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Research Article

# Drug Resistance Microbial of *Staphylococcus aureus*

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## Abstract

**Introduction:** Antimicrobial resistance (AMR) is a natural evolutionary response to exposure to antimicrobials. By 2050, approximately 10 million deaths are expected annually, directly or indirectly displacing neoplasia as the leading cause of death. Staphylococcus aureus is a gram-positive pathogenic bacterium with an incidence of 20 to 50 cases per year.

**Objective:** To describe the behavior of microbial drug resistance in Staphylococcus aureus.

**Material and Methods:** A bibliographic review was carried out between July and August 2024, of 26 references in Spanish and English in the SciELO, Elsevier, PubMed and Google Scholar search engine databases. The most recent published literature in accordance with the novelty of the topic in question was considered as a selection criterion.

**Development:** Staphylococcus aureus has particular characteristics of virulence and resistance to antibiotics. It presents indigenous forms of resistance: it reduces membrane permeability, limits drug absorption and the flow system by promoting drug leakage and the overproduction of β-lactamase. Resistance to methicillin and β-lactam antibiotics is determined in more than 85% by the presence of the mecA gene.

**Conclusions:** Antimicrobial resistance is a threat to human, animal and environmental health. Staphylococcus aureus is a microorganism that has very distinctive characteristics regarding its virulence and pathogenicity factors of resistance to various antibiotics. Several studies agree that resistance to methicillin and β-lactam antibiotics is determined in more than 85% by the mecA gene.

**Keywords:** Behavior; Drug Resistance Microbial; Staphylococcus aureus

## Introduction

Antimicrobial resistance is an evolutionary response to exposure to antimicrobials caused by human activity and environmental pollution. It restricts the ability to treat infections, thereby increasing the risk of future pandemics caused by resistant pathogens [1].

It arises when bacteria, viruses, fungi and parasites undergo changes over time and do not respond effectively to treatment. As a

result of the above, infections become increasingly difficult to treat, thus increasing drug resistance [2].

Since the first decade of the 20th century, the phenomenon of antimicrobial resistance has gained ground in the scientific community. It became more visible after the discovery of penicillin by Alexander Fleming in 1945 and his concern about the susceptibility it could develop to antibiotics [3].

By 2050, it is expected that there will be approximately 10 million deaths per year, directly or indirectly, which will displace neoplasia as the main cause of death [5]. In 2019, it directly caused the death of more than 1.5 million people. The largest number of cases was recorded in the sub-Saharan African region [6].

*Staphylococci* account for more than 80% of infectious diseases in routine clinical practice [7], which corresponds to what was stated by Aguayo-Reyes A., *et al*. [8], who points out that staphylococcal etiology is classified as the most frequent in a variety of entities in healthcare centers. It has an incidence that ranges between 20 and 50 cases/100,000 per year [9,10].

In Cuba, particularly in hospitals in the capital, an increasing incidence of diseases caused by this microorganism has been reported in recent years, with figures between 60 and 70% [11,12].

Inadequate behavior related to the use of antimicrobials by the population, the absence of control and prevention measures for infections associated with healthcare environments, and the absence of new antimicrobials are factors that favor bacterial resistance of *Staphylococcus aureus*, causing significant morbidity and mortality in the community, clinics, and hospitals.

## Objective

To describe the behavior of microbial drug resistance of *Staphylococcus aureus*.

## Material and Methods

A qualitative, documentary bibliographic review of 26 references was conducted from a total of 44 bibliographies between July and August 2024. Several primary digital sources of information were reviewed, including medical databases included in the Telematic Health Network in Cuba. The search was carried out in the SciELO, Elsevier, PubMed databases and the Google Scholar search engine. The following descriptors were used: Behavior, Microbial drug resistance and *Staphylococcus aureus*. Original articles and open access systematic reviews in peer-reviewed academic publications from the last 5 years and without geographical scope limitation were reviewed. AND and OR were used as Boolean operators.

- **Inclusion criteria:** Articles published in the last five years (2020-2024) because they are the most up-to-date and those that merit it due to their importance, language of the articles published in Spanish or English, articles that are freely published or that can be accessed through the Cuban Telematic Health Network INFOMED, documents that provide relevant information on low birth weight.
- **Exclusion criteria:** Articles for which the full text could not be accessed, editorial articles.

## Development

Bacterial resistance is a continuous process, whose origins date back to resistance to the antibiotic penicillin by *S. aureus*. During the 1960s, the incorporation of drugs, in this order penicillins that are resistant to penicillinases, brought with it resistance to methicillin and the appearance of strains of methicillin-resistant *S. aureus* (MRSA) [13].

According to the criteria of Cervantes-García E., *et al*. [13]. This mechanism is due to the penicillin-binding protein (PBP) called PBP2a or PBP2, which cannot be found in methicillin-susceptible *S. aureus* strains.

*Staphylococcus aureus* is a microorganism that has very distinctive characteristics regarding its virulence and pathogenicity factors of resistance to various antibiotics. Strains that present high antimicrobial resistance have been the most common in recent times in clinical practice, ideas with which the authors of this study agree [14].

To a greater extent, the nasal passages are its main route of transmission. All people have immediate susceptibility to this bacteria colonizing and initiating pathogenesis, thus adopting different modalities regarding the behavior of the evolutionary cycle, which will depend largely on the availability of the transport with which it can spread [14].

