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Prevalence of bacterial infection and somatic cell count in early postpartum milking goats

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ABSTRACT

This trial aimed to identify the bacterial pathogens associated with caprine mastitis and to determine the prevalence of infection in early lactation. Milk samples for bacteriology and somatic cell count (SCC) were collected from both glands of 400 goats in four herds. Bacteria were isolated from 28% (222/800) of the total glands sampled. Coagulase negative staphylococcus (12.9%), *Corynebacterium* spp. (11.5%) and *Staphylococcus aureus* (1.4%) were the most prevalent isolates. Infected glands had a significantly higher SCC than uninfected glands (473 x 10^3 (399 –563 x 10^3) vs. 123 x 10^3 (112 –136 x 10^3), geometric mean SCC and 95% confidence interval; $P < 0.05$). Infection increased SCC and the degree of increase in SCC varied between pathogens.

Keywords: goat; mastitis; somatic cell count; bacteriology.

INTRODUCTION

Mastitis is an inflammation of the mammary gland often caused by bacterial infection. In dairy goats, mastitis is usually a subclinical infection, although clinical mastitis does occur. Mastitis results in an increase in SCC, decrease in milk quality and a reduction in milk yield in goats (Dulin *et al.*, 1983; Sanchez *et al.*, 1999). The pathogens that cause both clinical and subclinical infections can be divided into two main groups. Major pathogens are defined as a bacterial species causing a high degree of pathology, whereas minor pathogens have low pathogenicity. In cattle, *Staphylococcus aureus* (SA), *Streptococcus agalactiae*, *Streptococcus dysgalactiae* (SD), *Streptococcus uberis* (SU), and *Esherichia coli* are regarded as major pathogens.

Coagulase negative staphylococci (CNS) have been reported to be the most common isolates found in goats' milk in a number of New Zealand and overseas studies. Coagulase negative staphylococcus prevalences of between 23% and 29% have been reported in dairy goats (Manser, 1986; Lerondelle *et al.*, 1992; McDougall, 2000).

Subclinical intramammary infection is the major cause of increased SCC in dairy goats (de Cremoux *et al.*, 1995). Goats' SCC is also influenced by lactation number, stage of lactation, milk yield (Wilson *et al.*, 1995), breed, oestrus, management conditions (Poutrel *et al.*, 1997) and caprine arthritis-encephalitis virus (CAE) infection (Ryan *et al.*, 1993).

The aim of this research was to quantify the prevalence of bacterial infection and the different bacterial species in the mammary gland of dairy goats, during early lactation, in the Waikato region of New Zealand. Additionally, the effect of infection on SCC was evaluated.

MATERIALS AND METHODS

A total of four hundred dairy goats, 100 from each of four herds, were selected by sampling every second or third goat as they came into the afternoon milking. Goats in two of the herds were housed and fed indoors by cutting and carting pasture, while the other two herds were outdoor herds that grazed pasture between milkings (Table 1). All the goats were fed some form of mixed grain during milking, which occurred twice daily. Sampling occurred in August 1999 when the goats had been lactating for between 1 and 7 weeks. A ~5 ml sample was expressed from each mammary gland of the selected goats into a factory-clean vial, after teat sterilisation. Sterility was obtained by scrubbing the teat ends with cotton wool moistened in 70% methanol. The milk samples were refrigerated overnight before submission to the laboratory where 10ml of milk was streaked onto a sheep-blood agar plate and incubated at 37°C for 48 hours. Bacteria were speciated on the basis of colony morphology, Gram's stain, haemolysis pattern, aesculin reaction, tube coagulase and CAMP tests. Somatic cell counts were determined from a ~20ml milk sample of each half taken immediately after the milk sample for bacteriology. The SCC was determined using a Fossomatic 5000 counter.

Prevalence of infection was defined as the number of glands (or goats) from which a bacterial pathogen was isolated divided by the total number of glands (or goats) sampled. Differences in prevalence between herds and between age groups (coded as 1-2, 3, 4-5, >5 years) were tested by c^2. Somatic cell count was log ten transformed before analysis as the SCC were not normally distributed. Somatic cell count from glands infected with different pathogens was analysed by one-way ANOVA and these groups compared by least significant difference (LSD). Glands were assumed to be independent for analysis. For SCC, all pathogens were analysed separately by species and then by pathogens classified as major (SA, SD, SU) and minor pathogens (CNS, Corynebacterium (Coryn), *Proteus mirabilis* and *Enterococcus* spp).

