Detection of *Streptococcus agalactiae* in Danish Dairy Herds by Different Methods

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Introduction

Streptococcus agalactiae (*S. agalactiae*) is a contagious pathogen that infects the bovine mammary gland, causing primarily subclinical mastitis and high somatic cell count. Consequently, the pathogen is responsible for production losses and reduction in milk quality (Keefe, 2012). Although *S. agalactiae* is considered a persistent infection, monitoring the prevalence and infection rate of *S. agalactiae,* however is challenged due to the fluctuating or cyclic pattern of the shedding from infected mammary glands (Svennesen, et. al., 2019). In Denmark, *S. agalactiae* herd prevalence is monitored by a mandatory surveillance program which, over time, has changed the strategy and detection methods of monitoring the pathogen (Mweu et al., 2012). Since medio 2021, detection of *S. agalactiae* is performed on bi-annually collected bulk milk samples tested with PCR. In addition, upon detection of *S. agalactiae* from clinical mastitis cases (quarter level), or in voluntary cow-level milk samples, collected prior to dry off, normally during monthly milk recordings. Furthermore, herds purchasing livestock from herds infected with *S. agalactiae*, will be given the status "infected". Including additional detection methods, other than the standard mandatory collection of bulk milk samples, potentially improves the ability to find infected herds. However, this is yet to be confirmed. Accordingly, the aim of this study was, to evaluate the distribution of detection methods related to herds shifting status to "infected". Furthermore, to explore the extent to which *S. agalactiae* can be rediscovered in the standard mandatory bulk milk samples collected up to 3 months after the detection of infection.

Materials And Methods

Data was collected from the Danish Cattle Database and comprised of records of *S. agalactiae* status and dates of change in status, for all dairy herds within two years between July 2021 and June 2023. The status could either be "not infected" or "infected". These data were supplemented with findings of *S. agalactiae* from bulk milk samples, results from PCR or bacteriology

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determined presence of *S. agalactiae* from individual cow- or quarter milk samples, along with status of herds from where cows were being moved from. Altogether, this led to information on date of infection and the infection's detection method, either as bulk milk samples, individual samples from either bacteriology or PCR, or from purchasing livestock from an infected herd. In case of two or more methods detecting *S. agalactiae* within the same month and year, the method assigned to the detection was the first method appearing in the order mentioned above.

Results

The results showed that approximately 56 % of the herds changed status to "infected" due to findings of *S. agalactiae* in individual cow milk samples analyzed either by PCR or bacteriology. In 18 % of the herds, findings of *S. agalactiae* in bulk milk samples were the cause of getting the status "infected". In herds where *S. agalactiae* was detected due to individual milk samples, either analyzed by PCR or bacteriological culture, the pathogen was only rediscovered in the subsequent bulk milk sample, in approximately 11 % of the cases.

Conclusion

Combining different methods of detecting *S. agalactiae* in dairy herds, such as results from analysis of individual samples at cow- or quarter level, might improve the detection of infected herds. This is supported by the findings, that *S. agalactiae* was found in bulk milk samples in only a small proportion of infected herds detected by individual samples. It is hypothesized, that this is due to dilution of the pathogen in bulk milk of large herds. However, further research is needed to establish how the within herd prevalence of *S. agalactiae* and volume of the bulk milk of infected herds, affects the ability to correctly identify infected herds.

References

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