

AVMA 2013 guideline recommends use of a frontal site high on the forehead aiming towards the foramen magnum as an alternative site in horned goats. The OIE recommends the frontal site be used for gunshot only. Exact positioning of a PCB at the poll is poorly described in the literature. The objective of this study was to determine the optimal anatomical site for PCB placement in horned and polled goats to ensure brainstem disruption consistently occurs.

Materials and Methods

Eight cadaver skulls (horned and polled) were used to determine the ideal anatomical site for conducting euthanasia of goats. Using a metal protractor to evaluate the proper trajectory, anatomical sites were established for both horned and polled animals with the objective of determining simple and clear guidelines resulting in consistent placement of PCB for damage to the brainstem. Once determined these sites were confirmed as accurate by euthanasia of 10 anesthetized goats.

Results

The site determined to best result in brainstem damage from the cadaver study was on the midline

2 cm caudal to a line drawn between the lateral canthus of each eye. This site could also be determined by identifying the intersection of lines drawn from the lateral canthus of each eye to the middle of the opposite ear.

Confirmation of this site was established by the euthanasia of 10 adult anesthetized goats. Using the site as described above, investigators were able to effectively euthanize all 10 animals without the need for an adjunctive step to assure death. Post-mortem sagittal section of skulls demonstrated damage to the brainstem of all 10 goats using this site.

Significance

To ensure brainstem damage during euthanasia via penetrating captive bolt devices, the proper anatomical site must be used; otherwise animals are likely to undergo extreme distress. Frontal shots will not consistently result in penetration of the cranium and are unlikely to damage structures associated with the brainstem.

Producer concern and prevalence of subclinical intramammary infections between lactations on 10 dairy goat farms in Ontario, Canada

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Introduction

For many dairy goat producers, a key deciding factor for keeping does in the herd is the animal's ability to maintain milk production. Subclinical intramammary infections (IMIs) are known to decrease milk production in does by as much as 20% (Contreras et al, *Livest Prod Sci*, 2003). Somatic cell count (SCC) is a reliable and inexpensive predictor of infection in dairy cows; however, this measure is highly variable in goats depending on factors such milk production, stage of lactation, and estrus activity (Leitner et al, *J Dairy Sci*, 2004; Paape et al, *Small Rumin Res*, 2007; Persson et al, *Small Rumin Res*, 2014), making identification of infected glands by SCC level problematic. Thus, it is likely that producers underestimate infection prevalence on their

farms. While IMIs are possible throughout lactation, the highest risk period for infection is when does are transitioning from one lactation to the next. On many farms, goats are dried-off (i.e., milking is ceased) and during the dry period infections may go unchecked and new infections begin. In other situations, does are not dried-off between lactations. The aims of this study were 2-fold: 1) to assess the attitudes of the producers regarding IMIs on their farms, and 2) to determine the prevalence of these infections during the dry period.

Materials and Methods

A total of 400 does on 10 commercial farms in Southern Ontario (40 ± 19 does per farm) were studied. For each doe, 2 milk samples were aseptically collected

from each udder half, at the end of lactation (last day of milking, or “dry-off”) and in the next lactation (6 to 10 days post-kidding). Bacteriological analysis was performed according to established methodology, and samples were flagged as infected when 1 or more bacterial colonies were isolated. Basic practices, such as milking hygiene, were observed for each farm. A Spearman correlation was used to determine the relationship between producer attitudes and infection prevalence at kidding (Proc CORR, SAS 9.2). Infection prevalence at dry-off was compared to post-kidding prevalence using paired t-tests (Proc TTEST, SAS 9.2). Pre-kidding samples were missing for 2 farms; these farms were excluded from the between sample comparison but were considered in the correlation.

Results

When asked about subclinical IMIs on their farm, most producers expressed little to no concern, and there was no relationship between concern and infection prevalence ($R^2 = 0.006$; ns). The lack of concern was reflected in milking hygiene; none of the farms incorpor-

ated hygienic preparation of the udder prior to milking into their general practices. Subclinical IMI prevalence in at least 1 udder half was high, and increased from dry-off to after kidding (mean \pm SE: 40 versus $49 \pm 3\%$; $P = 0.02$). The prevalence of infection in both sides of the udder was similar before and after kidding (mean \pm SE: 12 versus $14 \pm 3\%$; ns). The spontaneous cure rate was high (mean \pm SD: $26 \pm 18\%$), but this was matched by a high rate of new infections (mean \pm SD: $30 \pm 8\%$).

Significance

These results illustrate a disconnect between producer concern by Ontario dairy goat producers and prevalence of IMIs in goats under their care. Subclinical IMI prevalence was high among the farms, and higher than previous estimates (5 to 30%; Contreras et al, *Livest Prod Sci*, 2003). Next steps are to inform the producers of the impact of these infections on doe welfare and milk production, and recommend practices for reducing prevalence. Incorporating some level of hygienic udder preparation prior to milking will be a key recommendation.

Comparison of *Staphylococcus aureus* from bovine and caprine milk

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Introduction

Staphylococcus aureus is a frequent cause of infection in humans and animals. It is the most common cause of chronic subclinical bovine mastitis. Genotypes of *S. aureus* associated with one host can be transmitted among species. The purpose of this study was to compare genotypes and antimicrobial susceptibilities of representative bovine and caprine *S. aureus* isolates, and determine possible interspecies transfer of genotypes. It was hypothesized that genotypes and antibiotic susceptibility patterns of *S. aureus* would be similar for bovine and caprine isolates.

Materials and Methods

Isolates of *S. aureus* included 32 caprine milks submitted to the Mastitis and Milk Quality Laboratory for diagnostics, and 60 bovine milks representative of the laboratory's database. Antimicrobial susceptibilities were determined against 12 antibiotics, and genotypes were

identified using pulsed-field gel electrophoresis following *Sma*I or *Cfr*9I digest. Genotypes were considered of the same group if they were $\geq 80\%$ similar. Testing by PCR for the *mecA* gene and specific DNA sequences was performed to identify methicillin resistant *S. aureus* (MRSA) and/or ST398, more commonly isolated from pigs, poultry, and humans.

Results

A total of 13 genotype groups were identified, with the proportion of common genotype groups (4/13) not differing from those specific to caprine dairies (3/13), and to bovine dairies (6/13). More caprine (9/32) than bovine (2/60) isolates were resistant to 3 or more antibiotics. ST398 was identified, as were resistant genotypes identical or closely related to human CDC MRSA strains, showing potential trans-infection from humans and other animals.