RESULTS

Nine different pathogens were isolated including SA, SU, SD, CNS, Coryn, *Bacillus* spp. (BAC), *Coliforms* (coli), *Enterococcus* spp., and *Proteus mirabilis*. Coagulase negative staphylococcus was the most common isolate followed by Coryn and SA (Figure 1, Table 2). Bacteria were isolated from 28% (222/800) of the total glands sampled (Table 1). Of the 400 goats tested, 59.8% were uninfected in either gland, 25.0% were infected in one gland and 15.2% were infected in both glands. The prevalence of infection increased significantly with age ($P<0.05$; Figure 2). There was also a significant difference in the gland and animal prevalence between the herds ($P<0.05$; Table 1).

Infected glands had a higher geometric mean SCC than uninfected glands (474 x 10^3 (399 – 563 x 10^3) cells/ml vs 123 x 10^3 (112 – 136 x 10^3) cells/ml, respectively, geometric mean and 95% confidence interval; $P < 0.05$; Table 2). Glands infected with SA had a significantly higher SCC than uninfected glands (2047 x 10^3 cells/ml vs 123 x 10^3 cells/ml; $P < 0.05$, Table 2). The SCC of a gland infected with a major pathogen was significantly higher than glands with minor pathogen infections or no infection (800 x 10^3, 481 x 10^3, and 123 x 10^3 cells/ml, respectively, $P < 0.05$).

In goats with one infected gland, the SCC of the contralateral gland was higher than goats in which both glands were uninfected (161 x 10^3 (125 – 207 x 10^3) cells/ml vs. 117 x 10^3 (105 – 129 x 10^3) cells/ml, geometric mean and 95% confidence interval respectively; $P < 0.05$).

There was a positive relationship found between the prevalence of infection and average SCC at herd level (SCC = 18.5 x % infected glands + 55.9 (x 1000); adjusted R^2= 0.68; P = 0.11; Table 1).

TABLE 1: Goat herd background information including housing and herd size, prevalence of infection for each mammary gland and animal, and the average somatic cell count for the sampled animals.

Herd	Housing	Total herd size	Gland prevalence		Animal prevalence	Average SCC
			n.	%	%	(x 1000)
A	Outdoor	275	86	43.0 [a]	59.0[a]	801[a]
B	Indoor	300	57	28.5 [b]	43.0[b]	768[a]
C	Indoor	480	55	27.5 [b]	41.0[b]	484[b]
D	Outdoor	250	24	12.0 [b]	18.0[c]	236[b]
Total/Average			222	27.8	40.2	572

[a, b] Herds with different superscripts differ significantly (P<0.05)

TABLE 2: Prevalence of each pathogen, the geometric mean somatic cell count (SCC) and 95% CI for the infected goat mammary glands.

Pathogen	Prevalence		SCC Mean **	95% CI	
	n.	%*	(x 1000)	Lower	Upper
Staph aureus	11	5	2047 [f,g]	484	8662
Strep uberis	4	2	136 [a,b,c,d,f]	12	1497
Strep dysgalactiae	2	1	330 [a,b,c,d,e,f]	72	1505
Coagulase negative Staphylococcus	102	46	518 [c,d,e,f]	401	671
Coryneforms	91	42	373 [b,c,d,e,f]	306	455
Coliforms	4	2	672 [c,d,e,f,g]	57	7925
Other°	5	2	553 [b,c,d,e,f]	70	4342
All Infected	219		474	399	563
All "No growth"	573		123 [a,b,c]	112	136

* % of infected mammary glands.
° Includes *Proteus mirabilis* and *Enterococcus spp.*
** Figures with different superscripts were significantly different (P<0.05)
Eight goats are missing due to missing SCC data

FIGURE 1: Prevalence of bacterial species from 800 goat mammary glands (No growth (ng), *Staphylococcus aureus* (SA), *Streptococcus uberis* (SU), *Streptococcus dysgalactiae* (SD), Coagulase negative staphylococcus (CNS), *Corynebacterium* (Coryn), *Coliforms* (Coli)).

