

Analysis of the pathogen spectrum and risk factors associated with coliform mastitis in sows

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Summary

In this study, the spectrum of pathogens involved in sows' mastitis was analysed and associated risk factors were evaluated. Milk samples from 444 sows with coliform mastitis (CM) and 471 non-infected sows of different age were obtained on piglet farrowing units of six different farms. Bacteria involved in pathogenesis were identified by advanced bacteriological analysis including molecular techniques like PCR. The results were interpreted with regard to the sow lines, cycles and the effect of the farm and the season. A wide spectrum of pathogens was isolated, belonging mainly to coliform bacteria, with no explicit differences between healthy and diseased sows. The influence of the farm on the occurrence of specific bacteria was confirmed statistically. The line, farm and season had no effect on the incidence of CM, whereas the parity number presented a significant effect. Further studies will include the examination of a larger animal base and more detailed bacteriology.

Introduction

Coliform mastitis (CM), as central clinical sign of the Mastitis-Metritis-Agalactia (MMA) syndrome in sows, is an economically important disease [1]. After farrowing, the infection of the mammary gland results in reduced productivity of the sows and increased mortality of the piglets. The affected animals suffer from fever and an inflammation of the mammary glands followed by a reduced milk secretion 24 to 48 hours post partum. The sows fail to meet the needs of their piglets. High pre-weaning piglet mortality and growth retardation are the consequences [2]. Incidences in herds can be as high as 60 % with an average of 13% [3, 4].

CM is not transmitted through animal-animal-contact, but influenced by various factors like husbandry, management, nutrition and hygiene. Furthermore, bacterial pathogens play an important role, but detailed information is lacking. In several studies and infection experiments, especially coliform bacteria including the genera *Escherichia*, *Citrobacter*, *Enterobacter* and *Klebsiella* were isolated [5-7]. The most important agent of these pathogens is *Escherichia (E.) coli*, a gram-negative, rod shaped bacterium with different virulence factors marking its pathogenicity [8].

This study is part of the FUGATO-plus-project 'geMMA - structural and functional analysis of the genetic variation of the MMA-syndrome'. In this examination, the spectrum of pathogens involved in CM was analysed and associated risk factors were evaluated.

Animals, Materials and Methods

A total of 915 milk samples were obtained, consisting of 444 samples from diseased and 471 samples from healthy sows. The animals were of different age and housed on six piglet rearing and fattening units. They were pure bred (Landrace, Large White) or cross bred (Landrace and Large White with Duroc). The sows were identified as CM-infected when the measured rectal temperature was above 39.5°C and the mammary glands showed defined signs of infection. In addition, the appearance and the performance of the piglets were evaluated.

Bacteria involved in the pathogenesis of CM were identified by advanced bacteriological analysis of the milk samples including molecular techniques like PCR. The results were interpreted with regard to the lines and the parities of the sows and the effect of the season and the farm. The statistical evaluation was performed with the GENMOD procedure of SAS.

Results and discussion

Spectrum of pathogens

A wide spectrum of pathogens was isolated, belonging mainly to coliform bacteria, *Staphylococcaceae*, *Streptococcaceae* and *Enterococcaceae*. *Escherichia coli*, *Staphylococcus aureus*, the coagulase-negative staphylococcal species *Staphylococcus simulans* and *Staphylococcus chromogenes* and environmental *Streptococci* were found most frequently. They are known to cause bovine mastitis, but have also been isolated in studies on porcine mastitis before [5, 9]. Figure 1 shows no explicit differences in the identified bacteria for both healthy and diseased sows.

