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The Effect of Genetic Diversity and Phylogenetic Relationships on Staphylococcus Aureus Strains in Clinical Specimens

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Introduction

Staphylococcus aureus is one of the most important nosocomial pathogens that as a significant pathogen causes various infectious diseases and can become a life-threatening pathogen so it can cause a wide range of clinical infections. At present, the prevalence of methicillin-resistant Staphylococcus aureus (MRSA) in some areas is around 72 to 90% Nose is the most common carrier for S. aureus [1]. Nasal carriers are at risk for S. aureus infections.In recent years, the increasing number of methicillin-resistant S. aureus (MRSA) infections and resistance to various antibiotics has been a major challenge for physicians [2, 3]. Also, the virulence factors and toxins produced by this bacterium are responsible for several infections, in which Pantone Valentine Leukocidin (PVL) and exfoliating toxins are most closely associated. The mecA gene, which is responsible for resistance Methicillin is carried by a motile genetic element, the staphylococcal cassette chromosome (SCCmec) [4] Recombinase chromosome cassette (ccr) is another important part of SCCmec, which is involved in the placement and application of SCCmec elements [5]. So far, 11 main types of SCCmec have been identified that differ in size and genetic content, in addition, these elements contain multiple resistance genes. Most MRSA health-related strains (HA-MRSA) are SCCmec, I, II, and III, while SCCmec IV and V are commonly associated with community-based MRSA (CA-MRSA) [6].The aim of this study was to investigate the effect of genetic diversity and phylogenetic relationships on Staphylococcus aureus strains in clinical specimens.

Materials and Methods

This study was conducted in 1399 by searching for keywords such as genetic diversity, phylogenetics, Staphylococcus aureus in reputable databases such as: pub med and google scholar, which finally found 30 articles, of which 30 articles 28articles were used

Results

Based on studies of articles, the results show that Staphylococcus aureus (S. aureus) is one of the most common human pathogens and is responsible for many community-acquired and nosocomial infections, thus raising public health concerns throughout The prevalence of methicillin-resistant Staphylococcus aureus (MRSA) in some areas is currently around 72 to 90% [7]. The most prominent pathogenic species in the genus Staphylococcus is S. Aureus, several species of which cause a variety of diseases [8]. PVL was first isolated from furuncles in 1936 [9]. This toxin consists of two subunits, S and F, which have synergistic activity by lukS-PV and lukF-PV genes [10]. Injection of pure PVL releases histamine from basophil granulocytes, chemotherapy Ebrahimzadeh Namvar et al. In the infection model, PVL secreted through mechanisms such as high regulation of protein A and other adhesions causes tissue invasion, inflammatory response, and necrotic pneumonia [11].The regulatory system of lateral genes (agr) is responsible for regulating growth, colonization, expression of exoenzymes, toxins, surface proteins and other virulence factors [12, 13]. This system also regulates the metabolic pathways of organisms as an effective growth factor Although many S. aureus isolates are clinically positive for Agr in humans,

several reports indicate that defective agr mutations have been isolated from infected patients In the last two decades, the emergence of antibiotic-resistant strains, especially beta-lactam, has increased the clinical significance of S. aureus [14]. Strategies for prevention and control of S. aureus infections by analysis of isolates by Different molecular types depend [15]. Pulse field gel electrophoresis (PFGE), multifocal sequence typing (MLST) and SCCmec typing are the safest typing methods. Among them, PFGE is the gold standard for MRSA molecular typing and inpatient prevalence assessment. In addition, MLST typing is based on the determination of allelic characteristics or sequence type (ST) of internal components of 7 household genes and can be used to determine the evolutionary and demographic biology of bacterial species [16].

Discussion

S. Aureus colonizes up to 25% of healthy individuals and is even more common among those with mucosal, skin, throat, and nasal surfaces. S. Aureus is able to produce various toxins in which the most important substance is PVL. PVL-SA is pathogenic compared to other strains and can also cause skin and soft tissue infections, but in some cases may lead to invasive infections such as necrotic hemorrhagic pneumonia [17]. Given the importance of these strains, evaluation of antibiotic resistance and genetic characteristics of positive PVL strains can

play an important role in determining health policies, therefore, rapid diagnosis and control of PVLSA is necessary for appropriate treatments. Can be useful in epidemiology. Shrestha et al. Also reported that PVL was produced by 35.6% of S. aureus strains and was detected from bacteria, surgical site, respiratory and urinary tract infections [18]. Osteomyelitis caused by PVL-SA is more complex and resembles deep vein thrombosis or chronic osteomyelitis [19]. On the other hand, MSSA pvl positive gene contains more virulence factor genes compared to MRSA, although they are more sensitive to antimicrobial agents [20]. Numerous studies have shown that the prevalence of PVL-positive strains among MSSAs is higher than MRSA strains [21, 22]. Genotyping methods for microbial pathogens can be used for two main purposes: 1) Prevalence research and 2) Assignment of phylogenetic relationships and clonal relationship with strains [23]. Pulse gel electrophoresis (PFGE) is required to investigate local epidemiological conditions or prevalence, although for many years, multiple enzyme enzyme (MLEE) and multimodal sequencing (MLST) have been used for global study. Epidemiology of pathogens, such as bacterial lineage[24]. Recently, Korin et al. Proposed spa typing as a useful method for assigning phylogenetic relationships to strains. Protein A (spa) is a 42 kDa protein and an important virulence factor involved in the pathogenesis of S. aureus. [25, 26]. The Spa gene contains several regions with different functions, including (1) the N-terminal region, which includes an S region (signal sequence) divided into four or five immunoglobulin G binding domains (A, B, C, E, and D). And (2) the C-terminal zone (X zone), which is divided into XR and XC domains. The XR region consists of variable iterations used to type the spa, and the XC region contains an LPXTG binding pattern that forms the cell wall [27]. Previous studies have shown that the spa gene can act as a genetic marker that can accurately distinguish strains, and the spa typing resolution can be determined by PFGE and DNA microarray of the entire genome for specific sets. Contract analogy [28].

Conclusion

According to the findings, it is better to set up a program to reduce the risk that the risk factor is not dangerous for us and it is recommended that we continue to do the treatment process and proper protection to do a good job of this study.

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