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The importance of intestinal microbiota and its role in the nosocomial infection

A importância da microbiota intestinal e seu papel na infecção hospitalar

La importancia de la microbiota intestinal y su papel en la infección nosocomial

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Abstract
The gastrointestinal tract houses the largest and most complex community of microorganisms, and this bacterial colonization of the human intestine by environmental microbes begins immediately after the birth. The intestinal microbiota has several important and unique functions, including metabolic functions such as the biotransformation of drugs and the digestion of dietary compounds; a mucosal barrier function by inhibiting the invasion of pathogens and an immunomodulatory function. On the other hand, some commensal bacteria can be pathogenic, causing infections if the natural host is compromised and, in predisposed hosts, the intestinal microbiota can be involved in nosocomial infection. The translocation of bacteria through the intestinal wall is considered one of the main causes of nosocomial infections. The aim of this review is to provide a comprehensive view of the human gut microbiota, its main functions, its role in health and disease, addressing the correlation between intestinal microbial composition and nosocomial infections.
Keywords: Infection; Gastrointestinal microbiome; Host microbial interactions.

Resumo
O trato gastrointestinal abriga a maior e mais complexa comunidade de microrganismos, sendo que essa colonização bacteriana do intestino humano por micróbios ambientais começa imediatamente após o nascimento. A microbiota intestinal possui diversas funções importantes e exclusivas, incluindo funções metabólicas, como a biotransformação de medicamentos e a digestão de compostos dietéticos; uma função de barreira da mucosa ao inibir a invasão de patógenos e uma função imunomoduladora. Por outro lado, algumas bactérias comensais podem ser patogênicas, causando infecções se o hospedeiro natural estiver comprometido e, em hospedeiros predispostos, a microbiota intestinal pode estar envolvida na infecção nosocomial. A translocação de bactérias através da parede intestinal é considerada uma das principais causas de infecções nosocomiais. O objetivo desta revisão é fornecer uma visão abrangente da microbiota intestinal humana, suas principais funções, seu papel na saúde e na doença, com abordagem da correlação entre a composição microbiana intestinal e as infecções nosocomiais.
Palavras-chave: Infecção hospitalar; Interações entre hospedeiro e microrganismos; Microbioma gastrointestinal.

Resumen
El tracto gastrointestinal alberga la comunidad de microorganismos más grande y compleja, y esta colonización bacteriana del intestino humano por microbios ambientales comienza inmediatamente después del nacimiento. La microbiota intestinal tiene várias funciones importantes y únicas, incluidas funciones metabólicas como la biotransformación de fármacos y la digestión de compuestos dietéticos; una función de barrera mucosa al inhibir la invasión de patógenos y una función inmunomoduladora. Por otro lado, algunas bacterias comensales pueden ser

patógenas, causando infecciones si el hospedador natural está comprometido y, en hospedadores predispuestos, la microbiota intestinal puede estar involucrada en la infección nosocomial. La translocación de bacterias a través de la pared intestinal se considera una de las principales causas de infecciones nosocomiales. El objetivo de esta revisión es proporcionar una visión integral de la microbiota intestinal humana, sus funciones principales, su papel en la salud y la enfermedad, abordando la correlación entre la composición microbiana intestinal y las infecciones nosocomiales.
Palabras clave: Infección hospitalaria; Interacciones microbiota-huesped; Microbioma gastrointestinal.

