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ORIGINAL RESEARCH

Community-Associated Methicillin-Resistant Staphylococcus Aureus in the Oral Cavity

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ABSTRACT

The oral cavity is habitat to a wide variety of commensal flora, which may act as a reservoir of factors that influence drug resistance. Bacteria in the oral cavity create biofilms, which makes it easier for horizontal gene transfer to result in the accumulation of antibiotic resistance genes. Methicillin-resistant Staphylococcus aureus (MRSA) carriage rates in the oral cavity are high, according to recent studies. The widespread use of antibiotic prophylaxis among at-risk dental procedure applicants may facilitate MRSA establishment in the mouth. These modifications in the epidemiology of MRSA have significant ramifications for clinical practice, methodological approaches to MRSA carriage studies, and MRSA prevention efforts.

Keywords: Methicillin-resistant Staphylococcus aureus (MRSA), Oral cavity, Bacteria, commensal flora.

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INTRODUCTION

Over the course of evolution, the oral micobiota and oral micro biome have co-evolved in a symbiotic connection with their human hosts. This population of microorganisms has an amazing ability to adjust to each particular host as they grow older. The availability of nutrients, physicochemical conditions, and host-related factors including hormonal levels, immunological status, and age all affect how the constituent microorganisms grow, function, and adapt overall in their unique micro environmental niche. (Belibasakis, 2018).

There are various dental types of infections that arise in the oral cavity of the patient, such as periodontal cancer, teeth loss, oral pain, dental disorder dental abscess, plaque, dental calculus, dentin hypersensitivity, acid erosion, hyperdontitis, Malocclusion, ulcerative gingivitis, fluorosis of the oral cavity, effect on teeth, acute necrotization, etc. Many oral illnesses, such as mucositis, periodontitis, endodontic peri-implantitis infections, and even tooth decay, are thought to be caused by Staphylococcus. Aureus (passariello et al., 2012)

Staphylococci-positive, the pathogen is attributable to invasiveness blend, toxic mediated virulence blend, and antibiotic resistance (Loir Baron and Gantier, 2003).

Staph. Aureus is a gram-positive, non-spore-forming, grape-forming, non-motile such as clusters and the most important coagulase, Staphylococci positive pathogen attributable to invasiveness blend, toxic mediated virulence blend, there are drug-resistant strains of Aureus (Faden and Saudi, 2019). Resistant to methicillin the Staph. Aureus (MRSA) (Rajaduraipand, et al.,2006).

The strains of Staph. Aureus that they were resistant to antibiotics containing beta-lactam, such as penicillins, amoxicillin, methicillin, cephalosporins, oxacillin, etc (David et al., 2010). The inclination of the acquisition of antibiotic resistance by Staph. Aureus led to a global clone distribution of distinct antimicrobial resistance expressions. It has been found that there are several bacterial infections of MRSA strains in the population and clinics (Peters et al.,2013)

Since have been using the antibiotics in random way in hospital conditions are inadequate, and crowding patients and healthcare worker help to spread the pathogenic bacteria, such as Staph. Aureus. (AL-Safani et al., 2018).

Theoretically, in tooth infection due to its resistance to most widely used antibiotics for dental infection caused by this pathogen (Vellappally et al., 2017).

To create colonization that is required before any protopathic or periodontopathic process, the oral cavity is an open growth environment in which the bacteria must adhere to the surface (Jevon et al., 2020).

More than 300-400 species of aerobic and anaerobic bacteria colonize the oral cavity, but only low number of these species are involved in dental infection development (Boykin et al., 2018).

The presence of secreted saliva containing epithelial debris makes the mouth a favorable habitat for a large variety of bacteria. Odontogenic infection is caused by the composition of plaque bacterial groups (Dye et al., 2008). Saliva micro biota is influenced by the dislocation of bacteria from colonization aggregations in various oral cavity sites (teeth, tongue, cheek, and pharyngeal mucous membrane) (Maisonneuve et al., 2020).

Streptococci, peptostreptococci, Staphylococci, Veillonella, Corynebacterium, Neisseria, and other bacteria are found in roughly 6 (6x109) bacterium/ml in adult human saliva.

