

Difference in Virulence Factor Genes Between Transient and Persistent Streptococcus Uberis Intramammary Infection in Dairy Cattle

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Abstract : Streptococcus uberis is one of the most common mastitis-causing pathogens, with a wide range of intramammary infection (IMI) durations and pathogenicity. This study aimed to compare shared or unique virulence factor gene clusters distinguishing persistent and transient strains of S. uberis. A total of 139 S. uberis strains were isolated from three small-holder dairy herds with a high prevalence of S. uberis mastitis. The duration of IMI was used to categorize bacteria into two groups: transient and persistent strains with an IMI duration of less than 1 month and longer than 2 months, respectively. Six representative S. uberis strains, three from each group (transience and persistence) were selected for analysis. All transient strains exhibited multi-locus sequence types (MLST), indicating a highly diverse population of transient S. uberis. In contrast, MLST of persistent strains was available in an online database (pubMLST). Identification of virulence genes was performed using whole-genome sequencing (WGS) data. Differences in genomic size and number of virulent genes were found. For example, the BCA gene or alpha-c protein and the gene associated with capsule formation (hasAB), found in persistent strains, are important for attachment and invasion, as well as the evasion of the antimicrobial mechanisms and survival persistence, respectively. These findings suggest a genetic-level difference between the two strain types. Consequently, a comprehensive study of 139 S. uberis isolates will be conducted to perform an in-depth genetic assessment through WGS analysis on an Illumina platform.

Keywords : Streptococcus Uberis, mastitis, whole genome sequence, intramammary infection, persistent S. Uberis, transient s. Uberis

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