



Mini Review

Staphylococcus aureus: A Perspective on Livestock Handlers and Food Safety

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Abstract | *Staphylococcus aureus* is a significant pathogen in livestock, posing risks to both animal health and food safety. This bacterium can be found in various livestock species, including cattle, pigs, and poultry, often asymptotically colonizing their skin and mucous membranes. Livestock handlers are particularly at risk, as direct contact with infected animals can lead to zoonotic transmission. *S. aureus* is notorious for its ability to produce enterotoxins, which can contaminate food products and cause foodborne illnesses in humans. Effective biosecurity measures are crucial in minimizing the risk of infection in livestock and preventing contamination in food processing. Regular veterinary check-ups, proper hygiene practices, and employee training are essential components of food safety protocols. Additionally, surveillance programs can help identify and manage outbreaks in livestock populations. By addressing the risks associated with *S. aureus*, stakeholders can enhance food safety and protect public health. Comprehensive strategies are necessary to mitigate the potential impacts of this pathogen on both livestock and consumers.

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Introduction

Staphylococcus aureus is a significant pathogen that poses risks to both livestock health and food safety. Found in various livestock species, such as cattle, pigs, and poultry, this bacterium can asymptotically

colonize animals, making it challenging to detect (Bannerman, 2003). The pathogen is known for producing enterotoxins that can contaminate food products, leading to foodborne illnesses in consumers. As the demand for livestock products increases, ensuring safe handling and processing practices

becomes critical (Schelin *et al.*, 2011). Effective biosecurity measures, including proper hygiene and sanitation protocols, are essential in minimizing the risk of *S. aureus* transmission. Additionally, regular monitoring and veterinary interventions can help identify potential outbreaks early. Education and training for livestock handlers are vital in promoting safe practices and reducing contamination risks. Raber *et al.* (2018) by understanding the dynamics of *S. aureus* in livestock settings, stakeholders can develop comprehensive strategies to enhance food safety and protect public health. Addressing this issue is crucial in the context of modern agriculture, where the intersection of animal health and food safety is increasingly important (Campos *et al.*, 2022; Lozano *et al.*, 2020; Jing-Qian *et al.*, 2022).

Current trend in antimicrobial resistance has been discussed in several areas (Olowe *et al.*, 2024) Methicillin Resistant Staphylococcus Aureus (MRSA) is resistant pathogen to numerous medications, it poses a serious threat to public health. MRSA infections can happen in a variety of contexts, such as the community (CA-MRSA) and hospitals (HA-MRSA) (Nandhini *et al.*, 2022). MRSA is frequently linked to skin infections, but it can also cause bloodstream infections and pneumonia, among other more serious illnesses (CDC, 2024). Contaminated surfaces and direct contact are the primary means of transmission, making infection control and hygiene practices essential. Given the limited treatment options available, ongoing research into novel antibiotics and countermeasures for this resilient infection is necessary (Figure 1) (Taiwo *et al.*, 2005; Olowe *et al.*, 2013; Taylor and Unakal, 2022). *Staphylococcus aureus* is a common pathogen found in clinical samples, in animals, and among people who met them. This bacterium is well known for its capacity to cause a wide range of illnesses, from infections of the skin and soft tissues to more serious conditions like sepsis and pneumonia (CDC, 2024). Treatment choices are complicated when isolates from laboratory specimens show resistance to various antibiotics, including methicillin (Olowe *et al.*, 2013; Balaji-Maddiboyina *et al.*, 2023). According to Dubourg *et al.* (2017) reported that, the skin and mucous membranes of most healthy individuals harbor *Staphylococcus aureus*, a common part of normal human flora and the environment. While *S. aureus* typically does not cause infections on healthy skin, it can lead to serious, potentially fatal diseases if it

enters the bloodstream or internal tissues.

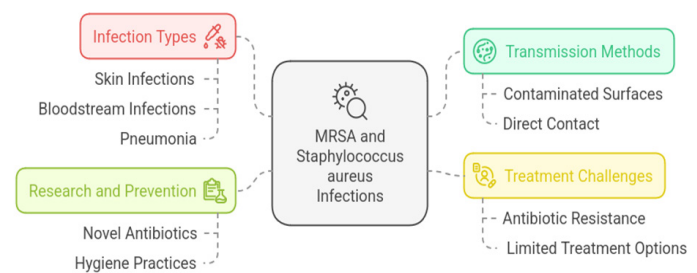


Figure 1: MRSA and staphylococcus infections.

A range of virulence factors released by *S. aureus* promotes its adhesion to host cells, cellular division, invasiveness, and evasion of the immune response. Notable among these factors are Panton-Valentine leukocidin (PVL), exfoliative toxins (ETs), hemolysins, enterotoxins (SEs), and toxic shock syndrome toxin 1 (TSST-1) (Figure 2), all of which contribute to the bacterium's virulence (Jarraud, 2002). The location of the infection on the body influences the symptoms of any *S. aureus* infection, including MRSA. MRSA infections commonly occur in cuts or scrapes that break the skin. Most *S. aureus* skin infections, including MRSA, present as a pimple or skin infection that may be red, swollen, painful, warm to the touch, filled with pus or other fluid and accompanied by a fever (Figure 3) (CDC, 2024). *S. aureus* in livestock has been linked to mastitis and other health problems that impact food safety as well as animal welfare (Campos *et al.*, 2022). Because handlers are primary carrier and capable of spreading zoonotic diseases, agricultural settings require strict hygienic measures (Crespo-Piazuelo and Lawlor, 2021). It is essential to comprehend the traits and resistance profiles of *S. aureus* from various sources to create efficient management strategies and guarantee the safety of the public's health. The virulence of MRSA strains has been linked also to the presence of the *pvl* gene.

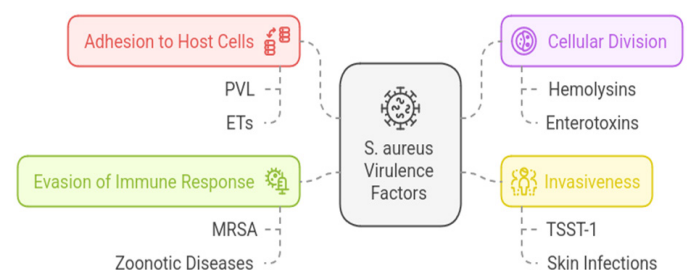


Figure 2: Virulence factors and impact of Staphylococcus aureus.

