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