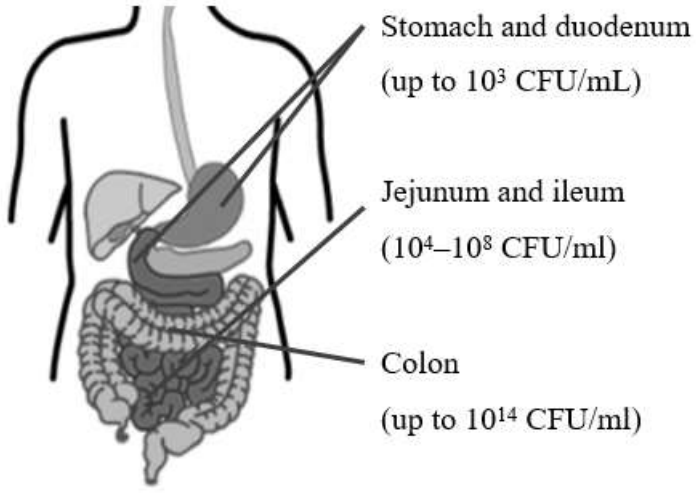
1. Introduction

The intestines form the largest organ of the body in length. Anatomically, they are divided into two zones with different functions, which are the small intestine and the large intestine. The small intestine is a tube around 7 m long and 2.5 cm in diameter, situated between the stomach and large intestine, which performs digestive functions, absorption of nutrients and conduction of undigested material into the large intestine. The large intestine is situated between the anus and small intestine, with a diameter three times longer than the anterior portion of the intestine, and its functions are related to the absorption of water, minerals, nutrients and vitamins, as well as the preparation and storage of feces before elimination. It is habited by rich bacterial flora that usually lives in symbiosis with the host, and is of great importance to human body (Udager et al., 2010).

In particular, the digestive tract harbours the largest and most complex community of microorganisms. The exact number of bacterial cells present in the human gut and which species they all belong to is unknown but some studies suggest that it is a number of approximately 100 trillion bacteria that play an important role in the human body (Souza et al., 2021).

The gastrointestinal microflora is considerably different in each part (stomach, duodenum, jejunum and ileum) and its distribution is uneven (Figure 1).

Figure 1. Number of bacteria in different sections of gastrointestinal tract.



Source: Authors.

As shown in Figure 1, in the stomach and duodenum is found low concentration of bacteria, up to 10^3 UFC/mL, meanwhile in jejunum and ileum is found about 10^4–10^5 CFU/ml. Colon possess the highest concentrations (up to 10^{12} CFU/ml (Koulas et al., 2021).

There are bacteria adhered to the mucosal epithelium or in microhabitats (trapped in the mucous gel layer or in the intestinal lumen probably associated with either food particles or with each other) (Paone & Cani, 2020). The genera

Bacteroides, Bifidobacterium, Clostridium, Eubacterium, Fusobacterium and *Lactobacillus* are the most common anaerobic enteric bacteria. Among the aerobes are the Gram-positive cocci, as *Enterococcus, Staphylococcus* and *Streptococcus*, and the Gram-negative such as *Escherichia coli* and *Salmonella spp*. moreover, fungal species are also present, such as *Candida albicans* (Montalto et al., 2009). However, its own composition is still unknown, since it is estimated that at least 40% of its species have not been cultured (Dominguez-Bello et al., 2011).

Recent attention has been drawn to the role of the intestinal microbiota, a complex community of microorganisms inhabiting the gut that plays an important role in human health and disease (Manor et al., 2020). In the healthy state, microbiota and host interact in a mutually beneficial manner, in which the host provides both the environment and a consistent source of nutrients, and the microbiota participates in the digestion, metabolism, immune homeostasis, and resistance to infection. In hospitalized patients, the normal host-microbiota interaction can be disrupted by interventions that may cause diarrhea such as antibiotic use (Polage et al., 2012). Furthermore, translocation of commensal bacteria across the intestinal wall is considered to be an important cause of nosocomial infections (Fine et al., 2020).

Since the intestinal microbiota is an integral part of normal human physiology, the imbalance of the normal gut microbiology may be involved in many health issues. This review intends to characterize the normal microbiota of the gastrointestinal tract, its installation process, functions and specificities. In addition, we discuss the composition of intestinal microbiota associated with nosocomial infections.

2. Methodology

The present study is a narrative review on the importance of the intestinal microbiota and its role in nosocomial infection. The qualitative narrative review of scientific literature enables a comprehensive theoretical discussion by the author about the object of study (Cordeiro et al., 2007; Pereira et al., 2018). To develop it, this review covered scientific articles published and available in the following databases: PubMed, Scielo (Scientific Electronic Library Online) and Academic Google. Studies that did not contain the abstract and that did not address the topic under study were discarded. In addition, opinionated articles that were not supported by research data or that did not support systematic data collection were discarded.

3. Discussion

3.1 Formation of the intestinal microbiota and its installation process

Bacterial colonization of human gut by environmental microbes begins immediately after birth. The composition of intestinal microbiota is relatively simple in infants, and become more complex with the body development and increasing age, exhibiting a high degree of variability among individuals (Lee et al., 2020). The intestine of the fetus is sterile. The newborn delivered vaginally receives the initial colonization of the intestine by bacteria from fecal and vaginal flora of the mother (Rasmussen et al., 2020). On the other hand, infants born by caesarean section are colonized by bacteria from the environment. Besides the type of delivery, the type of feeding is very important in determining the intestinal microbiota of infants (Fan & Pedersen, 2021).

