

Mastitis, an Economically Significant Bacterial Disease of Dairy Cattle Having Immense Public Health Importance: A Comprehensive & Exclusive Review

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ABSTRACT

Mastitis is a multietiopathogenic condition of mammary gland affecting dairy cows and remains the most economically important disease of dairy industries around the world. It is characterized by physical, chemical and microbiological changes in the milk and pathological changes in the glandular tissues of the udder¹. The changes in the milk include changes of colour, consistency and presence of abnormally large number of leukocytes. Production per cow due to the clinical and subclinical prevalence of mastitis is usually recognized as the main pathway in causing the economic losses due to the disease^{2,3}.

Key words: Dairy cattle, Mammary gland, Mastitis, Milk.

INTRODUCTION

Large numbers of infectious agents are responsible in causing the disease in dairy animals. Bacterial agents like *Staphylococcus spp.*, *Streptococcus spp.*, *Escherichia coli*, *Corynebacterium spp.*, *Klebsiella spp.*, *Pseudomonas spp.*, Mycoplasmal agents, fungal agents, viral agents are responsible for the disease^{4,5}. About 95% of intramammary infections are caused by *Staphylococcus spp.* and *Streptococcus spp.* The remaining 5% are caused by other organisms (NAIP Sub-Project at PD-ADMAS). *Staphylococcus aureus* is a major pathogen in dairy cattle mastitis⁵⁻⁷. Streptococcal species isolated from dairy cows with clinical mastitis were obtained from mastitis research workers in Florida, Louisiana, New York, Vermont, Washington, and West Virginia.

Reported cases of mastitis and related scientific investigations

Reports from different parts of India indicate high prevalence of both subclinical and clinical mastitis in dairy herds⁸. Frequency of occurrence of mastitis is influenced by different managerial, environmental and genetic factors. Klastrup *et al.*⁹ estimated that 25% of susceptibility to infection is attributed to environmental factors, 20% to genetic factors and 50% to herd management. Therefore prevalence of mastitis can be used as a litmus test to judge the management practices and hygienic conditions of any organized dairy farm. Though there are a long list of microorganisms are held to be responsible for the disease, but the most common pathogens are *Staphylococci spp.*, and *Streptococci spp.*

Konte *et al.*¹⁰ reported one year observation on mastitis in dairy herds of pure bred Monthbeliared and Pakistani Zebu near Dakar, 28 cases yield 20 bacterial species, the commonest being *Staphylococcus aureus* (50%) and *E. coli* (36%). Nine cases of mixed infection with 2-5 species were considered to have developed after treatment failure in single infection.

Firat *et al.*¹¹ isolated the organisms from 406 cows with clinical and subclinical cases of mastitis. Out of 390 isolates which showed CMT positive, 132 (34%) were coagulase positive Staphylococci, 63 (16%)

coagulase negative Staphylococci, 51 (13%) gram negative bacteria, 28 *Streptococcus agalactiae*, 27 *Streptococcus uberis*, 22 *Streptococcus faecali* and 21 *Streptococcus dysgalactiae*.

Lafi *et al.*¹² claimed that the most common organism isolated from clinical cases of mastitis was coagulase positive *Staphylococcus* spp.

Turutoglu *et al.*¹³ examined 1594 mastitis milk samples and yielded aerobic bacteria from 1126 samples. Among the positive samples *Staphylococcus aureus* was 28%, *Staphylococcus epidermidis* 23%, *Streptococcus agalactiae* 19%, *E. coli* 8%, *Streptococcus dysgalactiae* 4%.

Waage *et al.*¹⁴ examined milk samples taken from 2491 quarters of 2233 cows with acute clinical mastitis and were found that *Staphylococcus aureus* predominated (48%), followed by enterobacteria (18%), *Streptococcus dysgalactiae* (12%), *Str. uberis* and *Actinomyces pyogenes* (3% each) and other streptococci (4%).

Pampori¹⁵ found that out of 190 milk samples, 174 samples were positive for bacterial growth. 88 (50.57%) yielded Staphylococci, 81 (45.55%) Streptococci and 5 samples (2.87%) yielded mixed growth of gram positive rods and gram negative cocci.

Ghose and Sharda¹⁶ obtained 168 (15.85%) milk samples out of 1060 bacterial growth on cultural examination. A total of 224 isolates were obtained, out of which 74 (33.04%) were characterized as *Streptococcus* spp., i.e. *Str. agalactiae* (58.11%), *Str. pyogenes* (20.27%), *Str. dysgalactiae* (18.92%) and *Str. uberis* (2.7%).

