Comparative Genomic Insights into *Staphylococcus pseudintermedius* from Healthy Dogs and Those with Pyoderma

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Staphylococcus pseudintermedius (*S. pseudintermedius*) is commonly found as a normal flora on the skin of canines. The bacterium is also associated with one of the most common cutaneous diseases of dogs called canine pyoderma. The disease is becoming difficult to treat due to the increased emergence of multidrug resistant *S. pseudintermedius*. The differences in the nature of the bacteria from healthy vs. sick dogs is not well studied. Therefore, the objectives of this study were phenotypic and whole genome sequence-based comparison of isolates obtained from canine pyoderma cases and those from healthy dog's skin. Bacterial isolates were subjected to antimicrobial susceptibility test by the minimum inhibitory concentration (MIC) method. Concurrently, DNA was extracted from 22 isolates from healthy dogs and 26 isolates from cases of pyoderma for whole genome sequencing. DNA sequence libraries were prepared using Oxford nanopore's ligation sequencing kit and sequenced using the Mk1b device. Quality control and genome assembly was performed using the EPI2ME bioinformatic platform. Genomes were annotated using the Prokka tool. Presence of virulence, antimicrobial resistance and plasmid replicon genes were identified employing VFDB, CARD and PlasmidFinder databases, respectively. Core genome alignment and phylogenetic tree inference were conducted using Roary and IQ-TREE software's, respectively. Statistical analysis was performed using R, and data were visualized with the ggplot2 package. Isolates from dogs with pyoderma exhibited greater phenotypic antimicrobial resistance compared to isolates from healthy dogs. Pyoderma-associated isolates also carried a higher number of antimicrobial resistance (AMR) genes and accessory genes. In addition, plasmid replicon genes were detected more frequently in the genomes of isolates from pyoderma cases. However, no difference was observed in the number of virulence genes carried between the two groups. Based on phylogenetic tree analysis, no specific *S. pseudintermedius* lineages were associated with either pyoderma or healthy skin.

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