | *Staphylococcus hominis* | 0 | 0 | 0 | 0.3 (0.5) | 0 | 0.1 (0.1) | 0 | 0 | 0 | 0 | 0 | 0 | 0.03 (0.1) |
|  | *Staphylococcus hyicus* | 0 | 0 | 0.8 (0.03) | 0 | 0 | 0.2 (0.4) | 0 | 0.8 (0.5) | 0 | 0 | 0 | 0.2 (0.3) | 0.2 (0.3) |
|  | *Staphylococcus pseudintermedius* | 0 | 1 (0.2) | 0 | 0 | 0 | 0.2 (0.4) | 0 | 0 | 0 | 0 | 0 | 0 | 0.1 (0.3) |
|  | *Staphylococcus saprophyticus* | 0 | 0.3 (0.5) | 0 | 0 | 0 | 0.1 (0.1) | 0 | 0 | 0 | 0 | 0 | 0 | 0.03 (0.1) |
|  | *Staphylococcus simulans* | 1 (0.1) | 0 | 3.3 (0.9) | 3.3 (0.2) | 0 | 1.5 (1.7) | 2.4 (0.04) | 0 | 0.9 (0.05) | 0.9 (0.1) | 1.4 (0.5) | 1.1 (0.9) | 1.3 (1.3) |
|  | *Staphylococcus succinus* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.3 (0.5) | 0 | 0 | 0 | 0.1 (0.1) | 0.03 (0.1) |
|  | *Staphylococcus warneri* | 0 | 0 | 2.5 (0.1) | 1.6 (0.1) | 0 | 0.8 (1.2) | 1.6 (0.8) | 0 | 0 | 0 | 0 | 0.3 (0.7) | 0.6 (1) |
|  | *Staphylococcus xylosus* | 0 | 0 | 0 | 0 | 1.2 (0.5) | 0.2 (0.5) | 0 | 0.5 (0.6) | 0 | 0.9 (0.1) | 0.8 (0.1) | 0.5 (0.4) | 0.3 (0.5) |
|  | *Mammaliicoccus fleurettii* | 0 | 0 | 0 | 0 | 0.9 (0.9) | 0.2 (0.4) | 0 | 0 | 0 | 0 | 0 | 0 | 0.1 (0.3) |
|  | *Mammaliicoccus sciuri* | 0.3 (0.5) | 0 | 0 | 0.3 (0.5) | 0 | 0.1 (0.2) | 0 | 0 | 0 | 0 | 0 | 0 | 0.1 (0.1) |
|  | *Mammaliicoccus vitilinus* | 0 | 0 | 0 | 0 | 0.3 (0.5) | 0.1 (0.1) | 0 | 0 | 0 | 0 | 0 | 0 | 0.03 (0.1) |
|  | |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | *Streptococcus dysgalactiae* | 0 | 4.5 (2.5) | 1.4 (0.5) | 0.8 (0.05) | 0 | 1.3 (1.9) | 0 | 1.5 (0.5) | 0.9 (0.9) | 0 | 0 | 0.5 (0.7) | 0.9 (1.4) |
|  | *Streptococcus uberis* | 1 (0.1) | 5.6 (0.5) | 4.7 (0.6) | 2.5 (0.1) | 0.9 (0.1) | 2.9 (2.1) | 4.1 (1.2) | 3.9 (2.1) | 2.6 (0.9) | 0.4 (0.6) | 5 (0.8) | 3.2 (1.8) | 3.1 (1.9) |
|  | *Aerococcus* spp.1 | 0.9 (0.9) | 0.6 (1) | 0.6 (1) | 0.5 (0.9) | 0.3 (0.5) | 0.6 (0.2) | 1.6 (2.8) | 1.3 (1.9) | 0.3 (0.5) | 0 | 1.8 (1.9) | 1 (0.8) | 0.8 (0.6) |
|  | Other streptococcal and streptococcal-like organisms2 | 0 | 0.3 (0.5) | 0.3 (0.5) | 0 | 0 | 0.1 (0.1) | 0.4 (0.7) | 0.5 (0.6) | 0.5 (0.9) | 0 | 0.8 (0.8) | 0.5 (0.3) | 0.3 (0.3) |
|  | |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | *Corynebacterium* spp.3 | 3.7 (2.7) | 8.4 (2.3) | 1.9 (1) | 1.1 (0.9) | 0.3 (0.5) | 3.1 (3.2) | 3.1 (4.7) | 12.1 (6.3) | 0 | 0.4 (0.6) | 0 | 3.1 (5.2) | 3.1 (4.1) |
|  | *Kocuria* spp.4 | 1.5 (1.8) | 0.3 (0.5) | 1.4 (1.3) | 0.5 (0.9) | 0.3 (0.5) | 0.8 (0.6) | 0.5 (0.9) | 0 | 0.9 (1.5) | 0 | 0 | 0.3 (0.4) | 0.5 (0.6) |
|  | Other gram-positive bacteria | 1 (0.1) | 0.4 (0.7) | 0.5 (0.5) | 0.8 (0.8) | 0.6 (1) | 0.7 (0.2) | 0.5 (0.5) | 2.4 (1.4) | 0 | 1.3 (0.7) | 0.5 (0.5) | 1 (0.9) | 0.8 (0.7) |
|  | |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | Coliforms5 | 0 | 0.3 (0.5) | 0 | 0 | 0 | 0.1 (0.1) | 0 | 1.3 (0.5) | 1.4 (1.3) | 0.5 (0.6) | 0 | 0.6 (0.7) | 0.3 (0.6) |
|  | Other gram-negative bacteria | 1 (1) | 1 (0.2) | 0 | 0.5 (0.5) | 0.6 (0.5) | 0.6 (0.4) | 0 | 0.8 (1) | 0.3 (0.5) | 0.8 (1.2) | 0.3 (0.5) | 0.4 (0.4) | 0.5 (0.4) |
|  | |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | *Candida rugosa* | 0 | 0 | 0 | 0 | 0 | 0 | 0.4 (0.7) | 0 | 0 | 0 | 0 | 0.1 (0.2) | 0.04 (0.1) |
|  | Unable to be identified | 0 | 0 | 0.3 (0.5) | 0 | 0 | 0.1 (0.1) | 0 | 0 | 0 | 0 | 0 | 0 | 0.03 (0.1) |
| 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***

