

SUMMARY

Detection of Virulence Genes in *Streptococcus uberis* Isolated from Bovine Mastitis in Aydın Province by Multiplex Polymerase Chain Reaction (mPCR)

In this study, a total of 200 milk samples were brought to Adnan Menderes University Faculty of Veterinary Medicine Department of Microbiology and examined with regard of *Streptococcus uberis*. The multiplex PCR method was applied in order to determine the prevalence of virulence associated genes.

35 (% 17.5) *Streptococcus uberis* isolation was made from the examined 200 milk samples.

The strains which were conventionally identified as *S. uberis* were examined with Polymerase Chain Reaction and in complete (% 100) 35 isolates, 16S rRNA gene was detected. While virulence associated genes are examined individually, *hasB* was identified out of 32 (91 %) strains, *gapC* was identified out of 32 (91 %) strains, *skc* was identified out of 32 (91 %) strains, *cfu* was identified out of 30 (86 %) strains, *hasC* was identified out of 30 (86 %) strains, *hasA* was identified out of 30 (86 %) strains, *sua* was identified out of 29 (83 %) strains, *oppF* was identified out of 28 (80 %) strains, *pauA* was identified out of 25 (71 %) strains, *Ibp* was identified out of 9 (26 %) strains. There was not made any *pauB* gene identification.

As a result, when the prevalence of virulence genes are examined which belongs to *S. uberis* agents that are isolated from mastitis cases, it is exhibited that the genes which expresses the capsule formation play an important role with regard to the pathogenicity of the agent, in addition, it is seen that the genes which employ the synthesis of serine protease enzymes shown significant prevalence.

Keywords: *Streptococcus uberis*, mastitis, virulence genes, mPCR