Background

Staph. aureus is a gram-positive coccioccus aureus that appears under a microscope as blue-violet clusters, between (1.2-0.4 μm) and has a

yellow-pigmented colony called (aureus; means golden) because of their (carotenoid) pigments that develop during their development (Yan et al, 2016). Staph. aureus typically functions as a commensal of the human microbiome, but it can sometimes develop into an opportunistic pathogen. It is a common cause of food poisoning, sinusitis, and skin infections like abscesses. By creating virulence factors including strong protein toxins and the production of a cell-surface protein that binds and inactivates antibodies, pathogenic strains frequently aid in the spread of diseases. One of the primary causes of antimicrobial resistance-related mortality is Staph. aureus, and the rise of antibiotic-resistant strains, such methicillin-resistant Staph. aureus (MRSA), is an issue that affects clinical care all over the world. (Al-Talib et al., 2014; Yılmaz and Aslantaş, 2017; Suhaili et al;2018).

Staph aureus grows well under high osmotic pressure conditions and low humidity (Hau 2017), and no spores forming and resistant to dry conditions and high salt concentration, 15% NaCl and readily develops at fixations up to 10% NaCl and tolerant to 4.2-9.3 of pH range, with an ideal pH 7.0-7.5, It could grow at temperature between 15 C and 45 C, these bacteria rapidly multiply at room temperature and produce toxins that cause disease (Wu et al., 2018; Hau, 2017).

The response rates of Staph. aureus clinical isolates to chemical pressures and are relatively similar in growth rates, there were specific strains that responded to stresses by changing their lifestyles to form a biofilm and/or small colony variants in extreme conditions (but stress levels are still under lethal), it has been suggested that phenotype alteration depends on bacterial and host factors, and indicate that some specific strains may have a unique pathway that remains at stress (Otto, 2009; Kostakioti at el., 2013).

One of the important reasons that made Staph. aureus is more infectious is its ability to survive for several months on different surfaces (Kramer et al., 2006). Staph. aureus causes many diseases, including minor skin, soft-tissue infections and severe diseases such as pneumonia, septicemia, endocarditis, and catheter-related infections through the formation of biofilm, and it is also one of the most pathogens cause eye diseases (Hesje et al., 2011; Suzuki et al.,2012; Hussain, et al., 2019; Farah et al., 2020).

Interventions such as hospitalization or episodes of immunosuppression may lead to invasive Staph. aureus is naturally present in the skin and mucous membranes and causes skin or respiratory diseases, or life-threatening bacteremia. (Yang et al., 2019).

Genetic Diagnostic

The bacterial genome consists of core and accessory genomes. All genes necessary for cellular viability, including those that code for chemicals used in metabolism, DNA and RNA synthesis, and replication, are found in the core genome. By encoding the proteins necessary for bacteria to adapt to various ecological niches, the accessory gene pool serves as a representation of diversity within bacterial species. (resistance, virulence factors, etc.). Accessory genes frequently differ in G + C composition from those in the core genome because they are derived from other bacterial species (Hacker & Kaper, 2000).

Whole genome sequencing (WGS), unlike sequence-based methods, which determine the exact arrangement of nucleotides and evaluate DNA sequence evaluations (for example, Multi-locus Sequence Typing (MLST), Staph. aureus protein a (spa) typing, Amplified Fragment Length Polymorphism (AFLP), Random Amplified Polymorphic DNA (RAPD), and Multiple Locus Variable Number of tandem repeat analysis (MLVA), the sequence-based methods. These typing methods were created to better understand Staph. aureus' epidemiology and evolution (Nazareth et al., 2012; Moore, et al., 2015; Wu, et al., 2018).

Pathogenesis:

Staph. aureus is one of the most prevalent pathogenic bacteria because its biology is based on many virulence factors that cause illness and the disease's host. (Al Fatemi et al., 2014).