The virulence of the MRSA strain may not be due to the *pvl* gene alone, according to earlier studies, which also revealed that the presence of *pvl* and other

virulent components may increase virulence (Watkins *et al.*, 2012). However, the mechanism of *S. aureus*'s antibiotic resistance genes in Nigeria, has not be clarified.

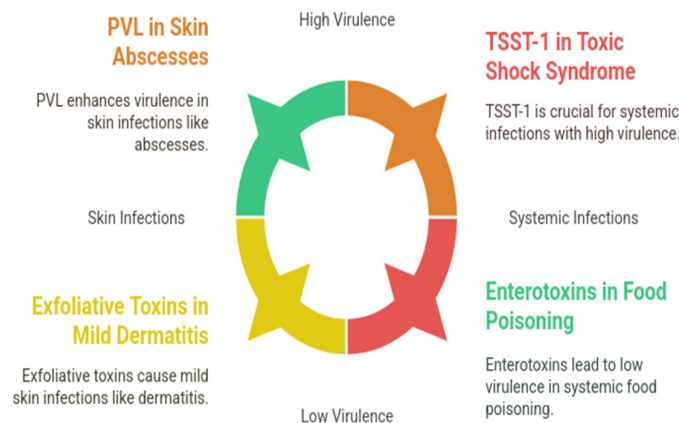


Figure 3: Virulence factors and infection locations of *S. aureus* infections.

Historical review of MRSA

Antibiotic-resistant *S. aureus* strain infections are a great concern worldwide in both clinical and community settings. Jevons (1961), referenced in Matuszewska *et al.* (2020), reported that MRSA was first isolated in 1961, just a few years after methicillin was initially used in clinical settings. MRSA infections were initially exclusively seen in patients admitted in hospitals or those who had been exposed to medical facilities, but they gradually spread to more people in the general community. This resulted in the classification of MRSA strains as either community-associated or healthcare-associated MRSA based on the patient's background (DeLeo *et al.*, 2010). A third epidemiological group, referred to as livestock-associated MRSA, has emerged in the last ten years, with human MRSA infections increasingly associated to contact with livestock (Voss *et al.*, 2005; Lee *et al.*, 2018; Matuszewska *et al.*, 2020). A diverse range of mammals, including insectivores, rodents, carnivores, ruminants, and birds, have been identified as carriers of *S. aureus* (Mrochen *et al.*, 2018a, b; Schaumburg *et al.*, 2012; Lozano *et al.*, 2016; Feßler *et al.*, 2018).

Any host that is colonized by *S. aureus* has the potential to be a source of infection for different host species. Reports from 2005 indicate that pig farmers in France and the Netherlands contracted *S. aureus* infections due to a high prevalence of MRSA carriage in livestock (Armand-Lefevre *et al.*, 2005; Voss *et al.*, 2005). The risk of zoonotic spread from other host species can be evaluated by considering three

factors: the species incidence (which species harbor the pathogen), the prevalence rates (the proportion of individuals within a species that are colonized), and the frequency of interactions or contact between humans and these species. The zoonotic risk picture changes if strains are regionally adapted to a specific species or group of species. Therefore, it's crucial to comprehend host specificity and switching.

Epidemiology of *Staphylococcus aureus* infections

Because *S. aureus* is a prominent cause of hospital acquired and community-acquired infections, it is critical to assess the relatedness of isolates obtained during an outbreak investigation. Typing systems must be repeatable, selective, and simple to understand and use. Phage typing is the standard method for identifying *S. aureus*. This approach is based on a phenotypic marker that is difficult to replicate. It also does not type many isolates (20% according to a recent survey at the Centers for Disease Control and Prevention), and it necessitates the upkeep of many phage stocks and propagating strains, so it can only be performed by specialized reference laboratories (Lakhundi and Zhang, 2018). Many molecular typing methods (Figure 4) have been used to study the epidemiology of *S. aureus*, especially methicillin-resistant strains (MRSA). Plasmid analysis has been widely utilized with a successful outcome, but it has the problem that plasmids are quickly lost and acquired, making it fundamentally unpredictable. In the epidemiology of MRSA, techniques developed to identify restriction fragment length polymorphisms (RFLP) employing a range of gene probes, particularly rRNA genes (ribotyping), have had little success. The restriction enzyme employed to cut the genomic DNA, as well as the probes, is critical in this method. Although random primer PCR can differentiate across strains, an appropriate primer for *S. aureus* has yet to be discovered. The most successful approach is pulsed field gel electrophoresis, in which genomic DNA is cleaved using a restriction enzyme, yielding huge fragments of 50-700 kb (Lopez-Canovas *et al.*, 2019).

Etiology

Staphylococcus aureus is a type of cocci-shaped, gram-positive bacteria that is stained purple by the Gram stain and forms clusters that are grape-like. These organisms can grow in salt-containing media, up to 10%, and their colonies are frequently golden or yellow. These organisms can thrive either aerobically

or anaerobically (facultatively) at temperatures between 18 °C and 40 °C (Taylor and Unakal, 2021). Biochemical tests are catalase positive (all pathogenic *Staphylococcus* species), coagulase-positive (to differentiate *Staphylococcus aureus* from other *Staphylococcus* species), novobiocin sensitive (to differentiate from *Staphylococcus saprophyticus*), and mannitol fermentation positive (to differentiate from *Staphylococcus epidermidis*) (Taylor and Unakal, 2022). MRSA strains have the *mecA* gene on their bacterial chromosome, which is a part of the wider Staphylococcal chromosomal cassette *mec* (SCC*mec*) area and allows resistance to a variety of antibiotics, according to the type of SCC*mec*, (Rasigade *et al.*, 2014). The PBP-2a (penicillin-binding protein 2a) protein is encoded by the *mec* gene. The PBP-2a, a penicillin-binding protein (PBP), is an important cell wall enzyme of the bacteria that induce the synthesis of the peptidoglycan in the bacterial cell wall. PBP-2A continues to accelerate the formation of the bacterial cell wall even in the presence of several antibiotics because it has a lower affinity to bind to beta-lactams (and other antibiotics derived from penicillin) than other PBPs. Because of this, MRSA strains of *S. aureus* that produce PBP-2A can flourish amid a wide variety of antibiotics. Methicillin, nafcillin, oxacillin, and cephalosporin resistance are common among MRSA strains (Rasigade and Vandenesch, 2014).

(Rasigade *et al.*, 2014).

