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The role of bacterial pathogens in coliform mastitis in sows

Zur Bedeutung bakterieller Erreger bei der coliformen Mastitis der Sau

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Summary

Even in modern piglet production, mastitis and lactation failure in sows represent a considerable health problem post partum, affecting in its consequences both the sow and her piglets. Known as a multifactorial syndrome, Mastitis-Metritis-Agalactia (MMA) has been topic of several studies investigating possible influencing factors at farm and sow level in the recent past. However, there is a lack of current investigations on the causative pathogens, especially with advanced laboratory methods and with an adequate control group of healthy animals. Therefore, 1026 milk samples from coliform mastitis (CM)-affected, and 972 samples from healthy sows on six farms were examined bacteriologically in this study. The spectrum of isolated bacteria did not differ significantly between diseased and healthy animals for most species, with *Escherichia coli* as predominant species with 70.4% positive samples from diseased, and 78.0% positive samples from healthy animals. Furthermore, other Enterobacteriaceae, Staphylococcaceae, Streptococcaceae and Enterococcaceae were isolated both from CM-affected and non-affected animals. The similar bacteria distribution underlines the multifactorial pathogenesis of CM: Only with further adverse – endogen or exogen – factors being present, ubiquitous bacteria from the sow's environment can contribute to the development of clinical signs of infection.

Keywords: dysgalactia, *Escherichia coli*, endotoxins, mastitis-metritis-agalactia (MMA), postpartum dysgalactia syndrome (PDS), swine

Zusammenfassung

Auch in der modernen Ferkelerzeugung stellt die Gesäugeentzündung der Sau im postpartalen Zeitraum nach wie vor ein Gesundheitsproblem dar, welches in seiner Konsequenz sowohl Sauen als auch Ferkel betrifft. Einige Studien in der jüngeren Vergangenheit analysierten mögliche Einflussfaktoren auf Betriebs- und Sauenebene, die das Auftreten des Mastitis-Metritis-Agalaktie(MMA)-Syndroms als typische multifaktorielle Erkrankung begünstigen. Es fehlen allerdings aktuelle Studien zu den ursächlichen pathogenen Keimen, insbesondere unter Anwendung moderner Labormethoden und der Beprobung einer passenden Kontrollgruppe gesunder Tiere. Deshalb wurden in dieser Studie 1026 Milchproben von an coliformer Mastitis (CM) erkrankten Tieren sowie 972 Proben gesunder Sauen von sechs Betrieben bakteriologisch untersucht. Das Spektrum der isolierten Bakterien unterschied sich bei den meisten Spezies nicht signifikant zwischen gesunden und erkrankten Tieren. *Escherichia coli* wurde am häufigsten isoliert und in 70,4 % der Proben erkrankter sowie in 78,0 % der Proben gesunder Tiere nachgewiesen. Des Weiteren wurden andere Enterobacteriaceae, Staphylococcaceae, Streptococcaceae und Enterococcaceae sowohl von CM-betroffenen als auch gesunden Tieren isoliert. Das ähnliche Bakterien-Spektrum verdeutlicht die multifaktorielle Pathogenese von CM: Bei Vorliegen weiterer ungünstiger, endogener oder exogener, Einflussfaktoren können ubiquitär in der Sauen-Umwelt vorhandene Bakterien zur Entwicklung eines klinischen Erkrankungsbildes beitragen.

Schlüsselwörter: Dysgalaktie, *Escherichia coli*, Endotoxine, Mastitis-Metritis-Agalaktie (MMA), Postpartum-Dysgalactia-Syndrom (PDS), Schwein