It's also an "ESKAPE" species, which may lead to a range of severe illnesses. As a result, it is regarded as a significant and rising worldwide threat that affects a wide range of individuals and causes serious nosocomial infections. (Liang et al.,2019). by immunity, which prevents opsonophagocytic killing by expressing surface-linked proteins and polysaccharide capsules.

- **The ability of Staph. aureus:**

1. To infiltrate and cause inflammation. This involves colonization, and the synthesis of extracellular structures of molecules that aid in adherence and help them resist host defenses. (Haghkhah, 2003).
2. To produce toxins. Despite Staphylococcus's multiple resistance, neutrophils are the most important body defense against in regulating the colonization and dissemination of Staph. aureus. Induction of neutrophil cell death is one of these techniques, which results in inflammation, tissue injury, and a worsening of the disease (Yang, et al., 2019). Furthermore, strategies are the induction of neutrophil cell death, which triggers tissue and inflammation loss and increased the severity of diseases. Staph. aureus creates several virulence variables, in addition to the capacity to generate septic products, enzymes and toxins. Shock by stimulating the immune system and communicating with it and with coagulation (Gordon and Iowy, 2008; Rigby and Deleo, 2012).

Staphylococci Virulence Factors

Staph. aureus virulence requires the synthesis of numerous excessive or superficial compounds, toxins, and immune evasion mechanisms. Because neutralization of one molecule does not always destroy the bacteria's capacity to cause infection, the exact sequence of these virulence factors varies between isolates, and some components are redundant in their action (Walton,2013).

Staph. aureus toxins

Staph. aureus produces a wide range of enterotoxins, which have been assigned to the pyrogenic toxin superantigen family based on their biological activity and structural similarity, toxic shock toxin-1 (TSST-1), which induces super antigenic activity, and exfoliative toxins (ETs), which are responsible for exfoliation. Staphylococcus enterotoxins cause food poisoning, and staphylococcal scarlet fever (a moderate type of TSS), and both of these toxins share structural and biological properties, indicating that they are belonging to the same family (Thomas et al,2006).

Staphylococcal enzymes:

Many of the secreted enzymes of Staph. aureus will break down certain molecules in the host or interact with cascades in host metabolism.

Coagulase

Two coagulase forms are produced by Staph. aureus; staphyloma coagulase and von Willebrand factor (VWF), which contribute to the formation of a complex called staphyloma-thrombin (after binding to fibrin clots prothrombin) and several other proteins from plasma that contribute to the fibrinogen conversion causes fibrin to clot fibrin on the surface of the fibrinogen inhibiting phagocytosis, Staph. aureus causes abscess and adhesion to Staph. aureus during infection and biofilm development (McAdow, et al., 2012; Otto, 2014).

Catalase

In several bacterial species, this enzyme is present and can influence the survival of bacteria by removing the superoxide within phagocytosis created by the response of the respiratory burst. Bacterial variables that are disrupting hydrogen peroxide allow bacteria to persist and stay, such as catalase, cells, and tissues within the host (Das and Bishayi, 2010).

Hyaluronidase

Hyaluronic acid hydrolysis, hyaluronic acids intracellular tissue matrix with acidic mucopolysaccharides, contributing to the propagation of staphylococci and their invasion of adjacent areas (Haghkhah, 2003).

Staphylokinase

One of the essential enzymes in host avoidance is staphylokinase innate immunity, as the connection between plasminogen and staphylocinase. It contributes to the development of a wide proteolytic enzyme spectrum that facilitates penetration of Staph. aureus into the underlying tissues (active plasmin) (Bokarewa, et al., 2006).

Lipases

Staph. aureus lipase (also known as glycerol ester hydrolase), like other microbial lipases, Staph. aureus lipase can cause human skin diseases due to its importance in the metabolism of bacterial lipids and participation in pathogenic processes (Rosenstein and Götz, 2000; Kitadokoro, et al., 2020).