Pathogenesis of *S. aureus* infections

Many extracellular and cell surface-associated proteins that *S. aureus* generates could play a role in the pathogen's pathogenicity. Nearly every infection caused by this organism has a complicated etiology. As such, determining the exact role of a given element might be difficult. It also draws attention to the shortcomings of many animal models used to study staphylococcal infections. Certain factors may play a role in pathogenesis since their expression has been linked to strains derived from various illnesses. The expression of certain factors has been associated with strains obtained from different infections, indicating their potential role in pathogenesis. Replication of these infections in animal models has been made possible (Wójcik-Bojek *et al.*, 2022). Recent progress has been made in our understanding of the pathophysiology of staphylococcal illnesses, thanks to the application of molecular biology, proteins have been isolated and purified due to cloning and sequencing of genes encoding putative virulence factors. This has made it easier to conduct molecular research on their routes of action in model systems.

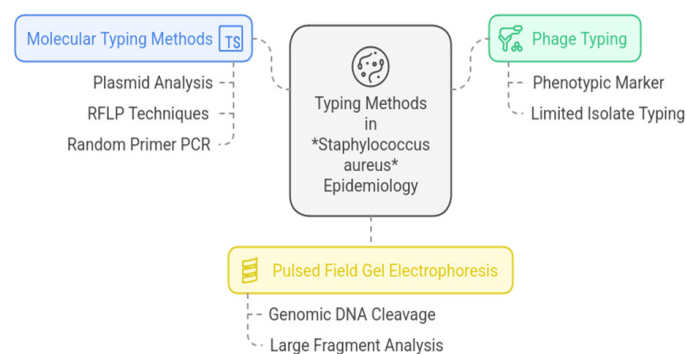


Figure 4: Typing methods in *Staphylococcus aureus* epidemiology.

Structure

Gram-positive cocci with a diameter of 0.5–1.0 μm is called staphylococci. As they enlarge, they can form short chains, pairs, or clusters. The clusters are the result of Staphylococci splitting into two planes. The arrangement of streptococci sets them apart from micrococci and staphylococci, as they usually grow in chains. Cultures grown in broth must be monitored since streptococci produced in solid media may manifest as clumps. Several fields should be evaluated before deciding whether clumps or chains are present

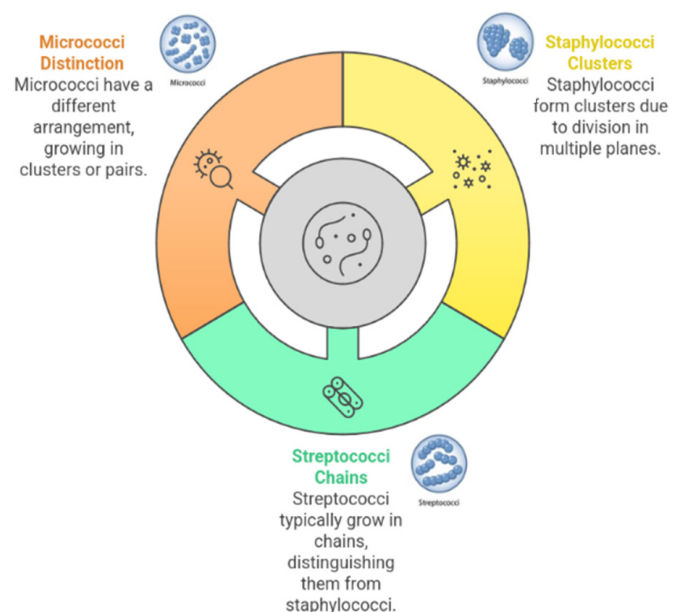


Figure 5: Morphology of gram-positive cocci.

Additionally, suspected virulence factor-encoding genes have been silenced, and in animal models, the virulence of the mutant strain has been compared to the wild-type strain. Any decrease in virulence implies the presence of the missing element. When the gene is transferred back to the mutant, virulence should recover, proving the Molecular Koch's Postulates to

be true. This method has confirmed several *S. aureus* pathogenicity factors.

infections are more prevalent after an influenza virus infection and a Cystic Fibrosis diagnosis.

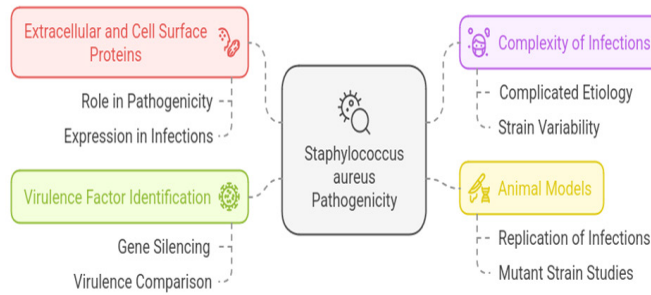


Figure 6: Exploring the *Staphylococcus aureus* pathogenicity.

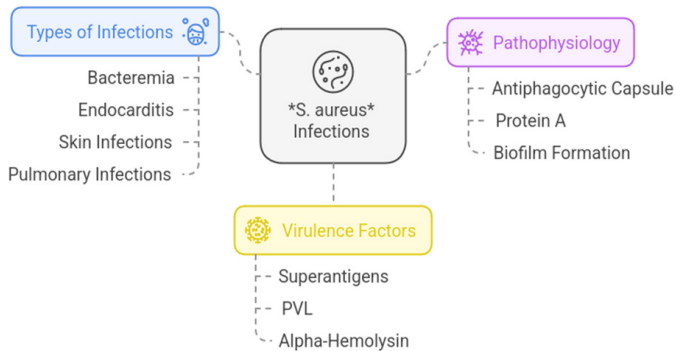


Figure 7: *S. aureus* infections: Types, pathophysiology, and virulence factors.