Introduction

Postparturient disorders in sows are commonly categorized under the terms mastitis-metritis-agalactia (MMA) complex in European countries (Martin et al., 1967) or as postpartum dysgalactia syndrome (PPDS or PDS) in English-speaking countries (Klopfenstein et al., 2006; Waldmann and Wendt, 2001). Although the syndrome varies with respect to clinical signs, mastitis has been shown to be the predominating symptom (Heinritzi and Hagn, 1999; Ross et al., 1981; Wegmann et al., 1986). Since the mastitis is similar to the coliform mastitis in cows, the term "coliform mastitis" has been suggested also for peripartal mastitis in the sow (Bertschinger, 1999; Gerjets and Kemper, 2009). The coliform mastitis (CM) in pigs is an inflammation of the mammary glands which is associated with fever and reduced milk production for the first 12 to 48 hours post partum. The syndrome therefore decreases lactation performance of the sows as well as negatively affects growth and the preweaning mortality of piglets. It is a serious problem for the economy and animal welfare in pig production, and reported worldwide with an average incidence at herd level of approximately 13% (Bäckström et al., 1984; Bertschinger, 1999; Jorsal, 1983; Krieter and Presuhn, 2009; Madec and Josse, 1992; Thorup, 2000). Even though CM is definitely a multifactorial syndrome with more than 30 identified aetiological factors so far (Gerjets and Kemper, 2009; Klopfenstein et al., 2006), bacteria play a major role as the causative agents of infection. Bacteria most commonly isolated from affected sows are coliforms, including the genera *Escherichia, Citrobacter, Enterobacter*, and *Klebsiella* (Awad Masalmeh et al., 1990; Hirsch et al., 2003; Ross et al., 1981; Wegmann et al., 1986). The predominant role of *Escherichia coli* in mastitis in sows has been demonstrated by several infection experiments (Magnusson et al., 2001; Osterlundh et al., 2002; Ross et al., 1983). However, considering the age of the published studies on bacteria in milk from affected sows, there is a lack of further investigations into the topic, particularly with regard to the improvements in the methodology of the bacteriological identification of genera, species, and pathotypes over the last decade. Moreover, the number of examined animals per study has not exceeded 188 diseased (Heinritzi and Hagn, 1999) and 41 healthy sows (Awad Masalmeh et al., 1990) in previous studies (Tab. 1). Therefore, the presence of bacteria in mammary glands of diseased and healthy animals in a comparable environment and an adequate sample size was examined in this study. The aim of this study was to present the bacteriological results in total and with respect to a family-based case-control design in modern, high-prolific sows.

Material and methods

Animals and study design

The investigation was carried out between April 2008 and August 2010 on six nucleus and supplier herds in Northern Germany (A–F), supervised by PIC Germany GmbH Schleswig (Tab. 2) (animal trial, subject to registration: reference no. 33.9-42502-05-09A600).

The farms were of high health status and under control of the PIC-health-program. The number of sows housed in the farms ranged from 700 to 1800. The sows were in different parities (1–11) and of different lines (Landrace, Large White and crossbreds, partly with Duroc).

They were identified as CM-affected when their rectal temperature was above 39.5°C (Furniss, 1987) and the mammary glands showed defined signs of inflammation like reddening, swelling or hardening. In addition, the appearance and the performance of the piglets were evaluated with regard to their behavior and body condition. As control sows, healthy half- or full-sib sows from the same farrowing group were chosen. The family-based case-control design was applied to perform studies on the genetic background via genotyping (Preißler et al., 2013). In total, 1998 milk samples were examined (1026 milk samples from sows with CM and 972 from healthy sows). Before gathering a pooled sample of several teats, mammary glands were cleaned and disinfected with disinfection swabs containing 70% iso-

TABLE 1: *Examples of other studies on the occurrence of bacteria in milk samples from CM-affected (CM^+) and healthy (CM^-) sows*

Literature	Number of examined CM^+ samples/sows	Number of examined CM^- samples/sows	Bacteriological results with regard to CM-status	CM^+	CM^-
Ringarp,1960	167/167	15/15	*Escherichia coli*	46.7%	–
Morkoc et al., 1983	24/24	12/12	only gram+	33.3%	33.3%
			only gram–	20.8%	–
			mixed flora	20.8%	8.8%
			no bacterial growth	25.0%	58.3%
Bertschinger et al., 1990	16/16		*Escherichia coli*	100.0%	
Awad Masalmeh et al., 1990	705/67	517/41	*Escherichia coli*	15.2%	1.5%
			Streptococcus spp.	24.5%	3.9%
			Staphylococcus aureus	8.2%	3.7%
			no bacterial growth	49.9%	90.9%
Heinritzi and Hagn, 1999	188/188		*Micrococcus* spp.	41.0%	
			Streptococcus spp.	35.1%	
			Escherichia coli	33.0%	
Hirsch et al., 2004	187/187		*Staphylococcus* spp.	46.0%	
			Escherichia coli	45.0%	
			Streptococcus spp.	45.0%	
Gerjets and Kemper, 2009	54/27	58/29	*Escherichia coli*	38.9%	44.8%
			Enterococcus spp.	33.3%	31.0%
			Staphylococcus aureus	14.8%	10.3%

TABLE 2: *Number of milk samples from six different farms*

Farm	Number of milk samples	
	from CM-affected sows	from healthy sows
A	501	492
B	15	13
C	1	1
D	322	274
E	20	25
F	167	167
total	1026	972

propyl-alcohol. The first streams of milk were discarded before the following streams were milked on transport swabs with Amies medium (transwab, medical wire & equipment, Corsham, England). The milk samples were stored at 4 °C and sent to the laboratory within 72 hours.

