

PVL related differences in Protein expression profile in MRSA and MSSA

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Since its early discovery as an opportunistic pathogen, *Staphylococcus aureus* continues to be a major cause of mortality with a wide variety of clinical affections. Panton-Valentine Leukocidin (PVL) is a staphylococcal synergohymenotropic exotoxin (one of virulence factors) belonging to the pore-forming toxin family, induces lysis of host defense cells such as human neutrophils, monocytes, and macrophages, and recently been associated with necrotizing pneumonia. Although MRSA was considered a worldwide major threat, recent records demonstrated several clinical cases of staphylococci infections caused by MSSA with high prevalence of (PVL)⁺ isolates. Hence, understanding mechanisms of both cell physiology and pathophysiology is necessary to contrast the diffusion of this pathogen, the aim of this project is to study the proteome of MSSA and MRSA with special emphasis on PVL⁺ and PVL⁻ strains to identify proteins that may be related to virulence using 2-D electrophoresis and mass spectrometry. Proteomic analysis revealed 8 differentially expressed proteins between MSSA (PVL⁻) and MSSA (PVL⁺) groups. Five of them showed over expression in MSSA (PVL⁻) while 3 proteins were over expressed in MSSA (PVL⁺). These proteins were successfully identified by mass spectrometry. Focusing on the function of identified proteins, it was found that proteins overexpressed in PVL⁺ are linked with catalysis of polypeptides and with energy production pathways. While the ones overexpressed in PVL⁻ are related to transcription pathways. Results can explain the reason because PVL⁺ strains are more pathogenic than PVL⁻.

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