Pathophysiology

Infections caused by *S. aureus* are among the most prevalent bacterial infections in people. These infections include bacteremia, infective endocarditis, skin, and soft tissue infections (such as impetigo, folliculitis, furuncles, carbuncles, cellulitis, and others), osteomyelitis, septic arthritis, infections of prosthetic devices, pulmonary infections (such as pneumonia and empyema), gastroenteritis, meningitis, these bacteria can result in invasive infections and/or toxin-mediated illnesses, based on the strains present and the site where they infect (Foster, 2005). Depending on the type of *S. aureus* infection, the pathophysiology differs significantly (Figure 7). The creation of an antiphagocytic capsule, concealing of antibodies produced by the host or antigen covering by Protein A, biofilm formation, intracellular longevity, and preventing chemotaxis of white blood cells are all ways of evading the host immune response by the bacteria (Salgado-Pabón et al., 2013). Furthermore, *Staphylococcal superantigens* (TSST-1 or toxic shock syndrome toxin 1) play a crucial role in the virulence of infected endocarditis, sepsis, and toxic shock syndrome. Pneumonia infections are linked to bacterial synthesis of *pvl* (Panton-Valentine leukocidin), Protein A, and alpha-hemolysin, and

Methicillin-resistant *Staphylococcus aureus*

Methicillin-resistant *Staphylococcus aureus* (MRSA) has been a threat to public health for decades causes infection in both in clinical and outside the clinical settings that are difficult to treat due to the multi-resistance of the bacteria (Figure 8). The clonal lineages involved in those infections occurring in the community, i.e. ST8, ST30, and ST80 in Germany (Robert Koch-Institute, 2011) and globally (Mediavilla et al., 2012), often harbour genes encoding for Panton-Valentine leukocidin (*pvl*), which is one of the major exotoxins of *S. aureus*. *pvl* is a well-known virulence factor of *S. aureus* causing severe disease (Otto, 2013; Thurlow et al., 2012; Vandenesch et al., 2003). *pvl*-positive MRSA are also associated with chronic and recurrent sSSTIs (Stieber et al., 2014). The frequent detection of specific clonal MRSA lineages (CC398MRSA) among livestock, i.e., pigs, cattle, poultry, in recent years in several (European) countries is a matter of concern (de Neeling et al., 2007; Spohr et al., 2010; Richter et al., 2012). These so-called livestock-associated (LA)-MRSA are zoonotic (vanLoo et al., 2007; Witte et al., 2007b; Cuny et al., 2012) and people with occupational contact to livestock, e.g., farmers, veterinarians, workers at abattoirs, are frequently exposed and colonized. Typically, staphylococcal food poisoning (SFP) occurs after ingestion of foods that are contaminated with *S. aureus* by improper handling and subsequent storage at temperatures supporting the growth of the bacteria. *Staphylococcal* food poisoning is rarely fatal, but it can lead to severe *S. aureus* infections such as osteomyelitis and pneumonia (Mulder and Verwiel, 1980; Duben et al., 1988; Taiwo et al., 2005; Olowe et al., 2013, 2014). Although *S. aureus* is mainly involved in SFP, intoxications caused by the ingestion of SE produced by MRSA so far were only described occasionally. The MRSA phenotype is primarily due to the presence of *mecA*, which encodes a low-affinity penicillin-binding protein (PBP2a or PBP2) with degraded affinity for β -lactams (Oliveira and De Lencastre, 2011; Moellering, 2012). The virulence of community-associated MRSA strains surpasses that of hospital-associated (HA-MRSA) and livestock-associated (LA-MRSA) strains due to their frequent production of the Panton-Valentine leukocidin (*pvl*) toxin, as noted by Otto (2013). Other virulence factors of *S. aureus* include surface components (such

as the capsule, peptidoglycans, teichoic acid, protein A), enzymes (such as esterases, lipases, fatty-acid modifying enzymes, various proteases, hydrolytic enzymes, catalase, and β -lactamase), and various toxins (such as leukocidins, enterotoxins, TSST-1, and alpha, beta, gamma, and delta hemolysins) (Vasconcelos and Cunha, 2010).

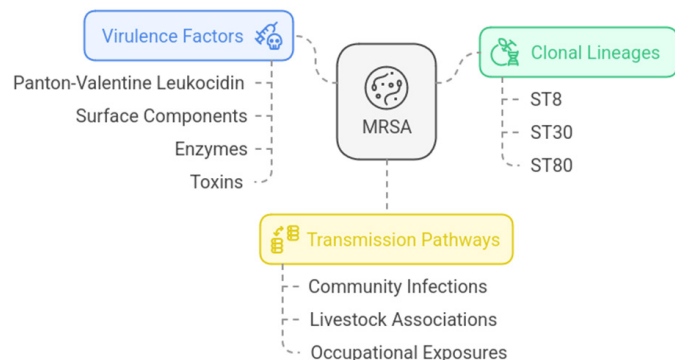


Figure 8: MRSA: Clonal lineages, virulence factors, and transmission.

Risk factors associated with *Staphylococcus aureus* bacteremia (SAB)

Staphylococcus aureus bacteremia (SAB) presents notable risk factors, particularly linked to age and ethnicity (Figure 9). Age is a significant determinant, with the highest incidence found at the extremes of life. Studies show that rates are elevated in infants, decrease through young adulthood, and then rise again in older adults. For instance, individuals over 70 years old experience over 100 cases per 100,000 person-years, compared to just 4.7 cases per 100,000 among younger, healthier U.S. military personnel. Research from Denmark indicates a 48% increase in SAB incidence from 2008 to 2015, particularly among those over 80, where rates surged by 90%. Despite a stable 30-day case-fatality rate of 24%, crude population death rates rose by 53% during the same period. The reasons behind this increase in elderly populations remain unclear.

Gender also plays a role, as males consistently exhibit a higher incidence of SAB, with a male to female ratio of approximately 1.5. The reasons for this discrepancy are not yet understood. Ethnic disparities are evident in the U.S., where the incidence of invasive MRSA is significantly higher in the Black population compared to Whites. Similar trends are observed in Australia and New Zealand among Indigenous populations. Socioeconomic factors alone do not account for these differences, and further research is needed to explore the role of genetic susceptibility in these ethnic

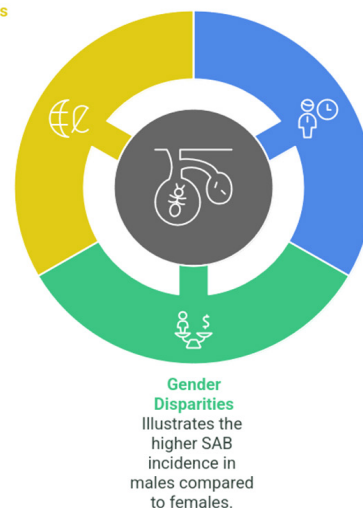
variations.

Ethnic Variations

Examines the higher SAB incidence in certain ethnic groups.

Age-Related Trends

Highlights the impact of age on SAB incidence rates.



Gender Disparities
Illustrates the higher SAB incidence in males compared to females.