Bacteriological analysis

Bacteriological analysis was performed by routine bacteriological diagnostics, including cultivation on Columbia sheep blood and Endo agar, Gram staining, and biochemical identification systems (ID32 STAPH, API20ST-REP, and API20E, bioMérieux, Craponne, France), as described previously (Kemper and Gerjets, 2009).

Statistical analysis

The univariate analysis of the bacteriological results in total was done with Chi-Square Test and Fisher's Exact Test using the procedure PROC FREQ from the statistical software SAS 9.2 (SAS Institute Inc., Cary, NC, USA).

Furthermore, a generalized linear mixed model (PROC GLIMMIX, SAS) was applied to analyse significant differences of bacteria species with a prevalence ≥ 5% with regard to the CM-status as a binary trait using the logit link function. This model included also other effects such as farm, line, season, parity number, birth assistance and partus induction:

$$y_{ijklmnoprst} = sow_i + farm\text{-}line_j + season_k + parity_l + coli_m + aureus_n + viridans_o + urinae_p + durans_q + faecium_r + faecalis_s + lactis_t + e_{ijklmnoprst}$$

with

$y_{ijklmnoprst}$	occurrence of CM as binary outcome (CM^+, CM^-)
sow_i	random effect of sow
$farm\text{-}line_j$	fixed effect of farm and line as a combined effect
$season_k$	fixed effect of season (spring, summer, autumn, winter)
$parity_l$	fixed effect of parity number (1,2,3,4,5,6, ≥ 7)
$coli_m$	fixed effect of bacteriological result of *Escherichia coli* (yes/no)
$aureus_n$	fixed effect of bacteriological result of *Staphylococcus aureus* (yes/no)
$viridans_o$	fixed effect of bacteriological result of *Aerococcus viridans* (yes/no)
$urinae_p$	fixed effect of bacteriological result of *Aerococcus urinae* (yes/no)
$durans_q$	fixed effect of bacteriological result of *Enterococcus durans* (yes/no)
$faecium_r$	fixed effect of bacteriological result of *Enterococcus faecium* (yes/no)
$faecalis_s$	fixed effect of bacteriological result of *Enterococcus faecalis* (yes/no)
$lactis_t$	fixed effect of bacteriological result of *Lactococcus lactis* (yes/no)
e	residual effect

This model was applied after quality control of the data set. Due to low sample size, farm C was excluded in further analyses. Other observations were excluded because of missing data regarding the fixed effect birth assistance or line or parity number. Moreover, parity numbers were classified (1–7, > 7). The fixed effects farm and line were used as combined effect in order to account for farm-specific usage of specific lines. After this quality control, 1986 observations remained for the model.

For the family-specific analyses, all available combinations between CM-affected sows and their possible paternal or maternal half- or full-sib healthy control sow from the same farrowing group were chosen. In total, 850 paired samples were analysed using the Wilcoxon signed-rank test and Kendall's tau correlation test. In a second full-sib approach, 73 CM-affected sows and their healthy 73 full-sibs from the same farrowing group were selected. The bacteriological results were screened for significant correlation using the Kendall's tau correlation test and differences were analysed using the Wilcoxon signed-rank test.

In general, a statistical significance level of $p \leq 0.05$ was used and Bonferroni correction method was applied to correct for multiple testing.

Results

In 99.1% of all samples, at least one bacteria species was isolated. The median number of different species was 3 (range from 0 to 6). Numbers of bacteria species did not differ significantly between samples from CM-positive and healthy sows (Tab. 3, Tab. 4).