*Description of enrolled herds and prevalence data set*

Participating herds milked an average of 69.5 cows (median: 70; range: 44-105) of various breeds. The mean rolling herd average for farms enrolled was 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. On average, 33.6 days elapsed between sequential farm visits for each herd (median: 34; range: 27-43). Five farms housed cows in a tiestall bedded with wood shavings, and 5 utilized a bedded pack system (3 actively managed for composting, 2 static). 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).

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).

*Intramammary infections: prevalence*

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%).

Twenty-seven percent of observations were the sole observation contributed to the data set by a given quarter, 41% came from quarters contributing 2 time points, and 31% and 1% came from quarters contributing 3 and 4 observations, respectively. The average time elapsed between sequential observations of a quarter was 37.1 days (median: 34.5; SD: 11.6), with an overall range of 27-96 days.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Table 1. Quarter-level prevalence of pathogens causing intramammary infections [mean (SD)] 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). A quarter-level prevalence for each pathogen causing IMI was calculated for each farm by visit, and 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 visit. Mean quarter-level prevalence for each farm was then calculated by averaging the quarter-level prevalence over all visits to a particular farm. Mean quarter-level prevalences for pathogens causing IMI in tiestalls (TS) and bedded packs (BP) were calculated by averaging the values for each of the five TS and BP farms, respectively. The overall quarter-level prevalence for each pathogen causing IMI was calculated by averaging the values of all 10 farms. | | | | | | | | | | | | | | |
|  | | 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 |  | 3 | 4 | 3 | 2 | 3 |  |  |
| Pathogen causing IMI | |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | *Staphylococcus aureus* | 1 (0-1.8) | 0 (0-1.7) | 0 (0-1.7) | 0 (0-1.6) | 0 (0-1.8) | 0 (0-0.9) | 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) |
|  | |  | 0 (0-0) | 0 (0-0.9) | 0 (0-0) | 0 (0-0) | 0 (0-0.9) | 0 (0-0) | 0 (0-0) | 1.1 (1-2) | 1.8 (0-2.4) | 0.5 (0-0.9) | 0 (0-0) | 0 (0-2.4) |
|  | Non-aureus staphylococci and mammaliicocci | 4 (0.9-6.3) | 7.5 (6.7-11) | 2.4 (0.8-2.6) | 1.6 (0-1.6) | 1.6 (0-11) | 0 (0-0.9) | 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) |
|  | *Staphylococcus agnetis* | 1 (0-3.5) | 0 (0-0.8) | 1.6 (0-2.6) | 0 (0-1.6) | 0 (0-3.5) | 0 (0-0.9) | 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) |
|  | *Staphylococcus auricularis* | 1 (0.9-1) | 0 (0-1.2) | 0.8 (0-0.8) | 0.8 (0-1.6) | 0.8 (0-1.8) | 0 (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) |
|  | *Staphylococcus capitis* | 0.9 (0-2) | 0.9 (0.8-1.2) | 0 (0-0) | 0.8 (0-0.8) | 0.8 (0-2) | 0.9 (0-0.9) | 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) |
|  | *Staphylococcus chromogenes* | 0 (0-0) | 0 (0-0.8) | 0 (0-0.8) | 0 (0-0) | 0 (0-0.8) | 0 (0-0) | 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) |
|  | *Staphylococcus cohnii* |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | *Staphylococcus devriesei* | 1 (0.9-1) | 5.6 (5-6.1) | 5 (4-5.1) | 2.4 (2.4-2.6) | 2.4 (0.9-6.1) | 0.9 (0.9-1) | 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) |
|  | *Staphylococcus epidermidis* | 3.5 (3.1-4) | 1.9 (1.7-2.4) | 4 (3.4-4.1) | 3.5 (3.2-3.9) | 3.2 (0.9-4.1) | 0.9 (0.9-1) | 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) |
|  | *Staphylococcus equorum* | 0 (0-0) | 3.3 (2.8-7.3) | 1.7 (0.8-1.7) | 0.8 (0.8-0.9) | 0.8 (0-7.3) | 0 (0-0) | 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) |