Figure 9: SAB incidence factors.

Clinical features and outcomes

Impetigo is the most prevalent bacterial skin infection in children, characterized by bullous or papular lesions that progress to crusted areas, typically on exposed skin like the face and extremities, without systemic symptoms (Nardi and Schaefer, 2021). Recovery rates for impetiginous lesions are reported at 29-90% for *Streptococcus pyogenes* and 57-81% for *Staphylococcus aureus*. While cutaneous abscesses are commonly associated with *S. aureus* skin and soft tissue infections (SSTIs), other forms, such as nonpurulent cellulitis (Figure 10), can also occur, albeit less frequently. The diagnosis is complicated by the lack of a gold standard and variability in microbiological methods. *S. aureus* cellulitis typically affects the lower extremities but can also involve the upper extremities, abdomen, and face (Darboe et al., 2019).



Figure 10: Skin and soft tissue infections caused by *Staphylococcus aureus*.

These include an abscess located in the top left, cellulitis surrounding a pustule in the top right, embolic infarcts that complicate infective endocarditis in the bottom left, and impetigo that complicates scabies infection in the bottom right (DermNet).

Several reports have also discussed contamination of raw meat with *Staphylococcus aureus*. Raw meat contamination is a significant food safety concern in Nigeria, where challenges such as inadequate hygiene practices, poor infrastructure in meat markets, and limited enforcement of food safety standards contribute to the prevalence of microbial contamination. *Staphylococcus aureus*, including antibiotic-resistant strains, is among the pathogens frequently detected in raw meat, posing risks of foodborne illnesses to consumers. [Adesiji et al. \(2015\)](#) examined microbial contamination in retail raw meats sold in Sagamu markets, Nigeria, identifying notable levels of *S. aureus*. Their findings underscore the urgent need to implement stricter hygiene protocols in meat handling and processing to reduce contamination risks and protect public health.

Treatment/ management

The type of *S. aureus* infection and the presence of drug-resistant strains are critical factors in determining treatment. When antimicrobial therapy is required, the duration and mode of therapy are dependent on the infection type and other factors ([Tong et al., 2015](#)). Penicillin is the drug of choice for MSSA or methicillin-sensitive *S. aureus* strains, while vancomycin is preferred for MRSA strains ([Boucher et al., 2008](#)). However, alternative therapies may be necessary in addition to antimicrobial treatment ([Chambers, 2013](#)). For example, fluid-replacement management may be required for toxin-mediated illness, while the removal of foreign devices may be necessary for prosthetic valve endocarditis or catheter-associated infections. MRSA strains are becoming a significant threat in both hospital and community settings, as they are often resistant to multiple antibiotics ([Figure 11](#)).

Antimicrobial resistance poses a severe challenge in the treatment of animal and human infections. The presence of *S. aureus* and MRSA in the environment of livestock farms and slaughterhouses and the potential for transmission to meat and workers in these settings is a significant concern to the scientific community. Accurate detection of MRSA is critical, given the

changing epidemiology of *S. aureus* and MRSA, and up to date information is essential for effective control measures. Identifying possible sources and routes of meat contamination in processing facilities is essential to improve preventive measures targeting their transmission to final products and their dispersion in the community.

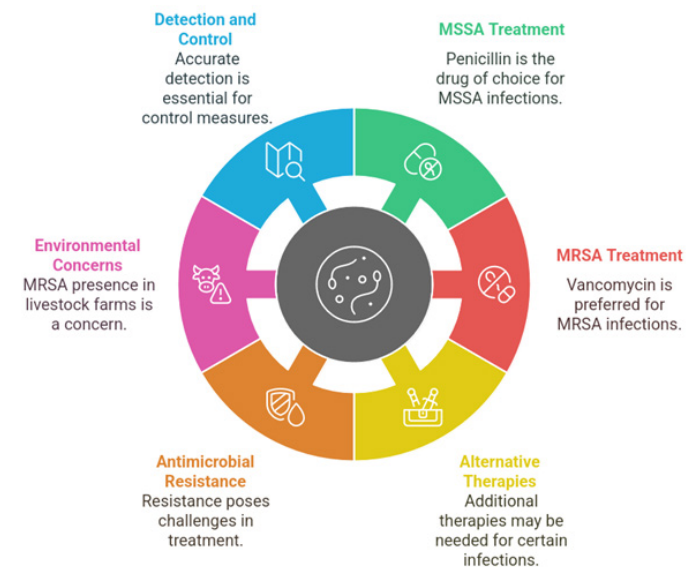


Figure 11: *S. aureus* infection management.

Conclusions

The investigation of *Staphylococcus aureus* isolated from clinical samples, animals, and their handlers raises serious questions about the pathogen's patterns of resistance and transmission. Similar strains have been identified in both humans and animals, suggesting a potential zoonotic relationship, and underscoring the interdependence of animal and human health. Additionally, the observed differences in resistance characteristics raise concerns about the efficacy of common antibiotics, complicating treatment choices for infections in both populations.

Recommendation

Establishing regular surveillance programs to monitor *Staphylococcus aureus* strains in clinical settings and livestock to track resistance and zoonotic transmission. Strengthening infection control measures and educating handlers on proper hygiene practices are essential for reducing transmission risks. Promoting responsible antibiotic use in both human and veterinary medicine can help mitigate the development of resistance, with guidelines ensuring that prescriptions are necessary. Additionally,

enhancing public awareness campaigns about the risks of *Staphylococcus aureus* and prevention strategies for consumers and livestock handlers is crucial for improving health outcomes.

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Novelty Statement

This review article, *Staphylococcus aureus: A Perspective on Livestock Handlers and Food Safety*, delves into the intricate zoonotic dynamics between animals and humans, emphasizing their interconnected health risks. It highlights critical disparities in antibiotic resistance patterns, raising concerns about the effectiveness of standard treatments and the growing challenge of managing infections across both populations.

Author's Contribution

OOO and AYO collected and analyzed the data. AEF and OFD collected the data online and did further comparative analysis. AO designed the review and wrote the manuscript. OAO edited the manuscript and supervised activities. All authors read and approved the final version of the manuscript.

Conflict of interest

The authors have declared no conflict of interest.

