Detection of some virulence factors genes in *Staphylococcus aureus* isolated from different clinical cases

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Introduction

Staphylococci include many species of pathogenic bacteria that cause infection to humans and animals, the species (*S. aureus*) is one of the most important pathogenic type to humans, and the most common species responsible for a wide range of diseases such as furuncles, various abscesses, wounds abscesses resulting from surgical operations, dermatitis, soft tissue inflammation, arthritis, bones inflammation, bronchial pneumonia, inflammation of internal parts of the heart and injuries caused by toxins such as toxic shock syndrome and *Staphylococcus aureus* syndrome and food poisoning (1). Due to a lot of Virulence factors, this bacterium has pathogenesis and ability to invade the host's tissue and spreading in it such as the production of Toxins and enzymes that help bacteria to cause infection (2). They have the ability to produce many toxins, extracellular enzymes such as coagulation enzyme of blood plasma that has the ability to inhibit phagocytosis, It also has the ability to produce other enzymes representing spreading factors such as Staphylokinase enzyme, proteinase enzyme and lipase enzyme which contribute to bacterial invasion of tissues and the spread of infection , It also works on the production of Alpha, Beta, Gama and Delta-type lipoproteins as well as the production of gastrointestinal toxins leading to food poisoning . Besides that, it has ability to produce exogenous toxins produced in cases of Toxic shock syndrome and Staphylococcal scalded skin syndrome (3). In addition to that, it has a wallet that helps bacteria to resist phagocytosis (4). This Bacteria also has cell wall, which is considered as an anti-genetic structure containing anti-genetic structures (peptidoglycan, teichoic acid and A protein). The cell wall works to resist the host's immune system and forms osmosis protection for the bacterial cell (5,6). One of the other Virulence factors is that some *S.aureus* strains is having *mecA* gene which is responsible for the resistance of the fixed penicillin group as a result of their encryption of PBPs Penicillin binding proteins which work to reduce the harmony with Meticillin antibiotic, the *Staphylococcus* resisting Meticillin are called MRSA which are characterized mainly by their institutionalization in hospitals and called HA(Hospital Acquired)-MRSA and when they take the community as a residence , they are called CA(Community acquired) MRSA. The importance of these antibiotica came through their resistance to many antibiotics such as resisting all the species of β-Lactam antibiotics and many other antibiotics (7). The first Meticillin Resistant *S.aureus*was recorded in England in 1961 and made a massive health disaster that moved to different parts of the world (8) . Due to the importance of MRSA in causing various infections of the body and the difficulty to find a medication and controlling them besides the lack of studies about their spread in the hospitals of Al-Diwaniyah city, Iraq, also we have lack of molecular studies related to pathologic factors (Virulence factors) of this bacteria. The current study