



Biochemical and Molecular Identification of Key Pathogens Causing Mastitis

Robert Shavulimo Shivairo

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Mastitis in dairy goats was investigated with the objective of establishing the effect of management and the identification of the key causative agents through common diagnostic procedures of somatic cell counts, bacteriological identification and, for the first time in goat mastitis, by use of Polymerase Chain Reaction. A cross-sectional survey, using a structured questionnaire was conducted in three agro-climatic regions of Coast, Nyanza and Rift Valley, with goat keeping clusters serving as sampling sub-units. The focus of the questions was on housing, feeding, labour, water sources, record keeping, socio-economic status of respondents and availability of extension service. California Mastitis Test (CMT) was done at the farm-level, Somatic Cell Counts (SCC) and bacterial isolation were done in the laboratory. Polymerase Chain Reaction (PCR) on the two key bacteria, Staphylococcus aureus and Escherichia coli were subsequently carried out on 16 randomly selected samples representative of the three dairy goat keeping agro-ecological zones. The management survey indicated that 56.9% of respondents were peasant farmers only 12% of respondents could afford hired labour. There was evidence of scarcity of quality water, with only 9% using water from rain catchment and the rest depending on wells, dams and rivers. There was no training package on dairy goats. The CMT scores for the two key organisms ranged between 2 and 3, making it a reliable test for udder infection. Somatic Cell Counts (SCC) was determined for 239 samples with scores ranging between 0.248 106 and 1.693 106 with a mean of 0.869 106. This study demonstrated significant SCC variations amongst the breeds, there was also significant variation in SCC scores for various locations. Other factors in the study were lactation length and parity all of which affected SCC scores. The bacterial isolation showed dominance of Staphylococcus aureus and Escherichia coli respectively. The two species of bacteria are significant indicators of the state of hygiene on the farms. The PCR identification of the two organisms showed that they were distributed in all three regions of study. There is a need for more intensive studies on the various diagnostic tools especially CMT, SCC, bacteriology and PCR to enable the development of quality standards in Kenya for goat milk which do not exist at the moment.



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