References

- Adesiji, Y.O., Adekanle, M.A. and Jolayemi, J.B., 2015. A study of microbial analysis of fresh fruits and vegetables in Sagamu markets, South-West Nigeria. *Afr. J. Microbiol. Res.*, 9(2): 111–117. <https://doi.org/10.4314/agrosh.v15i2.1>
- Armand-Lefevre, L., Ruimy, R. and Andreumont, A., 2005. Clonal comparison of *Staphylococcus aureus* isolates from healthy pig farmers, human controls, and pigs. *Emerg. Infect. Dis.*, 11(5): 711–714. <https://doi.org/10.3201/eid1105.040866>
- Balaji-Maddiboyina, R.H., Ramaiah, M., Sarvesh, C.N., Sahasra, H.K., Ramya, K.N. and Bhabani, S.N., 2023. Methicillin-resistant *Staphylococcus aureus*: Novel treatment approach breakthroughs. *Bull. Natl. Res. Centre*, 47(1). <https://doi.org/10.1186/s42269-023-01072-3>
- Bamigboye, B.T., Olowe, O.A. and Taiwo, S.S., 2018. Phenotypic and molecular identification of vancomycin resistance in clinical *Staphylococcus aureus* isolates in Osogbo, Nigeria. *Eur. J. Microbiol. Immunol.*, 8(1): 25–30. <https://doi.org/10.1556/1886.2018.00003>
- Bannerman, T.L., 2003. 2003. *Staphylococcus, Micrococcus and other catalase-positive cocci that grow aerobically*, p. 384–404. In P. R. Murray, E. J. Baron, J. H. Jorgensen, M. A. Tenover, and R. H. Tenover (ed.), *Manual of clinical microbiology*, 7th ed. ASM Press, Washington, DC
- Boucher, Helen, W. and Corey, G.R., 2008. Epidemiology of methicillin-resistant *Staphylococcus aureus*. *Clin. Infect. Dis.*, 46(S5): S344–S349. <https://doi.org/10.1086/533590>
- Campos, B., Pickering, A.J., Lis, P.R., Ananda, P.A., Mary, H.F-K., Tiago, J.R.F. and de, A., 2022. Diversity and pathogenesis of *Staphylococcus aureus* from bovine mastitis: Current understanding and future perspectives. *BMC Vet. Res.*, 18(1). <https://doi.org/10.1186/s12917-022-03197-5>
- CDC, 2024. Methicillin-resistant *Staphylococcus aureus* (MRSA) Basics. Methicillin-Resistant *Staphylococcus aureus* (MRSA). <https://www.cdc.gov/mrsa/about/index.html>
- Chambers, H.F., 2013. Editorial commentary: Cellulitis, by any other name. *Clin. Infect. Dis.*, 56(12): 1763–1764. <https://doi.org/10.1093/cid/cit126>
- Crespo-Piazuelo, D. and Lawlor, P.G., 2021. Livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA) prevalence in humans in close contact with animals and measures to reduce on-farm colonisation. *Irish Vet. J.*, 74(1). <https://doi.org/10.1186/s13620-021-00200-7>
- Cuny, C., Friedrich, A. W., and Witte, W. (2012). Absence of livestock-associated methicillin-resistant *Staphylococcus aureus* clonal complex CC398 as a nasal colonizer of pigs raised in an alternative system. *Applied and environmental microbiology*, 78(4), 1296–1297.
- Darboe, S., Dobreniecki, S., Jarju, S., Jallow, M.,

- Mohammed, N.I., Wathuo, M., Ceesay, B., Tweed, S., Basu Roy, R., Okomo, U., Kwambana-Adams, B., Antonio, M., Bradbury, R.S., de Silva, T., Forrest, K., Roca, A., Lawal, B.J., Nwakanma, D. and Secka, O., 2019. Prevalence of Pantone-Valentine Leukocidin (PVL) and antimicrobial resistance in community-acquired clinical *Staphylococcus aureus* in an Urban Gambian hospital: A 11-year period retrospective pilot study. *Front. Cell. Infect. Microbiol.*, 9. <https://doi.org/10.3389/fcimb.2019.00170>
- De Neeling, A.J., De Neeling, M.J.M., van den Broek, E.C., Spalburg, M.G., van Santen-Verheue, W.D.C., Dam-Deisz, H.C., Boshuizen, A.W., van de Giessen, E. and van Duiker, X.W., 2007. Huidscans High prevalence of methicillin-resistant *Staphylococcus aureus* in pigs. *Vet. Microbiol.*, 122(2007): 366-372. <https://doi.org/10.1016/j.vetmic.2007.01.027>
- DeLeo, F.R., Otto, M., Kreiswirth, B.N. and Chambers, H.F., 2010. Community associated methicillin-resistant *Staphylococcus aureus*. *Lancet* (London, England), 375(9725): 1557-1568. [https://doi.org/10.1016/S0140-6736\(09\)61999-1](https://doi.org/10.1016/S0140-6736(09)61999-1)
- DermNet. (n.d.). Staphylococcal skin infections. DermNet NZ. <https://dermnetnz.org/topics/staphylococcal-skin-infection>
- Duben, J., Šourek, J., and Bergdoll, M. S. (1988). A case of fatal enterotoxigenic complicated with acute bronchopneumonia caused by *Staphylococcus aureus* strains producing enterotoxin A. *Infection*, 16(3), 183-185. <https://doi.org/10.1016/j.ijantimicag.2016.11.015>
- Feßler, A.T., Thomas, P., Mühldorfer, K., Grobber, M., Brombach, J., Eichhorn, I., Monecke, S., Ralf Ehrlich, and Schwarz, Š., 2018. Phenotypic and genotypic characteristics of *Staphylococcus aureus* isolates from zoo and wild animals. *Vet. Microbiol.*, 218: 98-103. <https://doi.org/10.1016/j.vetmic.2018.03.020>
- Foster TJ. Immune evasion by staphylococci. *Nat Rev Microbiol.* 2005 Dec;3(12):948-58. [PubMed]
- Jarraud, S., 2002. Relationships between *Staphylococcus aureus* genetic background, virulence factors, agr groups (Alleles), and human disease. *Infect. Immun.*, 70(2): 631-641. <https://doi.org/10.1128/IAI.70.2.631-641.2002>
- Jevons M. "Celbenin"-resistant staphylococci. *Br Med J.* 1961;1:124-5. [Google Scholar]
- Jing-Qian, Z.W., Yongzhang, Z. and Chang, L., 2022. One health: A holistic approach for food safety in livestock. *Sci. One Health*, 1: 100015. <https://doi.org/10.1016/j.soh.2023.100015>
- Lakhundi, S. and Zhang, K., 2018. Methicillin-resistant *Staphylococcus aureus*: Molecular characterization, evolution, and epidemiology. *Clin. Microbiol. Rev.*, 31(4). <https://doi.org/10.1128/CMR.00020-18>
- Lee, A.S., de Lencastre, H., Garau, J., Kluytmans, J., Malhotra-Kumar, S., Peschel, A. and Harbarth, S., 2018. Methicillin-resistant *Staphylococcus aureus*. *Nat. Rev. Dis. Primers*, 4(18033): 18033. <https://doi.org/10.1038/nrdp.2018.33>
- Lopez-Canovas, L., Martinez, B.M.B., Herrera, I.J.A. and Flores, S.E., 2019. Pulsed field gel electrophoresis: Past, present, and future. *Anal. Biochem.*, 573: 17-29. <https://doi.org/10.1016/j.ab.2019.02.020>
- Lozano, C., Gharsa, H., Ben Slama, K., Zarazaga, M. and Torres, C., 2016. *Staphylococcus aureus* in animals and food: Methicillin resistance, prevalence and population structure. A review in the African continent. *Microorganisms*, 4(1): 12. <https://doi.org/10.3390/microorganisms4010012>
- Matuszewska, M., Murray, G.G.R., Harrison, E.M., Holmes, M.A. and Weinert, L.A., 2020. The evolutionary genomics of host specificity in *Staphylococcus aureus*. *Trends Microbiol.*, 28(6): 465-477. <https://doi.org/10.1016/j.tim.2019.12.007>
- Mediavilla, J.R., Chen, L., Mathema, B. and Kreiswirth, B.N., 2012. Global epidemiology of community-associated methicillin resistant *Staphylococcus aureus* (CA-MRSA). *Curr. Opin. Microbiol.*, 15 (2012), pp. 588-595. <https://doi.org/10.1016/j.mib.2012.08.003>
- Moellering, R.C., Jr. 2012. MRSA: The first half century. *J. Antimicrob. Chemother.*, 67: 4-11. (Google Scholar). <https://doi.org/10.1093/jac/dkr437>
- Mrochen, D.M., Dorothee, G., Schulz, D., Gumz, J., Trübe, P., Pritchett-Corning, K.R., Johnson, S.H., Nicklas, W., Kirsch, P., Martelet, K., van Berg, S., Bröker, B.M., Wiles, S. and Holtfreter, S., 2018. Global spread of mouse-adapted *Staphylococcus aureus* lineages CC1, CC15, and CC88 among mouse breeding facilities. *Int.*