β-Lactamase

The β-lactamase was among the first enzymes that destroy Penicillin; it was produced by several bacteria including Staph. aureus. The staphylococcal β-lactamase hydrolyzes the amide-bond of beta-lactam antibiotics, which helps to acquire the resistance against all β-lactam antibiotics. β-lactamase inhibitors can be combined with the old β-lactam antibiotics to restore their activity, and this phenomenon has been republished as an effective strategy to overcome the resistance mechanism. The presence of β-lactamase in the Staph aureus makes it one of the most antibiotic-resistant bacteria in the world (Kesharwani and Mishra, 2019).

Other virulence factor

Capsule

The cellular surface structure of the capsular polysaccharide, was another Factor in triggering the pathogenesis of Staph. aureus and bacterial evasion of immunological protection. The polysaccharide capsule synthesis is based on a complex regulatory network that guarantees its manufacturing only in the case of a proportion of phase-stationary cells (Keinhörster, et al., 2019).

Protein A

Protein A, located on the surface of bacteria, has 7% of the essential proteins of cells that contain the most essential proteins in Staph. aureus. Protein A of Staph. aureus binds to the portion of immunoglobulin (Fc). Many mammal forms may be useful in avoiding phagocytosis (Gao and Stewart, 2004).

The Genome of Staph aureus:

Staph. aureus genomes were sequenced for the first time in 2001 (Yan, et al., 2016). The Staph aureus genome is divided into three segments: the core genome, core variable genes, and mobile genetic element (MGE). The core genome is strongly conserved among isolates; however, single nucleotide polymorphisms (SNPs) that occur as a result of mutations cause a minor variation. Surface proteins and their regulatory genes are examples of core vector genes with established functions. MGEs are the most altered component of Staph.aureus genetic material, accounting for around 25% of all Staph. aureus genetic material (Hau, 2017). The core genome is mostly intact, and gene similarity between isolates is about 98–100% (Krmusaolu, 2017). By horizontal gene transfer, Staph. aureus was rapidly evolving (Dai, et al., 2019).

Staphylococcus aureus pathogenicity islands (SaPIs)

Staph. aureus contained not only (SaPIs), but also (vSa-gene family) variant surface antigens that encoded about 50% of virulence factors and toxins, vSa1 included enterotoxin coding genes such as Tst and Seb, while vSa2 contains genes that encoded enterotoxin genes such as Sec (HGT). (Krmusaolu, 2017; Lindsay, et al., 1998; Beda, et al., 2003)

Staph. aureus plasmids are divided into three kinds based on their capacity to conjugate and scale. Plasmids are classified as class I (the tiniest) less than 5kb and have the largest copy amount (Shien, 2014). Multiple environmental factors such as ph, oxygen, and carbon dioxide levels, bacterial cell density, regulate virulence expression. These factors all work across various regulatory mechanisms (Bronner, et al., 2004). In general, various combinations of virulence genes can lead to different infection outcomes (Luo, et al.,2018).

MecA Gene

In Staphylococcus genomes, the MecA gene is available. Most MRSA molecular tests are designed to detect the presence of the MecA gene in Staph. aureus. It facilitates virulence of Staph. aureus by inducing methicillin resistance in the genome region known as the Staphylococcus cassette chromosome (SCCmec) (Kırmusaoğlu, 2017; Gittens-St, et al., 2020). The MecA gene is a virulence gene found on the bacterial chromosome. Its length in MRSA is about 720bp, and the protein chain that encodes around 239 amino acids (NCBI, 2019). Penicillin-binding protein-2a (PBP2a), which is encoded by the MecA gene, is a mobile protein that binds penicillin. A genomic island's extrinsic genetic feature (SCCmec) (Alkharsah, et al., 2018). Since it prevents the active site from binding β -lactams, PBP-2a has a lower affinity for -lactams than standard penicillin-binding protein-2 (PBP2) developed by methicillin-susceptible Staph. aureus (MSSA) (Hussain, et al.,2019).

Tst Gene

Diseases lung inflammation, lung abscesses, urinary tract infections, food poisoning, osteoarthritis, endocarditis, meningitis, and a variety of other conditions another class of staphylococci genetic characteristics is a super-antigen encoded by the Tsst gene and borne on Mobile Genetic Elements (MGE) known as (SaPIs), around 15 kb of the genomic regions that denote a variety of virulence genes, (SaPIs) connected to separate S. aureus genetic families, known as lineages. (Shien, 2014; Sharma et al.,2018).