In total, 5580 bacteria isolates were detected in all samples. Out of the samples from CM-positive sows, 2844 isolates were identified, compared to 2736 isolates from samples of healthy sows. The isolated species mainly belonged to the families Enterobacteriaceae, Staphylococcaceae, Streptococcaceae, and Enterococcaceae (Tab. 5). *Escherichia coli* was the predominant bacteria species, however, this species was isolated significantly

TABLE 3: *Number of milk samples (n) and the number of isolated bacteria species (median, min-max, and total) from six different farms*

Farm	Number of isolated bacteria species			
	n	median	min–max	total
A	993	3	0–6	2862
B	28	3	1–5	82
C	2	2.5	2–3	5
D	596	3	1–5	1634
E	45	2	1–5	102
F	334	3	0–6	895
total	1998	3	0–6	5580

TABLE 4: *Number of isolated different bacteria species per sample in milk samples from CM-affected (CM^+) and healthy (CM^-) sows; absolute numbers, relative numbers in parentheses*

Number of different species per sample	Milk samples of CM^+ sows (n = 1026)	Milk samples of CM^- sows (n = 972)	Samples in total (n = 1998)
0	12 (1.2%)	7 (0.7%)	19 (0.9%)
1	70 (6.8%)	60 (6.2%)	130 (6.5%)
2	314 (30.6%)	302 (31.1%)	616 (30.8%)
3	413 (40.3%)	390 (40.1%)	803 (40.2%)
4	180 (17.5%)	167 (17.2%)	347 (17.4%)
5	35 (3.4%)	42 (4.3%)	77 (3.9%)
6	2 (0.2%)	4 (0.4%)	6 (0.3%)
total sample size	1026 (100%)	972 (100%)	1998 (100%)

more often in healthy sows. The same applies for *Streptococcus dysgalactiae* and *Enterococcus durans*. Significant differences were assessed for *Staphylococcus aureus* and *Lactococcus lactis* with more isolates observed for diseased animals.

Using a generalized linear mixed model approach, *Escherichia coli, Staphylococcus aureus* and *Lactococcus lactis* were significant effects on the occurrence of CM. For these species, the model confirmed the results of the univariate analysis (Tab. 5).

As already shown by Gerjets et al (2011a, b), birth assistance and parity number also affected CM significantly.

Regarding the full-sib comparison, neither significant correlations nor significant differences were found. In contrast, for the half-sib approach, significant differences were confirmed for *Escherichia coli* and *Staphylococcus aureus*. In addition, *Staphylococcus simulans* correlated significantly between the pair of siblings.

Discussion

In this study, milk samples of CM-affected and healthy sows were analysed bacteriologically, and compared in order to get information on differences in the spectrum and on possible causative pathogens. To the authors' knowledge, this is the first study comparing bacteriological results for CM-negative control sows and diseased animals with equal sample size including also family-based comparisons. It was shown, that S*taphylococcus aureus* was isolated more often from milk of CM-affected sows, while *Escherichia coli* was more often isolated from milk of healthy control sows. With regard to the comparability with other studies, the trait definition is of major importance. For instance, CM diagnosis in other studies is often restricted to rectal temperature measurement (Krieter and Presuhn, 2009), whereas in our study all CM-affected sows were defined through

TABLE 5: *Isolated bacteria from milk samples from CM-affected (CM^+) and healthy (CM^-) sows; absolute numbers, relative numbers in parentheses*

