IDENTIFICATION OF DIFFERENT HEMOLYTIC AND NON-HEMOLYTIC STRAINS OF BACTERIUM CAUSING MASTITIS BY DNA SEQUENCING OF 16S rDNA FROM GENOMIC DNA AND COMPARATIVE ANALYSIS OF SEQUENCES

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Abstract: Mastitis (inflammation of the mammary gland) is the disease of cattle. The disease is primarily caused by infection of udders by different bacterial species but may also be caused by trauma, injury or chemical irritants to the udders. It is the single most commonly occurring disease of dairy cattle (after foot and mouth viral disease) resulting in huge loss of quality and yield of milk. The estimated annual losses due to mastitis are about $184 per cow that includes reduced production, discarded milk, drug therapy, veterinarian costs, premature culling, and increased labor. Species specific highly conserved intergenic spacer region of rRNA operon can be used for identification of specific strain of bacterium. Molecular characterization of strains of bacterium allowed identification of mastitis causing strains in local population of cattle. This information can be used for designing species specific primers for rapid detection by PCR and therapeutic interventions. Sequencing of rDNA amplified from genomic DNA of different hemolytic and non-hemolytic colonies of bacterium identified different strains of Bacillus species such as Bacillus megaterium, B.subtilis, B.licheniformis, having sequence identity of 97 to 99 percent. Hemolytic ability was observed in all the Bacillus strains sequenced. Sequence analysis revealed the presence of unique sequences in intergenic region specific to strain.

Keywords: cattle mastitis, 16S rDNA operon, hemolytic ability, Bacillus strains, milk production

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