According to Pineda-Higuita S., *et al*. [14] and Washington-Win AS., *et al*. [15] it is one of the most important nosocomial pathogens in hospitals, as it causes numerous illnesses that can lead to complications such as folliculitis, furunculitis, and even severe infections such as endocarditis, septicemia, meningitis, pneumonia or bacteremia.

Washington-Win AS., *et al*. [15] also states that bacteremia and infectious endocarditis are entities that have this microorganism as a common denominator because it is the main gateway at the pathophysiological level, as well as alterations in the subcutaneous cellular tissue and joints [14].

The constant development of recombinant DNA technology and the access to the sequencing of the set of genes of *S. aureus* have made it possible to understand its pathophysiological mechanisms very easily. In this regard, Kuroda M., *et al*. [16] indicates that more than 45 % of the genome of *S. aureus* is similar to Bacillus subtilis, suggesting that these two microorganisms share a common ancestor [16].

*S. aureus* contains exogenous, mobile DNA, consisting of insertion sequences, transposons, bacteriophages and pathogenicity islands, which contain specific determinants responsible for the development of the disease and resistance to multiple antibiotics.

It is capable of carrying out horizontal transfer of all mobile elements supported by the set of genes, which is very effective because it allows it to do so with elements of its genus as well as with those of others. This exchange of genetic information is the cornerstone for the development of the genetic plasticity that is conferred on it and with it we can explain why the diseases it causes in humans are so common [16].

This microorganism has a circular chromosome on which the so-called "pathogenicity islands" rest, which are provided with genetic information valid for coding toxins that perform superantigen functions. More than 20 different staphylococcal toxins are known [18].

*Staphylococcus aureus* has different ways to develop its resistance. In this sense, the autochthonous forms are the fundamental ones. The limitation of the passage of substances through its membrane, the reduction by limit of the factors involved in the absorption of medicines and the flow systems in which the drugs leave and the production of β-lactamase begins are ways to develop its resistance according to Guo Y., *et al*. [17].

*Staphylococci* that show resistance to the antibiotic methicillin are also resistant to the group of beta-lactam drugs, as well as other groups of antimicrobials. Within this order of ideas, Castro-Orozco R., *et al*. [18] expresses that it has shown resistance to glycopeptides, in addition to quinolones, clindamycin, erythromycin, sulfamethoxazole and tetracyclines, which coincides with what was suggested by Espinosa C., *et al*. [19].

However, numerous strains have been found that show resistance to the group of antibiotics called MLSB macrolides, lincosamides and streptogramins B, which are used in the treatment of infections caused by *Su. aureus*. For this reason, it is necessary to monitor the antimicrobial susceptibility profile in order to find therapeutic alternatives in the evaluation of empirical therapy [18].

Several studies agree that resistance to methicillin and β-lactam antibiotics is determined in more than 85% by the mecA gene. It is the bacteria with the highest number of isolates according to Espinosa C., *et al*. [19]. Patients who present infection by *S. aureus* resistant to methicillin have more than 60% more probability of dying than patients with drug-susceptible infections [8].

*Staphylococcus aureus* uses a large number of carbohydrates and fats to carry out its metabolism. In the presence of oxygen, the final product of glucose catabolism is pyruvic acid and small amounts of carbon dioxide, substances that make it more resistant to different adverse situations than any other bacteria. They are viable for weeks in dried sputum, pus and water plates. They need at least 1 hour at more than 55°C for their destruction; they are resistant to chemical disinfectants [7].

Tălăpan D., *et al*. [21] and Hernández-Sarmiento R., *et al*. [22] agree that penicillin is the antimicrobial that acquires the greatest resistance to *S. aureus* strains, since as previously stated, it is due to the acquisition of the mecA gene that encodes the penicillin-binding protein PBP2a, which has low affinity for beta-lactams.

Vancomycin and Chloramphenicol have been reported as drugs that have also shown sensitivity to this bacteria. Differences are found with respect to the study of other investigations, where cefoxitin indicates the greatest susceptibility to *S. aureus* [22].

Sanmartín-Orbe ML., *et al*. [23] studied the antibiotic resistance of different strains of *Staphylococcus aureus* isolated in intra-hospital environments, of which all showed total resistance and a great sensitivity to trimethoprim, sulfamethoxazole, tetracycline, chloramphenicol and vancomycin, which coincides with the study carried out by Hernández-Moreno V., *et al*. [25].

Pardo L., *et al*. [24] during their investigation highlighted that the service that presented the greatest number of samples to *S. aureus* was the hemato-oncology service, results different to those achieved by the research of Abreu-Pereira., *et al*. [4] where the most affected services were Nephrology and the Intensive Care Unit (ICU).

Contributing risk factors such as stress enhance or delay the immune response of *S. aureus*, along with a possible vulnerability in the genetic aspect that they may have. In this way, the individual becomes more vulnerable and increases their probability of contracting infectious diseases [25].

Tables, stretchers, door knobs and cell phones are the main sites of settlement of this germ. Depending on the conditions of the place, the circumstances in which the sample is taken, the health care center, the cleaning tasks and the biosecurity standards, *Staphylococcus aureus* may show a high or low incidence with respect to the beginning of its infection, arguments raised by Sánchez-Zambrano AG., *et al*. [26].

## Conclusions

Antimicrobial resistance is a threat to human, animal and environmental health. *Staphylococcus aureus* is a microorganism that has very distinctive characteristics regarding its virulence and pathogenicity factors of resistance to various antibiotics. Several studies agree that resistance to methicillin and β-lactam antibiotics is determined by more than 85% by the mecA gene.

## Declaration of Conflict of Interest

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## Declaration of Authorship

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