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Clinical Presentation and Immune Response to Intramammary Infection of Holstein-Friesian Heifers with Isolates from Two Staphylococcus aureus Lineages

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Abstract : Staphylococcus aureus is the most frequent cause of clinical and subclinical bovine mastitis in Ireland. Mastitis caused by S. aureus is often chronic and tends to recur after antibiotic treatment. This may be due to several virulence factors, including attributes that enable the bacterium to internalize into bovine mammary epithelial cells, where it may evade antibiotic treatment, or evade the host immune response. Four bovine-adapted lineages (CC71, CC97, CC151 and ST136) were identified among a collection of Irish S. aureus mastitis isolates. Genotypic variation of mastitis-causing strains may contribute to different presentations of the disease, including differences in milk somatic cell count (SCC), the main method of mastitis detection. The objective of this study was to investigate the influence of bacterial strain and lineage on host immune response, by employing cell culture methods in vitro as well as an in vivo infection model. Twelve bovine adapted S. aureus strains were examined for internalization into bovine mammary epithelial cells (bMEC) and their ability to induce an immune response from bMEC (using qPCR and ELISA). In vitro studies found differences in a variety of virulence traits between the lineages. Strains from lineages CC97 and CC71 internalized more efficiently into bovine mammary epithelial cells (bMEC) than CC151 and ST136. CC97 strains also induced immune genes in bMEC more strongly than strains from the other 3 lineages. One strain each of CC151 and CC97 that differed in their ability to cause an immune response in bMEC were selected on the basis of the above in vitro experiments. Fourteen first-lactation Holstein-Friesian cows were purchased from 2 farms on the basis of low SCC (less than 50 000 cells/ml) and infection free status. Seven cows were infected with 1.73 x 102 c.f.u. of the CC97 strain (Group 1) and another seven with 5.83 x 102 c.f.u. of the CC151 strain (Group 2). The contralateral quarter of each cow was inoculated with PBS (vehicle). Clinical signs of infection (temperature, milk and udder appearance, milk yield) were monitored for 30 days. Blood and milk samples were taken to determine bacterial counts in milk, SCC, white blood cell populations and cytokines. Differences in disease presentation in vivo between groups were observed, with two animals from Group 2 developing clinical mastitis and requiring antibiotic treatment, while one animal from Group 1 did not develop an infection for the duration of the study. Fever (temperature > 39.5^{o}C) was observed in 3 animals from Group 2 and in none from Group 1. Significant differences in SCC and bacterial load between groups were observed in the initial stages of infection (week 1). Data is also being collected on cytokines and chemokines secreted during the course of infection. The results of this study suggest that a strain from lineage CC151 may cause more severe clinical mastitis, while a strain from lineage CC97 may cause mild, subclinical mastitis. Diversity between strains of S. aureus may therefore influence the clinical presentation of mastitis, which in turn may influence disease detection and treatment needs.

Keywords : Bovine mastitis, host immune response, host-pathogen interactions, Staphylococcus aureus
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