DISCUSSION AND CONCLUSIONS

1. Discussion

The objective of this study was to determine out the microbiological status (quantitatively and qualitatively) of raw goat milk and some potential risk factors associated with it, from commercial dairy goat farms in Indonesia. Despite of a limited sampling location, which include only three commercial dairy goat farms located in the Bogor District, West Java Province, it was likely that the results of this study would be useful to show some real data about the present situation of the microbiological status of goat milk in Indonesia. This was due to the fact that in Indonesia, dairy goat farms were concentrated in the West and Central Java Provinces and some other farms located in other provinces located on Java Island. Therefore the majority of the commercial dairy goat farms had approximately similar general characteristics of the management and milking practices.

It should be noted also that the milk produced from all sampling farms within this study, as well as from other dairy goat farms, was sold and consumed in raw condition by the consumers. Moreover, in Indonesia, the consumers preferred to consume the goat milk as fresh as possible, since they consider the milk to be fresher when they can consume it as soon as the milk is secreted from the goat udder.

Here, data on the counts and prevalence of indicator bacteria for the microbiological status of raw goat milk and also some potential risk factors associated with were obtained.

5.1.1 Quantitative data

There were 300 udder-half milk samples as the main sample and 30 bulk milk samples as a supporting sample collected from three commercial dairy goat farms with intensive breeding systems in the Bogor District, West Java Province, Indonesia. The samples were examined for the counts and presence of indicator bacteria, which
were TPC, coliforms, *Staphylococcus* spp., CPS and CNS. The information regarding some potential risk factors, which was predicted to have association with the indicator bacteria, was also assessed.

In this study the median values of indicator bacterial counts from overall udder-half milk samples were 3.74, 0.70, 3.00, 1.70 and 2.52 log cfu/ml for TPC, coliforms, *Staphylococcus* spp., CPS and CNS, respectively. Median values of indicator bacterial counts from overall bulk milk samples were 5.69, 2.98, 3.86, 3.66 and 3.32 log cfu/ml for TPC, coliforms, *Staphylococcus* spp., CPS and CNS, respectively.

Study or investigation reports regarding counts of bacteria in goat milk were very limited as compared to cow milk, and mostly concerned about proportion or prevalence of these bacteria. There was also no study/investigation report found in Indonesia regarding counts and prevalence of indicator bacteria in raw goat milk and potential risk factors associated with it.

This was due to the fact that commercial dairy goat farms in Indonesia just emerged about 10 – 15 years ago. In the past, goat milk was produced from backyard farming systems with a small number of animals. Today, the commercial dairy goat farms have from 100 to a thousand animals per farm.

The median of the TPC of overall udder-half milk samples in this study (3.74 log cfu/ml) was lower compared to the findings reported by Delgado-Pertinez *et al.* (2003) and Kyozaire *et al.* (2005). Delgado-Pertinez *et al.* (2003) reported that they collected udder-half goat milk samples from 28 farms in Spain and the mean value of TPC from those samples was 4.81 log cfu/ml. Whereas the mean values of TPC of 270 udder half milk samples collected from 3 commercial dairy goat farms which were using bucket milking machine, pipeline milking machine and hand milking machine in South Africa were 4.21, 4.56 and 4.68 log cfu/ml, respectively (Kyozaire *et al.*, 2005).
Other studies conducted in Switzerland and the USA reported lower TPC of bulk milk samples than here (5.69 log cfu/ml): the median of TPC of 344 bulk milk samples from three commercial dairy goat farms in Switzerland was 4.68 log cfu/ml (Muehlherr et al., 2003; Zweifel et al., 2005), whereas the mean of TPC of bulk milk samples from three commercial dairy goat farms located in Arkansas and Oklahoma was 2.95 log cfu/ml (Zeng and Escobar, 1996).

The results of this study for the bulk milk samples were relatively higher as compared to the following findings: Morgan et al. (2003) collected bulk milk samples from intensive breeding systems of small and medium scale dairy goat farms in France. The mean values of goat milk from those farms in France were 5.03, 2.15 and 4.34 log cfu/ml for TPC, coliforms and Staphylococcus spp. (CPS and CNS), respectively. Another finding was reported by Feschino et al. (2002), who collected 66 bulk milk samples from 10 dairy goat farms during a six month period in Italy. The mean values of TPC, coliforms, S. aureus and CNS of Italian raw goat milk samples were 4.70, 2.96, 3.07 and 3.11 log cfu/ml, respectively.