- J. Med. Microbiol., 308(6): 598–606. <https://doi.org/10.1016/j.ijmm.2017.11.006>
- Mrochen, D.M., Schulz, D., Fischer, S., Jeske, K., Heba El-Gohary, Reil, D., Imholt, C., Trübe, P., Suchomel, J., Tricaud, E., Jacob, J., Heroldová, M., Bröker, B.M., Strommenger, B., Walther, B., Ulrich, R.G. and Holtfreter, S., 2017. Wild rodents and shrews are natural hosts of *Staphylococcus aureus*. Int. J. Med. Microbiol., 308(6): 590–597. <https://doi.org/10.1016/j.ijmm.2017.09.014>
- Mulder, C. J., and Verwiel, J. (1980). A case of vertebral osteomyelitis caused by *Staphylococcus aureus*; complication of a staphylococcal enterotoxigenosis caused by consumption of vanilla custard. Nederlands Tijdschrift Voor Geneeskunde, 124(19), 740–743.
- Nandhini, P., Kumar, P., Mickymaray, S., Alothaim, A.S., Somasundaram, J. and Rajan, M., 2022. Recent developments in methicillin-resistant *Staphylococcus aureus* (MRSA) treatment: A review. Antibiotics, 11(5): 606. <https://doi.org/10.3390/antibiotics11050606>
- Nardi NM, Schaefer TJ (2021) Impetigo. [Updated 2020 Nov 21]. In: StatPearls [Internet]. StatPearls Publishing, Treasure Island. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK430974/>
- Oliveira, D.C. and de Lencastre, H., 2011. Methicillin-resistance in *Staphylococcus aureus* is not affected by the overexpression in trans of the *mecA* gene repressor: A surprising observation. PLoS One, 6: e23287. <https://doi.org/10.1371/journal.pone.0023287>
- Olowe, O.A., Gilbert, C.E., Odewale, G.O. and Eniola, K.I.T., 2014. Multidrug resistant *Staphylococcus aureus* in selected health care facilities in south western Nigeria. Curr. Trends Technol. Sci., 3(4): 321–325.
- Olowe, O.A., Kukoyi, O.O., Taiwo, S.S., Ojurongbe, O., Opaleye, O.O., Bolaji, O.S., Adegoke, A.A., Makanjuola, O.B., Ogbolu, D.O. and Alli, O.T., 2013. Phenotypic and molecular characteristics of methicillin-resistant *Staphylococcus aureus* isolates from Ekiti State, Nigeria. Infect. Drug Resist., pp. 87–92. <https://doi.org/10.2147/IDR.S48809>
- Olowe, R.A., Olawumi, O. and Olowe, O.A., 2024. Current trends in antimalarial drug resistance in Nigeria: A mini review. BIMA J. Sci. Technol., (2536–6041) 8(3A): 171–188.
- Olowe, O.A., Eniola, K.I.T., Olowe, R.A. and Olayemi, A.B., 2007. Antimicrobial susceptibility and betalactamase detection of MRSA in Osogbo, SW Nigeria. Nat. Sci., 5(3): 44–48.
- Otto, M., 2013. Community-associated MRSA: What makes them special? Int. J. Med. Microbiol., 303(6–7): 324–330. <https://doi.org/10.1016/j.ijmm.2013.02.007>
- Raber, J.M., Niekrasz, M., Linkenhoker, J., James M. Raber, M. Niekrasz, J. Linkenhoker, and K.A. Perdue. 2018. Veterinary care. In: (eds. Weichbrod, R.H., Thompson, G.A.H., Norton, J.N.). Management of animal care and use programs in research, education, and testing. 2nd edition. Boca Raton (FL): CRC Press/Taylor and Francis; 2018. Chapter 31. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK500439/>
- Rasigade JP, Vandenesch F. 2014. *Staphylococcus aureus*: a pathogen with still unresolved issues. Infect Genet Evol. 21:510–4. doi: 10.1016/j.meegid.2013.08.018. Epub 2013 Aug 29. PMID: 23994773.
- Richter, A., Sting, R., Popp, C., Rau, J., Tenhagen, B.A., Guerra B, Hafez HM, Fetsch A. 2012. Prevalence of types of methicillin-resistant *Staphylococcus aureus* in turkey flocks and personnel attending the animals. Epidemiol. Infect., 10: 1–10.
- Robert Koch-Institut, 2013. Eigenschaften, häufigkeit und verbreitung von MRSA in Deutschland update 2011/2012 Epidemiol. Bull., 21: 187–196.
- Salgado-Pabón, W., Breshears, L., Spaulding, A.R., Merriman, J.A., Stach, C.S., Horswill, A.R., Peterson, M.L., and Schlievert, P.M., 2013. Superantigens are critical for *Staphylococcus aureus* infective endocarditis, sepsis, and acute kidney injury. MBio, 4(4). <https://doi.org/10.1128/mBio.00494-13>
- Schaumburg, F., Alabi, A., Köck, R., Mellmann, A., Kremsner, P. and Boesch, C., 2012. Highly divergent *Staphylococcus aureus* isolates from African non-human primates. Environ. Microbiol. Rep., 4(1): 141–146. <https://doi.org/10.1111/j.1758-2229.2011.00316.x>
- Schelin, J., Wallin-Carlquist, N., Cohn, M.T., Lindqvist, R., Barker, G.C., Rådström, P., 2011. The formation of *Staphylococcus aureus* enterotoxin in food environments and advances