Bacteria family	Bacteria species	Occurrence in milk samples of CM^+ sows (n = 1026)	Occurrence in milk samples of CM^- sows (n = 972)	Results of the Chi^2-Test	Results of the generalized model
Enterobacteriaceae	*Escherichia coli*[1]	722 (70.4%)	758 (78.0%)	$p < 0.05$	$p < 0.05$
	Enterobacter spp.	8 (0.8%)	6 (0.6%)	n. s.	–
	Citrobacter spp.	41 (4.0%)	33 (3.4%)	n. s.	–
	Proteus spp.	28 (2.7%)	28 (2.9%)	n. s.	–
	Klebsiella oxytoca	33 (3.2%)	24 (2.5%)	n. s.	–
	Klebsiella pneumoniae	27 (2.6%)	14 (1.4%)	n. s.	–
	Serratia spp.	6 (0.6%)	3 (0.3%)	–	–
	other Enterobacteriaceae	44 (4.3%)	42 (4.3%)	n. s.	–
Staphylococcaceae	*Staphylococcus aureus*[1]	59 (5.8%)	35 (3.6%)	$p < 0.05$	$p < 0.05$
	Staphylococcus hyicus	27 (2.6%)	37 (3.8%)	n. s.	–
	Staphylococcus simulans[1]	205 (20.0%)	197 (20.3%)	n. s.	n. s.
	Staphylococcus chromogenes	74 (7.2%)	67 (6.9%)	n. s.	n. s.
	Staphylococcus sciuri	24 (2.3%)	20 (2.1%)	n. s.	–
	Staphylococcus spp.	71 (6.9%)	63 (6.5%)	n. s.	–
	Gemella morbillorum	24 (2.3%)	19 (2.0%)	n. s.	–
	Gemella haemolysans	3 (0.3%)	3 (0.3%)	–	–
Streptococcaceae	*Streptococcus dysgalactiae*[1]	162 (15.8%)	192 (19.8%)	$p < 0.05$	n. s.
	Streptococcus agalactiae	11 (1.1%)	9 (0.9%)	n. s.	–
	Streptococcus porcinus	10 (1.0%)	13 (1.3%)	n. s.	–
	Streptococcus mitis	23 (2.2%)	16 (1.7%)	n. s.	–
	Streptococcus group L	7 (0.7%)	13 (1.3%)	n. s.	–
	Streptococcus spp.	21 (2.1%)	11 (1.1%)	n. s.	–
	Aerococcus viridans[1]	178 (17.4%)	188 (19.3%)	n. s.	n. s.
	Aerococcus urinae[1]	55 (5.4%)	40 (4.1%)	n. s.	n. s.
	Lactococcus lactis[1]	57 (5.6%)	30 (3.1%)	$p < 0.05$	$p < 0.05$
Enterococcaceae	*Enterococcus faecium*[1]	272 (26.5%)	222 (22.8%)	n. s.	n. s.
	Enterococcus faecalis[1]	392 (38.2%)	362 (37.2%)	n. s.	n. s.
	Enterococcus durans[1]	164 (16.0%)	190 (19.6%)	$p < 0.05$	n. s.
	Enterococcus avium	18 (1.8%)	19 (2.0%)	n. s.	–
Micrococcaceae	*Micrococcus luteus*	22 (2.1%)	17 (1.8%)	n. s.	–
Leuconostocaceae	*Leuconostoc* spp.	21 (2.1%)	20 (2.1%)	n. s.	–
Pseudomonadaceae	*Pseudomonas* spp.	4 (0.4%)	4 (0.4%)	–	–
Pasteurellaceae	*Pasteurella* spp.	3 (0.3%)	3 (0.3%)	–	–
Aeromonadaceae	*Aeromonas* spp.	3 (0.3%)	7 (0.7%)	–	–
others		25 (2.4%)	31 (3.2%)	n. s.	–

[1] species included in the generalized linear mixed model
n. s. = not significant; – = not statistically analysed due to low size

clinical examination 12–48 h post partum. Also the applied bacteriological methodology can differ between studies and influence comparability, especially with older studies.

The causative agents of CM and their role in pathogenesis have been discussed controversially in the literature. Many different bacterial species have been isolated from the milk of clinically diseased animals, and the results of our study confirm this broad bacteria spectrum. From both, diseased and healthy animals, the most frequently isolated bacteria were representatives of the families Enterobacteriaceae, Staphylococcaceae, Streptococcaceae, and Enterococcaceae. Regarding the samples from CM-positive sows, this spectrum is in agreement with other studies (Awad Masalmeh et al., 1990; Kobera, 2000). The most commonly isolated bacteria from mastitis-affected sows belong to the class of coliforms, covering the bacterial genera *Escherichia, Klebsiella, Enterobacter*, and *Citrobacter* (Awad Masalmeh et al., 1990; Hirsch et al., 2003; Ross et al., 1981). The importance of *Escherichia coli* has been discussed in several studies (Pedersen Mörner et al., 1998; Persson, 1997; Ross et al., 1981; Wegmann et al., 1986). Furthermore, the relevance was confirmed in infection experiments, where *Escherichia coli* provoked clinical and haematological changes comparable to natural infections (Magnusson et al., 2001; Ross et al., 1983). The role of gram-negative bacteria in pathogenesis, especially *Escherichia coli*, is mainly related to Lipopolysaccharide endotoxins (Elmore et al., 1978). These endotoxins induce hormonal imbalances by suppression of prolactin release from the anterior pituitary and lead to an increase of cortisol concentrations and a decrease of circulating thyroid hormone (Nachreiner and Ginther, 1974; Reiner et al., 2009). Production and secretion of milk are affected adversely by these changes.