Ghose *et al.*¹⁷ cultured bacteriologically 13 milk samples, 11 (84.6%) yielded one type of bacteria in the remaining 2 samples (15.4%) mixed infection were observed. Among the bacterial mastitogens *Staphylococcus aureus* (33.3%) was the major agent followed by *Streptococci agalactiae* (26.7%), *Corynebacterium* spp. (20%), *Streptococcus dysgalactiae* (13.3%) and *Staphylococcus epidermidis* (6.7%).

Kheirabadi *et al.*¹⁸ reported that subclinical bovine mastitis in west Iran was mainly caused by coagulase positive *Staphylococcus aureus* and *Streptococcus agalactiae*.

Balakrishnan *et al.*¹⁹ isolated a total of 40 bacterial isolates. The spectrum of organisms were *Staphylococcus aureus* (35%), *Escherichia coli* (27.5%), *Streptococcus agalactiae* (17.5%), *Pseudomonas aeruginosa* (12.5%), *Streptococcus dysgalactiae* (2.5%), *Pasteurella haemolytica* (2.5%) and *Actinobacillus capsulatum* (2.5%).

Involvement of protein components of the etiological agents in causing mastitis and relative drug resistance

Patnaik *et al.*²⁰ experimentally showed that mastitis, can have an infectious and non-infectious etiology. The whole cell protein profile analysis of *Staphylococcus aureus* and *S. epidermidis* by SDS-PAGE technique showed broad similarity in band pattern except 4 bands (36.35 KDa, 31.16 KDa, 24.05 KDa and 19.49 KDa and 2 bands (69.09 KDa and 32 Kda) respectively were highly expressed may be due to some strain variation or mutation or antibiotic resistance and virulence.

Besides virulence factors, the increased resistance of *S. aureus* isolated from mastitic cows to several antimicrobial agents has been reported which impacts on the effectiveness of therapy since control methods of this organism from dairy herds requires treatment of infected mammary glands with effective antimicrobial agents. The determination of antimicrobial susceptibility of clinical isolates is required not only for therapy but also for monitoring the spread of resistant strains throughout the populations²¹.

Gene based molecular identification with characterization for confirmed diagnosis and treatment of mastitis

Bhandari *et al.*²² isolated 43 *Staphylococcus aureus* from 121 clinical and subclinical mastitis cases of cows and buffaloes of Gujrat. All *S. aureus* were identified on the basis of morphological, cultural and biochemical properties. All 43 *S. aureus* were identified by PCR method using species specific oligonucleotide primer that encode the gene 23S rRNA. PCR based detection was carried out for virulence associated genes of *S. aureus* namely *clfA*, *spa*, *coa* and *mec* (methicillin resistant). Methicillin resistant gene of *S. aureus* isolates did not generate any amplified product.

Reddy *et al.*²³ briefed a relative increase in methicillin resistance among 48 cases of *Staphylococcus aureus*-associated postpartum mastitis during 1998–2005. Of 21 cases with methicillin resistance, 17 (81%) occurred in 2005. Twenty (95%) isolates contained the *Staphylococcus* cassette chromosome *mec* type IV gene.

Moon *et al.*²⁴ isolated 21 *Staphylococcus aureus* and 19 CNS strains which were resistant to methicillin. The *mecA* gene was also found in 13 methicillin-resistant *S. aureus* (MRSA) and 12 methicillin-resistant CNS (MRCNS) isolates.

Sixteen isolates were classified as methicillin resistant and 96 isolates as methicillin susceptible by disc diffusion and broth microdilution. The *mecA* gene was identified in 15 of the 16 resistant isolates²⁵.

Genotyping of the 17 methicillin-resistant *Staphylococcus aureus* (MRSA) isolated from each cow revealed two staphylococcal cassette chromosome *mec* (SCC *mec*) types (IV and IVa), three *spa* types (t286, t324, and untypable), and two sequence types (ST1 and ST72)²⁶.

CONCLUSION

It has been estimated that mastitis reduces milk yield by approximately 21% and butter fat by 25% in affected cattle as compared to normal one. The milk of the infected cow turns inferior in quality and the milk of the affected cow is unfit for human consumption²⁷⁻²⁸.

Many different techniques are available for tracing the spread of single *S. aureus* strain of human and animal origin, such as antibiotyping, the biochemotyping the phage typing, protein electrophoresis by SDS-PAGE, plasmid profiling and PCR. Despite the presence of all these methods, each of these techniques has advantages and disadvantages in their discriminatory power, reproducibility and type ability. Treatment and eradication of diseases caused by *Staphylococcus aureus* and its multidrug resistance require precise typing of various pathogenic strains so as to find out the common clones, their origins, sources and routes of transmission²⁹.

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