DYNAMICS OF INTRAMAMMARY INFECTION WITH NON-AUREUS STAPHYLOCOCCI ON 4 FARMS

Ricardo Bexiga¹, Márcia Rato², Ilda Santos-Sanches², Carla Carneiro¹, Abdelhak Lemsaddek³, Teresa Semedo-Lemsaddek⁴, Kathryn Ellis⁵, Cristina Vilela¹

¹Microbiologia e Imunologia, Faculdade de Medicina Veterinária, UTL, Lisboa, ²Centro de Biodiversidade, Genómica Integrativa e Funcional, Universidade de Lisboa, Faculdade de Ciências, Caparica, ³Instituto de Investigação Científica Tropical, CVZ, CIIISA, ⁴CIIISA, Faculdade de Medicina Veterinária, UTL, Lisboa, Portugal, ⁵Scottish Centre for Production Animal Health and Food Safety, Faculty of Veterinary Medicine, University of Glasgow, Glasgow, UK

Despite being present in the environment, not every species of coagulase-negative staphylococci (CNS) is equally detected in the mammary gland and in extramammary sites. The most frequent source of intramammary infection (IMI) with CNS is not well established: either other cows, via the milking machine, or the environment. Different bacterial species may behave differently and thus control measures might need to be targeted accordingly. The objectives of our study were: a) to compare individual quarter somatic cell count (SCC) in milk samples with IMI due to different CNS species; b) to compare the duration of infection for different CNS species; c) to get insight into forms of transmission for individual CNS species.

The study was performed on 4 commercial dairy farms, with individual quarter samples taken from 12 cows per visit, every 4 weeks, for 12 visits on each farm. On the initial visit, only cows with a SCC increase from below to above 200,000 cells/ml on the 2 previous milk recordings were selected for sampling. On subsequent visits, cows from which CNS had been isolated in the previous visit were resampled, with new cows being added, selected as before, up to a total of 12 cows per farm. Phenotypic identification of CNS was performed with the ID32 Staph® system (bioMérieux). Genotypic identification to species level was performed with an internal transcribed spacer PCR and to strain level with a pulsed-field gel electrophoresis. The Simpson index was calculated to estimate diversity between strains for each species-farm pair.

The percentage of quarters with CNS IMI per farm varied between 6% and 34%. S. epidermidis was detected on 2 farms and S. intermedius (identified phenotypically) on 1 farm. S. simulans and S. chromogenes were more frequently detected (mode) for 3 months in succession and led to SCC geometric means of 222,000 and 193,000 cells/ml. S. epidermidis was more often detected in 1 month and not in the next, and led to a mean SCC of 87,000 cells/ml. S. intermedius was detected on the longest succession of months (mode=4). The Simpson index was lowest for S. epidermidis indicating that a small number of strains was responsible for the majority of MASTITIS cases. S. chromogenes had the highest values for the Simpson index indicating multiple sources of infection.

The epidemiology and the impact of infection with individual CNS species seems to vary. This should be taken into account when recommending control measures.