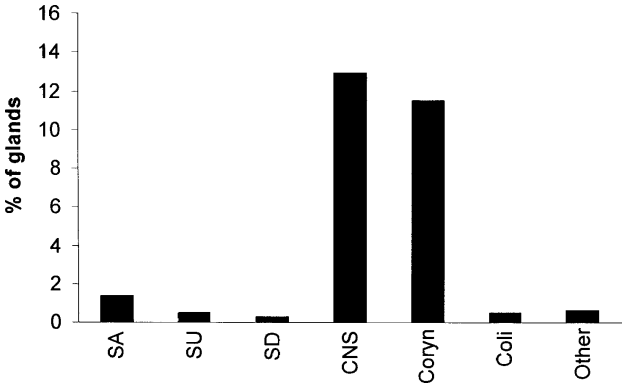
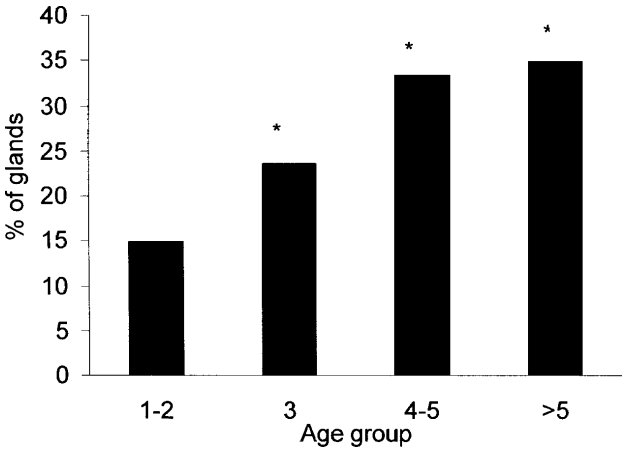


FIGURE 2: The effect of age on dairy goat udder half prevalence of infection (*prevalences differ significantly from the 1 and 2 year olds; P < 0.05).



DISCUSSION

The prevalence of infection was 40.2% of goats and 28.0% of glands in the present study (Table 1). These results are consistent with other studies by Manser (1986), Contreras *et al.* (1995) and Sanchez *et al.* (1999), who found between 30% and 47% of goats infected and 18% and 36% of glands infected, respectively.

CNS was the most commonly isolated organism here and in other studies (Dulin *et al*., 1983; Hunter, 1984; Lerondelle *et al*., 1992; Boscos *et al*., 1996; Poutrel *et al*., 1997; McDougall, 2000) (Table 2). Staphylococci are the main cause of clinical and subclinical mastitis in goats. Coagulase negative staphylococcus are commensals of the skin of the teat, the streak canal and the milker's hands (Smith & Roguinsky, 1997). While some consider CNS to be an insignificant pathogen in goats' (Hunter, 1984; Manser, 1986), others report that these infections may become chronic and lead to udder pathology, elevated SCC and decreased production (Smith and Roguinsky, 1977; Dulin *et al*., 1983; Poutrel and Lerondelle, 1983). Our results tend to agree with the latter as SCC was found to be three times greater with CNS infection than with no infection (Table 2). However, further research is required to determine whether CNS infections significantly decrease milk production, elevate SCC and result in udder pathology.

Corynebacterium spp. was the second most common organism isolated (Figure 1). However, the SCC associated with *Corynebacterium* spp. infection was not significantly higher than that of uninfected glands. High prevalences of *Corynebacterium* spp. have been associated with a failure of teat antisepsis (Contreras *et al.*, 1997).

The prevalence of infection increased with age (Figure 2) as previously reported (Boscos *et al*., 1996; Sanchez *et al*., 1999). This may be due to the older animals becoming infected in an earlier lactation and remaining infected through the subsequent lactations (Dulin *et al.*, 1983). Changes in mammary physiology with succeeding lactations or following infection, may also result in increased susceptibility to infection.

The geometric mean SCC of the infected glands was approximately four times greater than that of uninfected glands (Table 2). A significant difference was found between the SCC of glands infected with major and minor pathogens. This result is comparable with findings by Lerondelle *et al.* (1992) and Poutrel *et al.* (1997). Both papers report that milk samples from glands infected with SA had a much higher SCC than samples from uninfected glands or glands infected with CNS. The SCC of glands from which SA, CNS or no pathogens were isolated, were reported as between 2443 and 7890 x 10^3, 932 and 1040 x 10^3 and 272 and 520 x 10^3 cells/ml, respectively (Lerondelle *et al.*, 1992; Poutrel *et al.*, 1997).

Infection in one gland was found to increase the SCC of the contralateral uninfected gland in the present study. Dulin *et al*. (1983) found a similar results, however, Lerondelle *et al*. (1992) report that in their study bacterial infection in one gland did not increase the SCC of the opposite gland. The difference between studies may be explained if different pathogens were present in the study populations and if they produced different levels of response in the contralateral gland.

It is concluded that approximately a quarter of glands were infected within 8 weeks of parturition. However, there is considerable unexplained variation in prevalence between herds. Bacterial infection was associated with increased SCC, and at herd level increased bacterial prevalence was associated with increased herd average SCC.

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