At birth, newborns by vaginally delivered acquire bacteria from their mother's vagina (Rasmussen et al., 2020). These bacteria can be allocated in the skin and mouth and are already present in the first meconium. Sterile mucosal surfaces (digestive, urogenital, naso-buccal and respiratory as well as skin) constitute a set of ecological niches which provide highly favourable conditions to microbial colonization (Dominguez-Bello et al., 2011). In the absence of the sophisticated immunological mechanisms of the adult, the environment of digestive tract of the newborn is quickly colonized, reaching levels of 1011 bacteria per gram of stool (Doré & Corthier, 2010). The human vagina is an ecosystem dominated by relatively

few bacterial species.

Park et al., (2005) employed a molecular approach to c one infant on the first, third, and sixth days after birth and showed that microbiotic diversity changes very rapidly in the days following birth. On the first day of life were present in the infant's feces some species of *Enterobacter*, *Streptococcus mitis*, *Lactococcus lactis* and *Leuconostoc citreum*, with the largest taxonomic group in number of clones isolated being *Lactococcus lactis*. On the third day of life, *Enterobacter*, *Enterococcus faecalis*, *Escherichia coli*, *Streptococcus mitis*, and *Streptococcus salivarius* were present. On the sixth day, they found *Citrobacter*, *Clostridium difficile*, *Enterobacter sp.*, *Enterobacter cloacae*, and *Escherichia coli*. At this point, the largest taxonomic group was *Escherichia coli*.

Anaerobic bacteria that dominate the adult intestinal microbiota are among the first microorganisms encountered after vaginal delivery. They will develop and become dominant in the intestine, following facultative anaerobes that will settle in the intestine and help reduce the environment so that strict anaerobes can be established in sequence. Eventually anaerobic bacteria will dominate facultative anaerobes one thousandfold. This first succession of species occurs in the very first few hours following birth. Furthermore, bacterial from the skin microbiota may become part of the intestinal microbiota (Doré & Corthier, 2010). On the other hand, the intestinal microbiota of the mother is an important microbial source for the newborn (Van Daele et al., 2019). Anaerobic bacteria that dominate the adult intestinal microbiota are among the first microorganisms encountered after vaginal delivery (Doré & Corthier, 2010). Physiochemical and immunological properties as well as diet characterize the diverse niches of the stomach and small and large intestines. Among mammals, gastrointestinal tract physiology is a powerful predictor of bacterial community composition of feces and genetic differences can also affect the composition of the microbiota (Dominguez-Bello et al., 2011).

Since the maternal vaginal and perineal microbiota extensively contribute to colonization of vaginally delivered newborns, the skin and nosocomial environment play a significant role in cesarean section-born infants. Infants delivered by cesarian section had bacterial communities that were more similar to those of the mother's skin and were dominated by *Staphylococcus spp.*, *Corynebacterium spp*., and *Propionibacterium spp.* (Dominguez-Bello et al., 2011). The *Bifidobacterium* colonization has been shown to be acquired until one month of age, whereas in vaginally delivered infants it occurs at 10 days.

During the first year of life, the immunological functions are influenced by intestinal microbiota development, and babies that were born by cesarean section have lower bacteria number in fecal samples. Vaginal microbes that were transmissed to the baby might have a defensive role, since they can reduce colonization by pathogens. On the other hand, the intestinal microbiota could contribute to the risk for some diseases as allergies, and asthma, which are higher in cesarean section than in vaginally delivered babies (Dominguez-Bello et al., 2011). Regarding innate effectors, these are involved in the regulation of gut microbiota colonization, such as the production of secretory IgA, defensins, antimicrobial peptides that are produced and secreted by mucosal epithelial cells. Interactions between bacteria are also very important for the intestinal colonization. Some bacterial metabolic activities can modify the intestinal ecology, such as the synthesis of bacteriocins, which creates an environment that is appropriate for some kinds of bacteria but becomes hostile to others (Montalto et al., 2009).

Maternal milk may contain live bacteria that constitute one of the main sources of bacteria to the infant gut, which may be transferred to the baby via breastfeeding (Nyangahu & Jaspan, 2019). After one week of a diet of breast milk can be detected the development of a flora rich in *Bifidobacterium spp.* (Doré & Corthier, 2010). Other obligate anaerobes such as *Clostridium spp.* and *Bacteroides spp.* are isolated less frequently, and enterobacteria and enterococci are also rare. *Clostridia* have consistently been found at lower levels in breast-fed babies; thus the presence of this group of bacteria may indicate the babies have been fed formula (Cochetière & Montassier, 2011).