|  | *Staphylococcus gallinarum* | 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) |
|  | *Staphylococcus haemolyticus* | 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) | 0 (0-0.8) |
|  | *Staphylococcus hominis* |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | *Staphylococcus hyicus* | 6 (5.3-6.3) | 13.1 (11.7-15.9) | 16.2 (14.9-16.8) | 8.8 (7.1-8.9) | 13.1 (5.3-16.8) | 15.5 (13.8-15.5) | 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 pseudintermedius* | 1 (0.9-1) | 0 (0-0) | 0.8 (0.8-1.7) | 1.6 (1.6-1.8) | 0.9 (0-1.8) | 0 (0-0.9) | 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 saprophyticus* | 1 (0.9-1) | 0 (0-0) | 3.2 (2.5-4.3) | 3.2 (3.1-3.5) | 1 (0-4.3) | 0 (0-0) | 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 simulans* | 0 (0-0) | 3.7 (1.7-3.7) | 0 (0-0) | 0 (0-0) | 0 (0-3.7) | 1 (0.9-1.7) | 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 succinus* | 2 (1.8-2.1) | 0 (0-0) | 0 (0-0.8) | 0 (0-0) | 0 (0-2.1) | 0 (0-0.9) | 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 warneri* | 0 (0-0) | 0.9 (0.8-1.2) | 0 (0-0) | 0 (0-0) | 0 (0-2.7) | 1.9 (1.7-2.7) | 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 xylosus* | 0 (0-0) | 0 (0-0) | 2.5 (2.4-2.6) | 1.6 (1.6-1.8) | 0 (0-2.6) | 0 (0-0) | 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) |
|  | *Mammaliicoccus fleurettii* |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | *Mammaliicoccus sciuri* | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1.8) | 1 (0.9-1.8) | 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 vitilinus* | 0 (0-0.9) | 0 (0-0) | 0 (0-0) | 0 (0-0.8) | 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) | 0 (0-0.9) |
|  | |  | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0.8) | 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) |
|  | *Streptococcus dysgalactiae* | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0.8 (0-0.8) | 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) | 0 (0-0.8) |
|  | *Streptococcus uberis* | 0 (0-0) | 0.9 (0.8-1.2) | 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 (0-0) | 0 (0-1.2) |
|  | *Aerococcus* spp.1 | 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) |
|  | Other streptococcal and streptococcal-like organisms2 | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1.8) | 1 (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) |
|  | |  | 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) |
|  | *Corynebacterium* spp.3 | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-0.8) | 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) | 0 (0-0.8) |
|  | *Kocuria* spp.4 | 0 (0-0) | 0.9 (0.8-1.2) | 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 (0-0) | 0 (0-1.2) |
|  | Other gram-positive bacteria | 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) | 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) | 0 (0-1) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1) |
|  | Coliforms5 | 0 (0-0) | 0 (0-0) | 0.8 (0.8-0.9) | 0 (0-0) | 0 (0-0.9) | 0 (0-0) | 0 (0-0) | 1 (0-1.1) | 0 (0-0) | 0 (0-0) | 0 (0-0) | 0 (0-1.1) | 0 (0-1.1) |
|  | Other gram-negative bacteria | 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) |
|  | |  | 1 (0-1.8) | 0 (0-1.7) | 0 (0-1.7) | 0 (0-1.6) | 0 (0-1.8) | 0 (0-0.9) | 0 (0-4.8) | 0.5 (0-4) | 0 (0-0.9) | 0 (0-0) | 1.6 (0-3.7) | 0 (0-4.8) |
|  | *Candida rugosa* | 0 (0-0) | 0 (0-0.9) | 0 (0-0) | 0 (0-0) | 0 (0-0.9) | 0 (0-0) | 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) |
|  | Unable to be identified | 4 (0.9-6.3) | 7.5 (6.7-11) | 2.4 (0.8-2.6) | 1.6 (0-1.6) | 1.6 (0-11) | 0 (0-0.9) | 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) |
| 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* | | | | | | | | | | | | | | |

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