However, these study results were relatively lower compared to the finding which was also reported by Morgan et al. (2003) from small and medium scale dairy goat farms under extensive breeding systems in Greece and Portugal. They reported that mean values of indicator bacteria in goat bulk milk in Greece and Portugal were TPC = 7.5 and 7.6 log cfu/ml; coliforms = 6.25 and 6.39 log cfu/ml; Staphylococcus spp. = 5.23 and 4.28 log cfu/ml, respectively. The results of CNS counts here were also comparable to the finding of CNS counts in three commercial milking goat herds in the UK by Hall and Rycroft (2007), which ranged from 3.00 to 5.08 log cfu/ml.

This study result of coliform counts was comparable to the finding reported by Little and de Luvois (1999), who did a pilot study to determine microbiological quality of unpasteurized milk from goat and sheep taken along the food chain in England and Wales, UK. They found that 11 out of 100 unpasteurized goat milk samples had coliform counts of more than 2 log cfu/ml, whereas 38 samples contained coliform counts less than 2 log cfu/ml and no coliforms were detected in the rest of the samples.
Little and de Luvois (1999) also found that 15 out of 100 unpasteurized goat milk samples were \textit{S. aureus} positive and 6 out of 15 samples had \textit{S. aureus} counts of more than 2 log cfu/ml.

The indicator bacterial counts from udder-half milk samples were significantly different (P<0.05) among farms except for the CPS count (Table 3), but for the bulk milk samples, only the coliform counts were observed to have statistically significant difference among farms (Table 18). The results from bulk milk samples was contrary to a study which also used bulk milk samples carried out by Foschino et al. (2002). They reported that in Italy, sample source was the major factor affecting the microbial composition of goat milk, significant differences (P<0.01) were observed among samples from different farms for TPC, coliforms, lactococci, lactobacilli and halotolerant bacteria.

In general, microbiological standards for fresh or raw milk were based on bulk milk samples, however in this discussion, the results from bulk milk as well as udder-half milk samples were compared to the available standards. The median values of TPC in overall milk samples either from udder-half milk or bulk milk did not exceed the maximum limit of TPC in Indonesian, German as well as European standards. For coliforms and CPS (as compared to \textit{S. aureus} standard), none of three standard maximum limits were exceeded by median values of coliforms and CPS from overall udder-half milk samples. However, the median values of these bacteria from overall bulk milk samples were beyond the maximum limits of those standards.

5.1.1.1 Indicator bacterial counts of udder-half milk samples among levels of some factors

The indicator bacterial counts except for CPS from udder-half milk samples were significantly different among levels of breeds. The difference of TPC among breeds of goats was in line with a study conducted by Zeng and Escobar (1996), which found that Nubian does produce milk with higher TPC than Alpine does (P<0.05). However this result was contrary to findings reported by Zweifel et al.
In Switzerland, which found that the median of TPC was not significantly different among breeds of goats.

In the parity factor, the indicator bacteria counts, except for coliforms, were significantly different among parity levels. TPC, Staphylococcus spp., CPS and CNS counts tended to increase as the does got older. Only for Staphylococcus spp. group bacterial counts, the statistically significant differences were observed among lactation stages.

Counts of indicator bacteria, except for coliforms, based on the teat end condition were observed to have statistically significant differences, in which normal teat ends had significantly lower counts of bacteria compared to teat ends with a smooth rough ring form. A similar pattern was found for the teat shape condition and udder inflammation status. In the teat shape condition, only the TPC showed a statistically significant difference. The TPC was significantly increased as the teat shape condition was more dilated, whereas in the normal udder, the counts of indicator bacteria except for coliforms had significantly lower counts compared to the udder with inflammation.

In the factor of milk appearance, indicator bacterial counts were not significantly different between the normal and abnormal milk appearance, except for TPC. TPC was significantly higher in the abnormal milk appearance than the normal one.

5.1.2 Qualitative data

Overall prevalence of coliforms, Staphylococcus spp., CPS and CNS from udder-half milk samples were 46.3, 78.7, 37.7 and 66.0%, respectively and from bulk milk samples were 86.7, 96.7, 76.7, and 86.7%, respectively.