Hemolysin

Alpha (α), Beta (β), Gamma (γ), and Delta (δ) hemolysins rupture red blood cells inside the host, and many classes of hemolysins vary in terms of the degree of hemolysis that happens and how it occurs (Kessel, 2017). The hla, hlb, hld, and hlg genes code for the hemolysins Alpha (α), Beta (β), Delta (δ), and Gamma (γ). These toxins are more effective in causing Staph. aureus infections (Hoseini, et al., 2014).

Enterotoxin

Staphylococcal enterotoxins (SEs) are broadly classified as super antigens, many types of staphylococcal enterotoxins have been reported including: enterotoxins type A is associated with Sea gene, enterotoxins type B associated with Seb gene , enterotoxinstype C is associated with Sec gene, enterotoxins type D associated with Sed gene, enterotoxins type E associated with See gene, enterotoxins type F associated with Sef gene , enterotoxins type G associated with Seg gene, enterotoxins type H associated with Seh gene, enterotoxins type I associated with Sei gene, enterotoxins type J associated with Sej gene, enterotoxins type K associated with Sek gene, enterotoxins type L associated with Sel gene, enterotoxins type M associated with Sem gene, enterotoxins type N associated with Sen gene,

enterotoxins type O associated with Seo gene, enterotoxins type P associated with Sep gene, enterotoxins type Q associated with Seq gene and enterotoxins type R associated with Ser gene, most of SEs genes are portable on (MGE) , the enterotoxins are similar to each other in terms of activity and biological structure, but differ in antigen characteristics Sea, Sed, and See share 70–90% sequence homology (Mehrotra, et al., 2000; Pinchuk, et al., 2010; Zhao, et al., 2020).

Antibiogram Against Staphylococcus:

In human, animal and agriculture, medicine results in the production of resistance genes in different bacteria classes (Subbiah, et al., 2020).

Increased risk of multidrug-resistant strains (MDR) has been a global issue in recent decades, posing significant health risks. Staph. aureus can easily respond to changing environmental factors and become resistant to almost all antibiotics. (Wu et al., 2018; El- Gohary et al., 2019). Staph. aureus is a pathogen that can cause both acquired and contagious infections (Akanbi et al., 2017). Infections caused by drug-resistant bacteria lengthen recovery times and keep patients in hospitals longer, resulting in higher healthcare costs and, most specifically, higher morbidity and mortality rates (Ylmaz & Aslantaş, 2017).

Methicillin resistance (MRSA) and vancomycin resistance (VRSA) are two of the antibiotic resistances that Staph. aureus has developed (Hiramatsu et al., 2014). Drug-resistant microbes arise, and these strains can rapidly spread across human populations by direct interaction, as shown by MRSA and vancomycin-resistant Staph. aureus (VRSA) outbreaks around the world (Bae et al.,2004).

Penicillin resistance was found in Staph. aureus barely five years after that drug's introduction in 1943, and it's estimated that more than 90% of Staph. aureus isolates worldwide are now resistant to it. In response to benzyl penicillin- resistant Staph. aureus, a penicillin-resistant lactamase that may inactivate β-lactam antibiotics was developed in 1959 (Audrey and Lazarus ,2019).

The MecA gene has been linked to resistance to ß-lactamase-resistant penicillins such as methicillin since the mid-1960s. MRSA's growth in European hospitals was limited until the 1970s, and it didn't spread globally until the late 1970s. MRSA strains first appeared in the early 1980s, displaying a wide range of resistance to antibiotics, cephalosporins, and carbapenems, and unrelated chemicals like antiseptics, and quickly spread throughout the world.

The most recent fourth wave of resistance is characterized by MRSA's competitively invading the population and resulting in the development of community-associated MRSA, (Alharbi, 2013; Shien, 2014). The most effective class of antibiotics to combat Staph. aureus infection for the last seventy-five years has been ß- lactam. Staph. aureus was responsible for more than 80% of all deaths in the pre-antibiotic era (Nazareth, et al., 2012).

