

# Gastrointestinal Colonization by *Staphylococcus aureus* Strains as Risk Factor for Different Infections (Brief Review)

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**Abstract**—*Staphylococcus aureus*, although identified as a commensal, is also a common cause of human bacterial infections. Certain strains of *S. aureus* are more competent colonizers than others. Their adhesion and virulence factors play a role in the switch from intestinal colonization to infection. In this review is discussed some aspects of gastrointestinal carriage of *S. aureus* and its involvement in some diseases. More studies will be needed to deep understanding of the importance of intestinal *S. aureus* colonization and its association with different diseases.

**Keywords**— *S. aureus*, multi-drug resistance, carriage of *S. aureus*, intestinal colonization.

*S. aureus* Infectious diseases remain one of the most prevalent causative agents of infections and leading agent of death worldwide. Although *Staphylococcus aureus* is a commensal microbe, it has the potential to cause a wide range of diseases [1]. *S. aureus* is the most isolated human bacterial pathogen and an important cause of broad spectrum of infections - boils, abscess formation, wound infection, septic arthritis, sepsis/septic shock, pneumonia, osteomyelitis, foreign body infections and endocarditis [2,3]. It is also often responsible for toxin-mediated diseases (toxic shock syndrome, scaled skin syndrome, and staphylococcal foodborne disease) [4]. *S. aureus* is a common cause of infections in patients in intensive care units in many countries. One of the reasons for the success of this human pathogen is its variability, occurring at different times and countries [5].

Currently, *S. aureus* is the main common cause of nosocomial infections, and as an increasing number of community acquires infections, is an increasing public concern [6]. In addition to its ability to outwit human immune system, its multi-drug resistance phenotype, particularly – in methicillin-resistant *S. aureus* (MRSA) strains makes it one of the most intractable pathogenic bacteria in the history of antibiotic chemotherapy [7,8]. *S. aureus* is a common cause of infections in patients in intensive care units, and in many countries, MRSA is one of the most common causes of clinical infections worldwide and has attracted significant public attention due to the increased mortality associated with multidrug resistance [9,10]. Nowadays, treatment failures are associated with multidrug resistant *S. aureus* strains also.

More than 100 trillion microorganisms live in the human intestine. They play an important role in health status and diseases, including cancer. *S. aureus* may cause nosocomial

antibiotic-associated diarrhea [11]. Decreased stomach acidity can facilitate colonization due to easy passing the gastric-acid barrier [12]. An Intestinal overgrowth of bacteria causes enteritis and/or diarrhea. This bacterium is involved in inflammatory bowel disease also [13,14].

The bacterial species *S. aureus*, including MRSA, primarily found in their ecological niche - the human nose, but is also can colonize the intestines and the perineal region. Colonization of the gastrointestinal system by *S. aureus* strains in hospitalized patients may lead to important clinical implications [4] and is able to acquire multiresistance [15,16]. Nasal colonization by *S. aureus* is a well-defined risk factor for different infections such as cutaneous, post-operative infections and other types of infections [17,18].

Prolonged colonization of *S. aureus* in the intestinal tract also occurs and results important clinical implications. Still, compared to nasal carriage, gastro-intestinal colonization by *S. aureus* has been sparsely studied.

The COVID-19 pandemic conditions increase MRSA incidences. Community acquired MRSA is now emerging as an apparent epidemic [19].

Changes in the interactions among the intestinal epithelial cells, intestinal microbiota, and host immune system are associated with many diseases, including cancer [10]. Besides of many factors (diet, family history, age, ethnicity), metabolic products of intestinal microbiota also influence and predispose to the development of colorectal cancer [9]. Some determinants of pathogenicity (urease, lecithinase production, hemolysis, proteolysis), also carbohydrate and mannitol fermentations in aerobic and anaerobic conditions are characterized with high activity in MDRSA and MRSA strains in comparison of non-MRSA strains. These enzymes are involved in the pathogenesis of *S. aureus* infections [3].

Intestinal carriage of *S. aureus* may increase incidences of intestinal infections. Antibiotic therapy causes overgrowth of bacteria and induces enteritis or antibiotic-associated diarrhea. MRSA has been suggested as a cause of antibiotic-associated diarrhea in hospitalized patients [22].

Study results revealed compelling evidence of MRSA etiological role in antibiotic-associated diarrhea by excluding *C. difficile*, other bacterial pathogens and parasites, several enteric viruses in patients with enterotoxin-producing MRSA intestinal carriage [23].

*S. aureus* produce different enzymes, which are correlated with the virulence of bacteria. Secreted enzymes

(exoenzymes) function to break down bacterial and host molecules for nutrient acquisition, bacterial survival, and dissemination [8]. For newborns MRSA intestinal colonization was detected in 1–2% and can be involved in the development of neonatal infectious disease. The colonization of the intestine with *S. aureus* in young children occurs at high frequency within the first 6 months of life, after which the frequency drops. Prolonged intestinal carriage among personnel can be an important factor of MRSA outbreaks in hospitals and become as important source of environmental contamination [19].

*S. aureus* strains are significantly spread in patients with different diseases as well as healthy persons. These strains revealed high enzymatic activity and intestinal carriage need to be considered as one of the significant factor for development of different diseases.

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