In the udder-half milk samples, statistically significant difference was observed only for prevalence of coliforms and CNS among farms, whereas in bulk milk samples no statistically significant difference was observed among prevalence of indicator bacteria within farm level.
The prevalence of coliforms in these study results, either from udder-half or bulk milk samples, were higher compared to a study result of coliform prevalence in unpasteurized goat milk in England and Wales, UK by Little and de Luvois (1999). They reported that the prevalence of coliforms was 12%. However within the farm level, farm 1 had a lower prevalence of Coliforms with only 6% in the udder-half milk samples.

Prevalence of *Staphylococcus* spp. both from udder-half and bulk milk samples from this study were higher to the prevalence of these bacteria reported in the previous reports from other countries by Kalogridou-Vassiliadou (1991); Contreras *et al.* (1995); White and Hinckley (1999); Sanchez *et al.* (1999); Ndegwa *et al.* (2001); Leitner *et al.* (2004); Moroni *et al.* (2005b) and Leitner *et al.* (2007), which were 3.1 (Greece), 4.1 (Italy), 38.2 (USA), 70.0 (Spain), 32.9 (Israel), 1.6 (Italy) and 28.8% (Israel), respectively.

However the prevalence of *Staphylococcus* spp. in the bulk milk samples found here was comparable to the study results reported by Contreras *et al.* (1999). They examined bulk tank milk from commercial dairy goats in Maryland, USA and it was found that most of the pathogen isolated was *Staphylococcus* spp. with 95.7% of prevalence.

As reported by many others studies, this study also recorded CNS as the most prevalent pathogens within *Staphylococcus* spp. *Staphylococcus* spp. is the most prevalent pathogen responsible for IMI in small ruminants and CNS is the most prevalent one within this group of bacteria (Contreras *et al.*, 2007). Although less pathogenic than *S. aureus*, CNS can also produce persistent subclinical mastitis, significantly increase MSCC and cause clinical mastitis (Deinahofer and Pernthaner, 1995; Contreras *et al.*, 1997).

Most studies on the IMI estimated the prevalence by halves and not by animals because the half is an anatomically independent unit (Sanchez *et al.*, 1999).
In this study 64.7% (97/150) of goats had infections in both of their udders (positive bacteriological isolation of *Staphylococcus* spp.) and it was found also that counts and prevalence of indicator bacteria were not observed to have statistically significant differences between samples from left and right udders (Table 20 and 21).

The results of this study showed that the CNS prevalence was higher compared to CPS. The CNS and CPS prevalence from udder-half milk samples were 66% and 37.7%, respectively.

Following studies reported to have lower CNS and CPS prevalence of udder-half goat milk samples than here: 44.5% and 17.2%, respectively in Greece (Kalogridou Vassiliadou, 1991); 61.1% and 18.5%, respectively in Greece (Boscos et al. 1996), 9.6% in Ethiopia (Wakwoya et al., 2006); 17.9% in Israel (Leitner et al., 2007) and 47% in UK (Hall and Rycroft, 2007) (the last three data only for CNS).

Whereas these following studies reported higher CNS prevalence compared to these study results: 76.1% in Austria (Deinhefer and Pernthaner, 1995); 71.4% in Spain (Concas et al., 1997); 68.1% in USA (White and Hinckley, 1999). Comparable results were found from the study in dairy goat farms in Vermont, USA which reported 66.7% prevalence of CNS from udder-half milk samples taken in 40 days after parturition (McDougall et al., 2002).

### 8.1.2.1 The assessment of associations between sample prevalence of indicator bacteria and potential risk factors

The evaluation of several potential risk factors in its association with the presence of indicator bacteria in the samples was shown in Tables 10 – 16. All potential risk factors were analyzed for the prevalence of each indicator bacteria both by univariate (Chi-square test) and by multivariate analysis of the logistic regression test. Multivariate analysis permits estimation of the real impact of a particular factor without interaction from other factors. The results show that some of those potential risk factors could be considered to be risk factors, which increased the risk of presence of each indicator bacteria.
Breed of goats: these study results show that the breed of goats was only significantly associated with the presence of coliforms in the samples, and the Saanen breed had a significantly higher chance of coliform contamination (P<0.05) than other breeds. No statistically significant association was found for the breed of goats with other indicator bacteria. This result was comparable with the previous finding by Boscos et al. (1996) who reported that no breed differences were observed with regard to the type of bacteria isolated.