Mechanisms for antibiotic resistance

Limiting drug absorption, modifying the drug's target to avoid binding, destroying the enzymatic drug, and reducing drug concentration by lowering drug permeability are some of these pathways. Bacteria can use one or more of these resistance mechanisms, in particular, the localization of resistance genes on (MGEs), which together form what is known as a "horizontal gene pool," depending on the antimicrobial involved. These components, which may travel inside and/or between genomes, can be transposons, convertible plasmids, interconnected genomic islands, or phages (Ylmaz and Aslantaş 2017; Top and Springael, 2003). Resistance genes in bacteria result in the development of genetically similar bacteria that can survive in the presence of antibiotics (Schinasi, 2012).

Penicillin

Penicillin in bacteria is caused by changes in the penicillin target enzymes, which cause the ring

structure of penicillin and other β-lactam antibiotics to be disrupted (Walton, 2013).

Vancomycin

The other kind of Vancomycin resistance (VISA) was obtained by adaptive mutations included in the gene coding regulation of bacterial cell physiology. Staph. aureus acquired resistance to Vancomycin (VRSA) by horizontal transport of the VanA-gene on the plasmid, the other form of Vancomycin resistance (VISA) was obtained by adaptive mutations included in the gene coding regulation of bacterial cell physiology (Hiramatsu, et al., 2014). The resistance mechanisms for VISA and VRSA strains are very different; for VISA strains, bacterial cell wall thickness is the suggested resistance mechanism, while for VRSA strains, receiving VanA-gene from Enterococcus spp. suggested resistance mechanism (Hadadi, et al., 2018).

Aminoglycosides

Changing the position of the ribosome target is one of the first pathways of bacterial resistance to aminoglycosides. Changes in ribosome structures result from mutations in genes that encode ribosome receptor proteins, and receptor proteins may not be present or the antibiotic may no longer bind. A second resistance mechanism weakens the antibiotic's absorption, lowering the antibiotic's effective intracellular concentration. It's obvious that permeability is caused by factors influencing the cell membrane's energy, but the precise mechanism is unclear (Özgen, 2008).

Macrolides

Tolerance to macrolides is often produced by a ribosome modification or active efflux of the antimicrobial drug by an ATP-dependent pump in Staph. aureus (Adaleti et al., 2010).

Tetracyclines

A broad-spectrum antibiotic is frequently used in human medicine; there are two types of tolerance in Staph. aureus active efflux (induced by plasmid gene acquisition) and passive efflux (caused by plasmid gene acquisition). Tetracycline resistance can also be acquired by Staph. aureus through ribosome defense, which is mediated by transposon or chromosomal determinants (Trzcinski and colleagues, 2000; Schmitz and colleagues, 2001).

Methicillin

Staph. aureus has developed resistance to methicillin by passing MecA genes between them, which is regulated by the methicillin resistance gene (MGE) (Liang et al., 2019; Hiramatsu, et al., 2014).

Resistance to the antibiotic methicillin the MecA gene, which encodes a modified penicillin-binding protein 2a, is immune to Staph. aureus (Al-Talib and colleagues, 2014).

Methicillin-resistant Staph. aureus (MRSA)

Antibiotic resistance is linked to Staph. aureus, one of the most common illnesses (MRSA) (Suhaili, 2018). MRSA infections have developed more common in recent years, accounting for about 90% of all Staph. aureus infections in humans. (Hussain, et al., 2019; Garazi et al., 2009). Macrolides, aminoglycosides, lincosamide, and all lactams are typically resistant to MRSA. Multidrug resistance (MDR) renders MRSA untreatable (Mahmoudi et al., 2019). The colonization of MRSA is usually asymptomatic in healthy people (Yang et al., 2019). The prevalence of MRSA varies considerably in hospitals (Hussain, 2019). Because of the increasing difficulty in dealing with and treating MRSA, medical research and practice have become increasingly concerned (Alkharsah et al., 2018).