- in risk assessment. *Virulence*, 2(6): 580-592. <https://doi.org/10.4161/viru.2.6.18122>
- Shallcross, L.J., Fragaszy, E., Johnson, A.M. and Hayward, A.C., 2013. The role of the Pantón-Valentine leucocidin toxin in staphylococcal disease: A systematic review and meta-analysis. *Lancet Infect. Dis.*, 13(1): 43-54. [https://doi.org/10.1016/S1473-3099\(12\)70238-4](https://doi.org/10.1016/S1473-3099(12)70238-4)
- Spohr, M., Rau, J., Friedrich, A., Klittich, G., Fetsch, A., Guerra, B., Hammerl, J.A., Tenhagen, B.A., 2010. Methicillin-resistant *Staphylococcus aureus* (MRSA) in three dairy herds in southwest Germany. *Zoon. Publ. Health*, 58: 252-261. <https://doi.org/10.1111/j.1863-2378.2010.01344.x>
- Stieber, B., Monecke, S., Müller, E., Baier, V., Coombs, G. W., and Ehrlich, R. (2014). Development and usage of protein microarrays for the quantitative measurement of Pantón-Valentine leukocidin. *Molecular and Cellular Probes*, 28(4), 123-132.
- Taiwo, S.S., Bamidele, M., Omonigbehin, E.A., Akinsinde, K.A., Smith, S.I., Smith, S.I., Onile, B.A., Olowe, A.O., 2005. Molecular epidemiology of methicillin-resistant *Staphylococcus aureus* in Ilorin, Nigeria. *West Afr. J. Med.*, 24(2): 100-106. <https://doi.org/10.4314/wajm.v24i2.28176>
- Taylor, T.A. and Unakal, C.G., 2021. *Staphylococcus aureus*. PubMed; StatPearls Publishing. <https://pubmed.ncbi.nlm.nih.gov/28722898/>
- Tong, S.Y.C., Bishop, E.J., Lilliebridge, R.A., Cheng, A.C., Spasova-Penkova, Z., Holt, D.C., Giffard, P.M., McDonald, M.I., Currie, B.J. and Boutlis, C.S., 2009. Community-associated strains of methicillin-resistant *Staphylococcus aureus* and methicillin-susceptible *S. aureus* in indigenous northern Australia: Epidemiol. Outcomes. *J. Infect. Dis.*, 199(10): 1461-1470. <https://doi.org/10.1086/598218>
- Thurlow, L. R., Joshi, G. S., and Richardson, A. R. (2012). Virulence strategies of the dominant USA300 lineage of community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA). *FEMS Immunology & Medical Microbiology*, 65(1), 5-22.
- VanLoo, X., Huijsdens, E., Tiemersma, A., de Neeling, van de Sande-Bruinsma, D., Beaujean, A. and Voss, J., 2007. Kluytmans emergence of methicillin-resistant *Staphylococcus aureus* of animal origin and in humans *Emerg. Infect. Dis.*, 13(2007): 1834-1839. <https://doi.org/10.3201/eid1312.070384>
- Vandenesch, F., Naimi, T., Enright, M. C., Lina, G., Nimmo, G. R., Heffernan, H.... Etienne, J. (2003). Community-Acquired Methicillin-Resistant *Staphylococcus aureus* Carrying Pantón-Valentine Leukocidin Genes: Worldwide Emergence. *Emerging Infectious Diseases*, 9(8), 978-984. <https://doi.org/10.3201/eid0908.030089>.
- Vasconcelos, N.G. and Cunha, M.L.R.S. (2010) *Staphylococcal Enterotoxins: Molecular Aspects and Detection Methods*. *Journal of Public Health and Epidemiology*, 2, 29-42.
- Voss, A., Loeffen, F., Bakker, J., Klaassen, C. and Wulf, M., 2005. Methicillin-resistant *Staphylococcus aureus* in pig farming. *Emerg. Infect. Dis.*, 11(12): 1965-1966. <https://doi.org/10.3201/eid1112.050428>
- Watkins, R.R., David, M.Z. and Salata, R.A., 2012. Current concepts on the virulence mechanisms of methicillin-resistant *Staphylococcus aureus*. *J. Med. Microbiol.*, 61(Pt 9): 1179-1193. <https://doi.org/10.1099/jmm.0.043513-0>
- Witte, W., Strommenger, B., Stanek, C. and Cuny, C., 2007. Methicillin-resistant *Staphylococcus aureus* ST398 in humans and animals. *Central Europe Emerg. Infect. Dis.*, 13: 255-258. <https://doi.org/10.3201/eid1302.060924>
- Wójcik-Bojek, U., Różalska, B. and Sadowska, B., 2022. *Staphylococcus aureus* a known opponent against host defense mechanisms and vaccine development do we still have a chance to win? *Int. J. Mol. Sci.*, 23(2): 948. <https://doi.org/10.3390/ijms23020948>