Parity: a significant association of the parity factor with the presence of indicator bacteria was observed only in CPS. Further analysis by logistic regression test showed that only goats in fifth parity had a significantly positive association and higher risk of having CPS in the samples (OR=6.033, P=0.050, 95%CI=0.999, 36.455). However, numerically the prevalence of indicator bacteria tended to increase as the does got older (increase in parity) in every indicator bacteria. This result was also comparable to some previous reports, i.e. Boscos et al. (1996), who also found that no parity differences in the prevalence of type of bacteria isolated, but the proportion of positive samples was significantly higher in multiparous than in primiparous Saanen goats; Sanchez et al. (1999) who reported that prevalence of IMI (which was mostly caused by Staphylococcus spp. [P=70%]) increased with the age of the goats, and they also found positive statistical association between subclinical intramammary infection and goats in greater than fifth parity (PR=1.80; 95% CI=1.21, 2.68); McDougall et al. (2001) reported that significant association in infection prevalence was found between goats older than 4 years and less than 4 years old and Moroni et al. (2005b) who reported that goats in third and fourth parities had significantly more infection than goats in first or second parities. McDougall et al. (2002) stated that increasing prevalence with age may be due to the increased length of exposure to pathogens in older compared to younger animals. Additionally, where the duration of infection was long and the spontaneous cure rate was low, the prevalence would increase.

Lactation stage: a significant association in univariate analysis was found for the lactation stage with the presence of Staphylococcus spp. and CPS, but further
Evaluation by logistic regression showed that the lactation stage was not a risk factor for those bacteria (Table 13 and 15). Bergonier et al. (2003) stated that the incidence of clinical IMI did not vary with the lactation stage in the same way as in dairy cattle, on the contrary, higher rates were observed during the first third of lactation. This statement was in agreement with the results presented in Tables 13 and 15. Bergonier et al. (2003) also stated that the variations of subclinical IMI incidence according to the stage of lactation should be assessed by systematic, monthly milk culturing of large numbers of healthy udders, and this kind of a study was very rare. However, a finding reported by Moroni et al. (2005b) was contrary to this study result. They concluded that later stages of lactation had more infection than earlier lactation stages.

Udder inflammation status: another potential risk factor, which was found to have a positive association with indicator bacteria, was the udder inflammation status. The status of udder inflammation was based on a CMT score by following the method suggested by Wakwoya et al. (2006). Udder inflammation status was found to have a significant association with the presence of Staphylococcus spp. and CPS. Moreover, results of logistic regression confirmed that the udder inflammation status was a risk factor for the presence of both bacteria in the milk samples. The udders with inflammation had a strong and significant association with and higher prevalence of Staphylococcus spp. [OR= 2.490, P= 0.002, 95%CI= 1.403, 4.418] and CPS [OR= 2.622, P= 0.001, 95%CI= 1.487, 4.623] compared to the udders without inflammation.

None of the potential risk factors was significantly associated with the presence of CNS in the samples, but as a member of Staphylococcus spp. and despite of statistical insignificance, numerical prevalence of CNS in the udder with inflammation was higher than in the normal udder (Table 16). Therefore the udder inflammation status could be used as an indicator of the presence of CNS in the milk samples.

Other potential risk factors (udder symmetry, udder hygiene status, teat end condition, teat skin condition, teat shape and milk appearance) were found to have no statistically significant association with the presence of indicator bacteria in the
samples either in univariate or multivariate analysis. Those potential risk factors were unrelated to indicator bacteria detection rates.

2. California Mastitis Test results

CMT was conducted on 300 udder-half milk samples for determining the udder inflammation status as well as for an indicator of the presence of subclinical mastitis or IMI. Regarding the CMT score, 62.7% (188/300) of the samples were CMT positive and 37.3% (112/300) of the samples were CMT negative. This result was different compared to the study result reported by Wakwoya et al. (2006) in Ethiopia, that showed from 680 udder-half goat milk samples, 278 (40.9%) milk samples were CMT positive, while 402 (59.1%) samples were CMT negative. On the other hand, 28 (10.1%) of the 278 CMT positive milk samples yielded no bacterial growth while the remaining 250 (89.9%) samples were also culture positive in which diverse bacterial pathogens were identified. They did not present a further proportion of the bacterial growth in CMT positive-negative samples for each identified bacteria.

In the isolation of indicator bacteria using conventional bacteriological isolation method, it was found that for coliforms 47.3% (89/188) of CMT positive samples yielded coliform growth, while the remaining 52.7% (99/188) of CMT positive samples yielded no coliform growth. On the other hand, 44.6% (50/112) of the CMT negative samples yielded coliform growth and 55.4% (62/112) of the CMT negative samples yielded no bacterial growth.

