Prevalence of various microbial organisms isolated from dairy goat milk samples in central Kenya highlands

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Abstract
Six-hundred and thirty (630) apparently normal milk samples from dairy goat flocks in Nyeri district (Kenya) were examined over a three-month period to determine the prevalence of bacterial organisms. Bacteria were isolated in 28.7% of the milk samples (181/630) either as a single bacterial organism (92.8%) or mixed bacterial organisms (7.2%). The most prevalent bacterial organisms isolated were Staphylococcus spp. (60.3%) followed by Micrococcus spp (17.7%), Acinetobacter spp (5%), Actinomycetes spp (5%) and Streptococcus spp (1.1%). No Coliforms or yeast were isolated from any of the milk samples. The Staphylococcus spp were mainly comprised of Coagulase negative staphylococcus (64.3%) and Coagulase positive staphylococcus (35.7%), these organisms accounted for 37.5% and 22.7% of the total bacterial isolates respectively.

The isolation of bacteria in the apparently normal Caprine milk, some of which are important in clinical and sub-clinical mastitis (especially Staphylococcus spp) means that particular attention should be given to the management of these dairy goat flocks in order to avoid cases of clinical mastitis.

Introduction
Dairy goat farming in Kenya is rapidly becoming an important enterprise especially in the central highlands where land fragmentation has led to small pieces of land. In these areas animal feed resource base has been reduced to crop residues, weeds and shrubs which can not sustain dairy cattle farming. Since goats have a more efficient digestive system than dairy cows, i.e. are able to convert poor feed stuffs into animal protein (Semenye and Hutchcroft 1992), they would form an alternative dairy animal in the areas where feed availability and quality can not sustain dairy cattle farming. Keeping of two to three dairy goats in such areas would result in an increased farm productivity and also provide a small but an all year round source of milk protein to the farmer (Kinuthia 1997). For example, a Kenyan Toggenberg goat can provide up to 521Kg of milk in a lactation period of 240 days (KARI/ODA Manual 1996). However, dairy goat keeping could be affected by a variety of diseases amongst which udder infections would be very important.

In Kenya there is dearth of information concerning the prevalence of bacterial infections in mammary glands of dairy goats, only a preliminary study in free-range goats has been reported (Maina et al. 1993). This study was therefore, undertaken to determine the prevalence of microorganisms in the milk of dairy goats in central Kenyan highlands, which have the highest dairy goat population in Kenya.

Materials and Methods
The study was carried out in seven dairy goat farmer groups in Nyeri district in Kenya. All the does in different stages of lactation from all the dairy goat groups were sampled once a month for three months. The number of does sampled were 130 in the first month, 108 in the second month and 77 in the third month. The does were mainly German Alpine crosses (87%) with a few Toggenberg, Saanen and Galla crosses (13%). The mammary glands of the does were examined visually for any injuries and by palpation for consistency and warmth. Milk samples (20 ml) from each mammary gland half were aseptically collected into sterile Bijoux bottles and kept at 4°C during transportation to the laboratory. In the laboratory the milk samples were streaked onto sheep blood and MacConkey agar plates and incubated aerobically at 37°C for 48 hours. Significant bacterial colonies at 24 and 48 hours were selected and sub-cultured for 24 hours after which they were gram stained and biochemically tested and classified according to standard methods (Holt 1986).
Results
Bacterial organisms were isolated in 181 (28.7%) of the 630 milk samples examined (Table 1). Of the 181 milk samples, 174 samples (96.1%) had only one type of bacteria while seven milk samples had mixed bacterial isolates. Most of the bacteria (88.4%) were isolated from single mammary gland halves. Staphylococcal spp were the most prevalent bacteria, accounting for 63.6% of all the bacterial isolates. Within this group, the Coagulase negative staphylococci (CNS) were the most prevalent and comprised 64.3% of the staphylococcal organisms and 37.6% of the total bacterial isolates. This was followed by Coagulase positive staphylococcus (CPS) which accounted for 35.7% of the staphylococci and 22.7% of the total bacterial isolates. The second most common microorganisms group was Micrococcus, which accounted for 17.7% of all the bacterial isolates. The other bacterial organisms isolated were Acinetobacter spp 5%, Actinomycetes spp 5% and Streptococcus spp 1.1% and mixed bacterial organisms (7.2%).

TABLE 1. The prevalence of microorganisms isolated from normal Caprine milk samples in central Kenyan highlands.

