STUDY OF VIRULENCE ASSOCIATED GENES IN STREPTOCOCCUS UBERIS ISOLATED FROM BOVINE MASTITIS

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Streptococcus uberis is a pathogen implicated in bovine MASTITIS, and it is predominantly associated with sub-clinical and clinical intramammary infections (IMI) in lactating and non-lactating cows. Prophylactic measures are often inadequate, simply because animals are constantly being re-exposed to infection from their surrounding environment. Molecular analysis of S. uberis suggested that a wide variety of strains were shown to be able to infect the mammary gland. At present, nothing has been reported about the occurrence of the virulence associated genes among S. uberis isolates from bovine MASTITIS in Argentina, and about the possible distribution of virulence patterns at various dairy herds. The aim of this work was to determine 11 putative virulence associated genes by polymerase chain reaction (PCR) in S. uberis strains isolated from bovine MASTITIS in dairy herds located in the east-central region of Argentina. The study included 78 S. uberis strains obtained from IMI in 21 dairy herds located in the central region of Argentina. The isolates were previously identified by two PCR protocols of the restriction fragment length polymorphism analysis of 16S ribosomal DNA. Individual PCR reactions based on specific oligonucleotide primers for the detection of ctx, hasAB, hasC, gapC, lbp, oppF, pauA/B, skc and sua genes were finally conducted. Results revealed that all virulence associated genes were not present in the 78 analyzed strains. Each S. uberis strain carried among 1 to 10 virulence genes. Of 78 strains examined, 57.7% isolates carried among seven and nine virulence associated genes. Further analysis showed 58 different virulence patterns being ctx + hasAB + hasC + gapC + lbp - oppF + pauA/B +/- skc + sua + the most prevalent (n = 7). In this work, we found a high number of virulence patterns associated with IMI. These results showed that any virulence associated gene was present in all the strains and therefore revealed the absence of classical virulence factors such as those present in other species of Streptococcus. This fact may indicate that others virulence factors could be involved. While many studies relating the distribution of one or a few virulence associated genes have been reported, to our knowledge this is the first study that investigates the presence of eleven virulence associated genes. Genotypic characterization of S. uberis strains carried out in our study contributes to a better understanding of the pathogenicity of S. uberis.