For the *Staphylococcus* spp., 84.0% (158/188) of CMT positive samples yielded bacterial growth and the rest [16.0% (30/188) of CMT positive samples] yielded no bacterial growth. Whereas 69.6% (78/112) of CMT negative samples yielded bacterial growth and the rest [30.4% (34/112)] yielded no growth.

In CPS, 44.1% (83/188) of CMT positive samples yielded bacterial growth and the remaining 55.9% (105/188) yielded no bacterial growth. In CMT negative samples, 26.8% (30/112) yielded bacterial growth and for the rest of the samples (73.2% (82/112)) yielded no growth of bacteria.
For CNS, 69.68% (131/188) of CMT positive samples yielded bacteria growth and the remaining 30.32% (57/188) of the samples yielded no growth of bacteria. In CMT negative samples, 59.82% (67/112) yielded bacterial growth, whereas 40.18% (45/112) of the remaining samples yielded no growth of bacteria.

The study results showed that except in coliforms and CPS, the proportion of CMT positive samples which yielded bacterial growth was higher compared to CMT positive samples with no bacterial growth. Wakwoya et al. (2006) explained that the CMT positive and culture negative samples (those which yielded no bacterial growth) could be partly explained in that the udder could be injured and was recovering from infection or the infection could be not due to a bacterial pathogen. It could also be due to an organism such as mycoplasma, which requires special media and cannot be detected using routine bacterial isolation techniques.

The proportion of CMT negative samples that yielded bacterial growth in each indicator bacteria, except for CPS, in this study was relatively higher than a report from Wakwoya et al. (2006). They found that from a total of 402 milk samples taken as CMT negative, 124 (30.8%) yielded bacterial growth on cultures. This study result was also higher compared to the study results in Kenya by Ndegwa et al. (2000), who reported that 22.5% of 568 CMT negative samples yielded bacterial growth. They suggested that bacterial organisms isolated from the CMT negative samples were either a latent cause of infections or did not stimulate any significant increase in somatic cell counts.

McNemar Chi-square test results showed that statistically significant differences (P<0.05) between CMT and bacterial isolation results were observed for coliforms, *Staphylococcus* spp. and CPS. It meant that the ability of two tests/methods to detect true proportions of indicator bacteria in the same samples was significantly different. Only in the CNS isolation, the results of CMT and bacterial isolation were not significantly different (P=0.419) and the sensitivity of the CMT test was moderate (66%) whereas specificity was relatively low (44%), even though the agreement between the two test results was poor (κ = 0.100).
The results were comparable with findings by Ndegwa et al. (2000), who reported no significant direct relationship between bacterial isolation and CMT in goat milk from dairy goat farms in Kenya; Winter and Baumgartner (1999) reported from their study results in Austria regarding the evaluation of CMT reaction in goat milk, that CMT was not specific for infected udder halves, but can be used as an additional diagnostic tool concerning goat mastitis without overestimation, due to the influence of different factors in cell counts.

Another previous report was comparable to the result here, Schaeren and Maurer (2006) had evaluated the relationship of subclinical udder infection and individual SCC as well as CMT in three dairy goat herds in Bern, Switzerland. They concluded that the relation between CMT reactions and udder infections was not very close. More than 20% of mammary halves infected with CNS showed negative CMT reactions. On the other hand, 25% of the samples from mammary halves without a proven infection reacted positively.

However, these study results showed that despite of statistical significance, numerically the proportion of CMT positive samples which yielded bacterial growth was higher compared to CMT negative samples which yielded bacterial growth in all indicator bacteria.

McDougall et al. (2001) stated that definite detection of infected animals relies on the positive culture of pathogens from aseptically collected milk samples. However bacteriology has limitations due to the requirements for laboratory support, the time delays for culture to occur and the costs associated with the bacteriology assessment. Contreras et al. (1996), Perrin et al. (1997) and McDougall et al. (2001) stated that CMT is a subjective screening test based on scoring the degree of gel formation of a milk and bromocresol reagent mixture. The CMT score has been shown to be positively associated with SCC and with the probability of bacterial infection.

McDougall et al. (2001) also stated that of the “animal side test” CMT was superior to other indirect test such as impedance. They concluded from their study that wide variation in the test characteristics of SCC, CMT and impedance were
reported in sheep and goat. This was at least partly due to differences in the infection within the population studied. Their study result showed the effect of changing prevalence on the test performances. Perrin et al. (1997) also suggested that CMT had to be used carefully for low milk-yield goats or for late lactations.