<table>
<thead>
<tr>
<th>Organism</th>
<th>1st Sampling N=130*</th>
<th>2nd Sampling N=108*</th>
<th>3rd Sampling N=77*</th>
<th>All Samplings N=630*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Right</td>
<td>Left</td>
<td>Right</td>
<td>Left</td>
</tr>
<tr>
<td>N'</td>
<td>95(73)</td>
<td>82(62)</td>
<td>81(75)</td>
<td>76(70)</td>
</tr>
<tr>
<td>CNS</td>
<td>15(12)</td>
<td>16(12)</td>
<td>12(11)</td>
<td>9(8)</td>
</tr>
<tr>
<td>CPS</td>
<td>6(5)</td>
<td>7(5)</td>
<td>7(7)</td>
<td>9(8)</td>
</tr>
<tr>
<td>Micrococcus spp</td>
<td>8(6)</td>
<td>13(10)</td>
<td>1(1)</td>
<td>4(4)</td>
</tr>
<tr>
<td>Acinetobacter spp</td>
<td>2(2)</td>
<td>1(1)</td>
<td>2(2)</td>
<td>2(2)</td>
</tr>
<tr>
<td>Actinomycetes spp</td>
<td>0(0)</td>
<td>3(4)</td>
<td>1(1)</td>
<td>3(3)</td>
</tr>
<tr>
<td>Streptococcus spp</td>
<td>1(1)</td>
<td>0(0)</td>
<td>0(0)</td>
<td>0(0)</td>
</tr>
<tr>
<td>Other spp</td>
<td>1(1)</td>
<td>3(4)</td>
<td>1(1)</td>
<td>2(2)</td>
</tr>
<tr>
<td>CNS + Micrococcus spp</td>
<td>1(1)</td>
<td>1(1)</td>
<td>1(1)</td>
<td>2(2)</td>
</tr>
<tr>
<td>Actinomycetes + others</td>
<td>1(1)</td>
<td>1(1)</td>
<td>1(1)</td>
<td>0(0)</td>
</tr>
<tr>
<td>Acinetobacter + others</td>
<td>0(0)</td>
<td>2(2)</td>
<td>1(1)</td>
<td>1(1)</td>
</tr>
<tr>
<td>CPS + others</td>
<td>0(0)</td>
<td>1(1)</td>
<td>0(0)</td>
<td>0(0)</td>
</tr>
</tbody>
</table>

N' = Number of milk samples (a) for either (right or left) mammary gland halves and (b) for all the mammary gland halves.
CNS = Coagulase negative Staphylococcus
CPS = Coagulase positive Staphylococcus
Number in parenthesis is percent (a) of the number of the quarter milk samples (b) total quarter milk samples and (c) of the total bacterial organisms (181).

Discussion
The prevalence of bacteria isolated from the milk samples was 28.7%. This was similar to the findings of by Dublin et al. (1983) and Bocos et al. 1996, who found that the prevalence of bacteria in Caprine milk without clinical mastitis was 39.0% and 29.0% respectively. However, the results of the present study differ from those of Manser (1986) and Kalogridou-Vassiliadou et al. (1992), who reported a higher percentage of bacteriologically positive Caprine milk samples (15-79%, and 81.4% respectively), and those of Ryan and Greenwood (1990) and Contreras et al. (1995), who reported a lower prevalence (16.9% and 18% respectively). The prevalence of bacteria in the milk of goats has been observed to be lower in hand milked goats than in the machine milked goats (Sheldrake et al. 1981). In our study, the does were hand-milked hence this could have influenced the prevalence of the bacterial isolation.

The finding that Staphylococcus spp. were the most prevalent bacteria in these flocks was similar to other observations (Contreras et al. 1995, Bocos et al. 1996). Among the
Staphylococcus spp, Coagulase-negative staphylococci (CNS) were the most predominant bacteria isolated (37.6%) from milk samples. This microorganism has been reported as the main bacterial organism associated with bacteriologically positive milk samples from lactating goats (Manser 1986, Boscos et al. 1996). However, it has been reported that CNS has been considered as non-pathogenic or of low pathogenicity for the mammary gland of domestic ruminants (Boscos et al. 1996). Generally, some observations have proposed CNS as one of the etiological agents of Caprine sub-clinical mastitis (Poutrel 1984).

There was a low prevalence of Actinomyces spp. and Streptococcal spp. in the milk samples. The main sources of infection of these organisms to dairy goats are infected dairy cows (Radosits et al. 1994). Thus, the absence of infected cattle around the environment of these does could have contributed to the low prevalence of these organisms. The high prevalence (28.7%) of bacterial isolation from apparently healthy udders shows that there were a high percentage of latent infections in these dairy goat flocks. This also shows that presence of bacterial organisms in the mammary gland halves of dairy goats does not necessarily result in clinical mastitis. However, the effect of these latent infections in the future status of the mammary glands of the does needs to be investigated.

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References