Also in the milk of healthy control sows, bacteria were detected. In this context, the risk for contamination should be considered. The procedure of milking sows in order to obtain samples is difficult and severely restricted by practical circumstances, but an absolutely needed prerequisite to obtain reliable results. Cleaning and disinfection are urgently required to eliminate skin microbiota or other contaminating – mainly faecal – microorganisms. Examinations on the skin microbiota on sows' teats showed that Staphylococci are the most common bacteria (Kemper and Preißler, 2011). The significant correlation of *Staphylococcus simulans* between the pair of siblings in this study demonstrated the family-specific microbiota in milk.

The fact that healthy animals possess nearly the same bacterial spectrum in their milk as diseased ones clearly shows that milk from sows is not sterile. This is in agreement with other studies (Awad Masalmeh et al., 1990). Even in milk obtained by percutaneous aspiration, bacteria were detected (Morkoc et al., 1983). This can also be related to the anatomy of the sow's mammary gland. In contrast to the cow, two or more complete gland systems end in two or more teat orifices per teat, without muscular sphincters (Klopfenstein et al., 2006).

The infectious dose for colonization of the mammary gland is extremely low at less than 100 organisms (Bertschinger and Bühlmann, 1990). Bacteria causing or at least accompanying CM may originate from the intestinal microbiota of the sow, from the environment or from the oral microbiota of the neonatal piglet. The hypothesis of a galactogenous route of infection was corroborated by experiments carried out by Bertschinger et al. (1990), in which a reduction of CM prevalence was noticed after protection of the mammary gland against faecal contamination. The faecal origin of *Escherichia coli* isolated from sows' milk was also reported by Awad Masalmeh et al. (1990): in one quarter of 67 CM-affected sows O-serogroup-identical *Escherichia coli* were detected in both milk and faecal samples. Regarding the analysis of isolated bacteria species beyond the species level, virulence profiles of *Escherichia coli*, taking into account 27 virulence genes, did not show any specific CM-associated patterns (Gerjets et al., 2011c).

In another study comparing the bacterial microbiota of the uterus, the caecum, the ileum and the mammary gland, the prevalence of only gram-negative bacteria in the mammary glands and in the ileum of CM-affected sows was remarkable (Morkoc et al., 1983), though the faecal route of infection could not be confirmed in this study due to the study design. The lack of gram-negative bacterial culture growth in uterine samples supports the theory that uterine involvement in CM is of minor importance (Armstrong et al., 1968; Martin, 1970; Nachreiner and Ginther, 1974). However, infections of the urinary tract especially with *Escherichia coli* are strongly related to puerperal diseases, even when urinary infections are not apparent clinically (Mauch and Bilkei, 2004; Waller et al., 2002).

The spectrum of analysed bacteria in our study represents bacteria that can origin both from faecal and urine contamination and have to be considered as ubiquitous in the sow's environment. The fact that only some sows develop clinical mastitis clearly emphasizes the multifactorial character of CM. Factors contributing to clinically apparent CM include the strongly related main issues of nutrition, housing microclimate, management in general, and aspects of hygiene in particular. Risk factors identified thus far for an increase in CM prevalence are discussed in detail elsewhere (Gerjets et al., 2011a; Papadopoulus et al., 2010). Besides these factors, the individual predisposition of the sow to cope with possible pathogens is one main contributing factor, of course influenced by all factors mentioned before. With an estimated heritability of approximately 9% (Preißler et al., 2012), a genetic background for CM cannot be excluded and there is the opportunity to use this trait for selection. Indeed, as shown by Heringstad et al. (1999, 2003) for mastitis resistance in dairy cattle, it is possible to achieve sustainable selection response even for low heritable disease traits.

In conclusion, even though also healthy animals show bacteria in their milk, the role of bacteria in the pathogenesis of CM should not be underestimated. Without any doubt, infection, as it is seen for mastitis, is caused by pathogenic agents. But to enable possibly pathogenic bacteria to cause clinical syndromes implies that other predisposing factors are also present in the sow herself or in her environment. Especially with respect to the continuous improvement of commercial sow lines in their reproductive capabilities, with large litters and high-milk-producing potential, and the physiologically extreme situation during and soon after birth, these adverse factors should be limited as far as possible.

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