Furthermore Gonzalez-Rodriguez and Carmenes (1996) reported their study results about the accuracy of CMT that was higher when compared with SCC, but an increase of false-positive samples was observed toward the end of lactation, which also implied a decrease in the predictive value of positive results. They also concluded that samples taken in the last month prior to the dry therapy would have a high error rate in predicting infected glands. They suggested taking the samples in the second and third months after parturition. Constant CMT positive reactions should be submitted for bacteriological analysis.

Based on these study results and the above mentioned previous reports, it should be stated that CMT can be used as an effective, reliable, cheap and “farm and farmer friendly test” for screen testing of IMI or subclinical mastitis in dairy goats.

5.2 Conclusions

Three hundred udder halves and thirty bulk milk samples from three commercial dairy goat farms, in the Bogor District, West Java Province, Indonesia were investigated for counts and prevalence indicator bacteria, which were TPC, coliforms, Staphylococcus spp., CPS and CNS. Ten potential risk factors were also evaluated in relation to the counts and prevalence of indicator bacteria.

The median values of the indicator bacterial counts from overall udder-half milk samples were 3.74, 0.70, 3.00, 1.70 and 2.52 log cfu/ml and from the bulk milk samples 5.68, 2.98, 3.86, 3.65 and 3.32 log cfu/ml for TPC, coliforms, Staphylococcus spp., CPS and CNS, respectively.
The indicator bacterial counts from udder-half milk samples were significantly different (P<0.05) among farms except for the CPS count, whereas for the bulk milk samples, it was only the coliform count that was observed to have statistically significant difference among farms.

None of the median values of overall udder-half milk samples exceeded the maximum limit of the available microbiological standards for TPC, coliforms and S. aureus, however the samples had maximum values which exceeded the maximum limit of those standards. In the bulk milk samples, it was only the median value of TPC that was below the maximum limit of the TPC standards, but all of the indicator bacteria had maximum values beyond the maximum limit.

Statistically significant differences (P<0.05) of indicator bacterial count among breeds of goat in each farm were observed only for TPC in Farm 1 and 3, coliforms and CNS count in Farm 3. For udder-half milk samples, 3 out of 10 factors, which were udder symmetry, udder hygiene and teat skin condition, had no statistically significant differences of indicator bacterial counts among their levels. The indicator bacterial counts within the level of the other seven factors varied statistically.

The overall prevalence of coliforms, Staphylococcus spp., CPS and CNS from udder-half milk samples was 46.3, 78.7, 37.7 and 66.0%, respectively, and from the bulk milk samples 86.7, 96.7, 76.7, and 86.7%, respectively. Prevalence from both types of samples was relatively higher compared to the majority of the study results from other countries. Data on the prevalence of indicator bacteria from udder-half milk samples among breeds of goat in each farm showed that statistically significant difference (P<0.05) was observed only for the prevalence of coliforms and Staphylococcus spp. among breeds of goat in Farm 3 and Farm 1, respectively.

Some of the potential risk factors could be considered to be risk factors which increase the risk of the presence of indicator bacteria in the milk samples, i.e. the Saanen crossbreed, that had a significantly higher chance of coliform contamination (P<0.05) than other breeds; fifth parity, that had a significantly positive association
and higher risk of having CPS in the samples, and udders with inflammation, that had
strong significant association and a higher chance of having contaminated samples
of Staphylococcus spp. or CPS, compared to udders without inflammation.

No statistically significant difference was observed either for counts or
prevalence of indicator bacteria between left and right udder milk samples.

A statistically insignificant difference (P>0.05) between the CMT result and
the bacterial isolation was only observed for CNS, but the agreement between the two
test results was poor (κ = 0.100) and the CMT had moderate sensitivity (66%) and a
relatively low specificity (44%). However, numerically, the proportion of CMT
positive samples that yielded bacterial growth was higher compared to the CMT
negative samples that yielded bacterial growth in all indicator bacteria. It was also
supported by the fact that udder with inflammation, which was determined based on
the CMT result, had been proved to have statistically significant higher results of
Staphylococcus spp. and CPS positive samples than udder without inflammation.

Therefore CMT could be used as an effective, reliable, cheap and “farm and farmer
friendly test” for screen testing of IMI or subclinical mastitis in dairy goats.