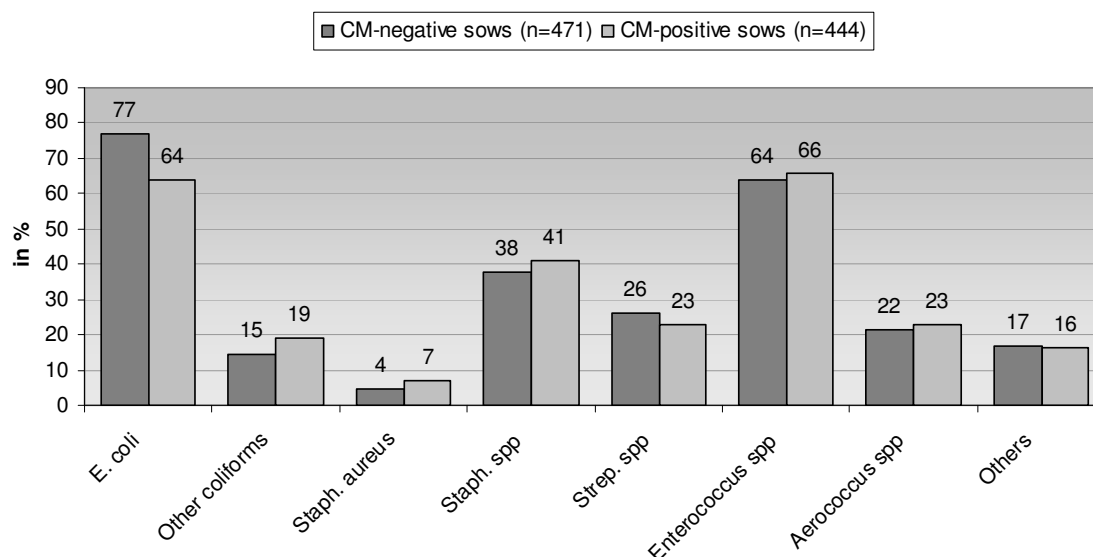


Figure 1: Bacteriological findings in milk samples in percentages

Coliform bacteria were found more often than the others pathogens. In particular, *E. coli* represented the major part of all isolated coliform bacteria. Other coliform bacteria included *Klebsiella* species (spp), *Citrobacter* spp and *Raoultella* spp in minor percentages. In 63.66 % of the samples from CM-affected sows, *E. coli* was found. These results are in accordance with several other investigations, showing that these pathogens are the causing agents in the etiology of CM [5-8].

Risk factors associated with CM

The results of this bacteriological analysis were statistically examined with regard to the parameters line, parity, season and farm (Table 1). The parity numbers and lines of the sows had no significant influence on the occurrence of specific bacteria. The influence of the farm, i.e. management and housing conditions, and the season were confirmed statistically. Indeed, faecal contamination of the sows' surroundings represents the most probable source of infection [5] and indicates distinctly the need for proper animal hygiene. Ravel et al. [10] reported that regular washing of the farrowing unit is associated with a lower preweaning mortality. Mammary complexes of sows should be kept clean by reducing the contact with faeces considerably. In a study by Bertschinger et al. [11], conventional farrowing crates and an experimental pen with a clean resting area were compared, showing a 10 times lower incidence of intramammary *E. coli* infections for sows in the experimental pen.

Table 1: Significances of the effects

effect	CM	<i>E. coli</i>	other coliforms	<i>Staph. aureus</i>	<i>Staph. spp.</i>	<i>Strep. spp.</i>	<i>Enterococcus spp.</i>	<i>Aerococcus spp.</i>
parity	0.0409	0.9609	0.5268	0.5695	0.1108	0.6607	0.6396	0.7746
line	0.0615	0.7347	0.3798	0.7024	0.0931	0.2990	0.0088	0.6367
farm	0.5537	<.0001	0.6405	0.2002	<.0001	<.0001	<.0001	0.0532
season	0.4273	0.0082	0.0312	0.0063	<.0001	0.5058	<.0001	0.2015

Due to the data material, the following tendencies regarding an occurrence of CM were calculated. The line did not influence the occurrence of CM, neither did the effect of the farm and the season. According to the data the parity has a significant influence on the occurrence of CM. Primiparous sows were in tendency more often infected with CM than multiparous ones. In literature, the impact of the parity number is discussed controversially. Baer and Bilkei [12] found a higher parity of the sows (> 4) increasing the occurrence of CM. Other investigations support the results of this study postulating a lower parity as factor contributing to a higher risk of CM [4, 13].

Conclusions

Most studies dealing with CM were conducted between 1970 and 1990. With particular respect to the economic damages, it is time for research to have a closer look at this syndrome again. Bacterial, environmental and animal factors may change the susceptibility for CM. These factors are interdependent and the relative influence of each factor depends on the type of pathogens [14]. A holistic approach, considering both husbandry and microbial influences, is needed to cope with future aspects of pig husbandry. This study is a first step in this direction and will be followed by detailed examinations on a larger animal base with further studies on the genetic background of CM. Beyond that, investigations concerning the isolated *E. coli* have been initiated to obtain knowledge of associated virulence factors and to compare both health and diseased sows.

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