Hospitals Acquired Infections

MRSA-associated hospital (AH) infections are normal, impairing patient conditions and rising the cost of healthcare, increasing hospital costs, use of antibiotics and mortality. Nosocomial diseases in clinics and primary care centers worldwide particularly in immunocompromised people (Yarbrough et al., 2018 and Schubert, et al., 2019). Diseases with HA-MRSA lead to morbidity and mortality. In patient hospitals that concede as an

important reservoir, healthcare jobs (HCWs), surfaces of the environment, and even through the air.

In a survey on the percentage (Muto et al., 2003 and Al-Talib et al., 2014). Staph. aureus was the bacterial infection of the operating theatres, in most Iraqi cities.

Acquired Pathogens from the Environment

In the past two decades, a large spread and worrying expansion of Staph. aureus has been witnessed the subsequent from society (CA-MRSA). Those (Junie, et al., 2018 and Copin et al., 2019) isolates of CA-MRSA have been a worldwide problem and have been found in the community climate, but also in health care globally, not only in equipment. CA-MRSA isolates have been reported by some hospitals as HA-MRSA isolates, they are dominant (Hesje, et al., 2011). These two group's differences in their susceptibility to antimicrobial agents also occur, creation of the methicillin resistance genetic cassette code and related cassette code profiles with external toxins. Since the link to CA-MRSA and HA-MRSA this knowledge may be about the vulnerability and fertility properties of microbes, useful in planning possible infection prevention and management plans (Hesje et al.,2011). The genetic variations found between HA-MRSA and CAMRA increased the virulence of CA-MRSA strains, which are borne by CA-MRSA, whereas HA-MRSA has SCCmec I, either SCCmec IV or VPantone - a cellular toxin developed by Staph. aureus is valentine leukocidin (PVL).

The significance of PVL in CA-MRSA virulence is fine for, HA MRSA and CAMRSA, produced particularly in the skin and soft tissues (Singh, et al., 2018), but is unclear due to the simple transmission of Staph. aureus epidemiological making, from the population to hospitals and vice versa, a far more nuanced interpretation of CA-MRSA (Harastani, et al., 2014). MRSA is one of the bacterial pathogens believed to be caused by the disease. MRSA transmission, especially among healthcare workers (Huang, et al., 2019).

Livestock-associated methicillin- resistant Staphylococcus aureus (LA-MRSA)

The Staphylococcus aureus LA-MRSA is a bacterium that is antimicrobial-resistant and affect humans and wildlife, the ability to be pathogenic. LA-MRSA involvement in animals originating from bovine mastitis was first recorded in Belgium in 1972. LA-MRSA samples have been found in many species in many European countries, the United States, and Asia (Krishnamoorthy, et al.,2019).

Methods for Molecular Typing of MRSA

Patterns of susceptibility and molecular typing methods that include; profile of DNA fragment restriction, pulsed-field electrophoresis gel (PFGE), multilocus pattern typing (MLST), and the protein A (spa-typing) accessory gene regulator (agr), direct repeat unit determination of the Mec linked area of hyper- variable (dru locus is strongly located in a Meca gene (SCCmec) variable region, Mec gene complexes in SCCmec the portion has been internationally standardized (Ho et al., 2015; Goudarzi et al., 2016; Ho et al., 2016; Rezai et al., 2020).

The excellent form of molecular typing should have sufficient discriminatory discrimination strength, be highly reproducible, have simple analysis and results, and be unchangeable, cheap, and non-time-consuming data generation (Nazareth et al; 2012).

CONCLUSION

Given the potential for increased MRSA transmission, the growing danger to the public health posed by MRSA in the oral cavity cannot be understated. Additionally, it adds fresh angles to the discussions about whether or not to give candidates for high-risk dental procedures antibiotic prophylaxis. Probably, each situation calls for a different decision to be taken. Therefore, the need for newer therapeutic agents is greater than ever. It's true that there is very little information on how S. aureus, and by extension MRSA, engage with the oral microbiota and how much the oral cavity facilitates the

development of S. aureus- and MRSA-caused endocarditis as a result of dental procedures.

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