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Detection of diverse virulence factors in phages Methicillin Resistance *Staphylococcus aureus* (MRSA) isolated from mastitic cows

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Staphylococcus aureus is an opportunistic human and animals' pathogen that is found passively colonizing a large percentage of the population primarily on the skin or mammary glands in cows. As the capacity of a given *S. aureus* strain to cause infection varies among strains and is determined by the presence or absence of many virulence-associated genes, some of which are encoded by phages. To determine the abundance and characterize the diversity of *S. aureus* strains which caused mastitis in cows in various provinces in Baghdad city, Polymerase Chain Reaction (PCR) was used to detect the presence of *S. aureus* phage-type specific DNA which carry genes coding for diverse virulence factors such as Panton-Valentine leukocidin (PVL), enterotoxins and exfoliative toxins. *Staphylococcus aureus* used in this study was isolated from mastitic cow milk grew on blood agar and methicillin-resistant *staphylococcus aureus* (MRSA) were selected as indicator strains to investigate the presences of phage segments. The isolates of wild lytic phages from the transient stocks were *S. aureus* phage was extracted and phage segments were investigated. Results showed that the phage content virulence factors in *S. aureus* isolates were, enterotoxin A, enterotoxin p, and exfoliative toxin A, toxic shock syndrome toxin-1 (TSST-1) and lipase. But Panton –valentine leukocidin gene failed to amplify among strains and the diversity of Baghdad city is relatively high. The current study concluded that the role of bacteriophages in changing ecology and virulence of *S. aureus* propagated with the corresponding host clinical MRSA isolates using the plate method. Plates were incubated overnight at 37°C and plaque morphology and growth characteristics were recorded.

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