Besides the delivery and feeding mode, the establishment of the intestinal microflora may be influenced by social contacts and enviromental factors (including geographic location) and household exposure (Vandenplas et al., 2020) . Thus,

the intestinal colonization pattern varies considerably between infants in developing and industrialized societies. Hygiene at birth and during the first moments of life will markedly influence the dynamics of colonization. It seems clear today that colonization by the usual early colonizing commensal species such as E. coli is delayed in industrialized countries when compared to developing countries, owing most likely to the hygiene conditions applied to date (Adlerberth et al., 2006; Doré & Corthier, 2010)

The newborn's gut community has relatively few species and lineages, but diversity increases rapidly (albeit with a considerable degree of instability) over the first few years of life. A complete microflora is obtained at 2-3 years of age, where more than 400 bacterial species can be found (Adlerberth et al., 2006). Exogenous factors include exposure to microorganisms of maternal (faecal, vaginal and cutaneous) and environmental origin, but also food intake and occasionally antibiotherapy which may induce significant perturbations (Doré & Corthier, 2010).

3.2 The human gastrointestinal microbiota and its function

The intestinal microbiota is essential for the intestinal homeostasis and protection against pathogens to such an extent that some researchers have referred to it as an "extra body" of the host (Sousa et al., 2008). The gastrointestinal tract is populated with large numbers of bacteria that contribute to normal digestive function. The microbiota secretes a diverse array of enzymes (mainly for the fermentation of carbohydrates and proteins) with substantial metabolic potential which presents important implications for drug metabolism. Bacterial metabolic reactions and their respective enzymes can extensively metabolise drugs and other chemical compounds more than any other part of the body (Adak & Khan, 2019).

3.2.1 Biotransformation of drugs

The oral route is the preferred route for drug administration (Zimmermann et al., 2019). The majority of drugs orally administered is rapidly and completely absorbed in the stomach and upper intestine and has minimal contact with intestinal bacteria. However, all drugs orally administered are subject to hepatic metabolism and it will be also subject to bacterial metabolism, which occurs mainly in the lower gastrointestinal tract if it is not totally absorbed in the upper gastrointestinal tract. Drugs that display low solubility, low permeability or both will reach the lower confines of the gastrointestinal tract, presenting themselves to the host microbiota. Drugs can also come in direct contact with bacteria via rectal administration in the form of suppositories or enemas (Sousa et al., 2008).

The liver is the main responsible for metabolism which performs reactions of oxidation and conjugation generating polar metabolites, while reductive and hydrolytic reactions occur in the gut microbiota generating nonpolar low molecular weight by products. Furthermore, all drugs that are delivered to, or absorbed into the blood stream, are subject to hepatic metabolism. However, rate and extent of bacterial metabolism will be influenced by the amount of drug that reaches the distal gut (Sousa et al., 2008; Zimmermann et al., 2019)

Microbial metabolism could yield a pharmacologically active, inactive or toxic metabolite. Intensive metabolism results in often low circulating levels of the original products, as a consequence, the final health effects of some drugs are often related to specific active metabolites which are produced in the body rather than being related to the product's original composition (Possemiers et al., 2011).

Intestinal bacteria are able to reduce the azo bond with the aid of azoreductase enzymes produced by the large intestinal microbiota, and some pro-drugs, as sulfasalazine, were developed to be directed to this metabolic reaction. Small amount of sulfasalazine is absorbed in the small intestinal and its azo bound of is reduced in the colon by bacteria, releasing 5-aminosalicylic acid which presents topical anti-inflammatory effect and sulfapyridine which is systemically absorbed (Sousa et al., 2008). Nitrazepam is recognized to cause fetal abnormalities (teratogenicity) by nitroreduction to 7-aminonitrazepam, and

intestinal bacteria with nitroreductase activity are the primary site for reductive metabolism (Flowers et al., 2020). *In vitro* studies showed that omeprazole is reduced to sulfide metabolites by intestinal contents, however, in vivo the gut microbiota did not affect the oral pharmacokinetics once the drug is completely absorbed before reaching the hindgut (Wilson & Nicholson, 2017).

A series of potential implications of bacterial metabolism on drug performance or toxicity, suggests that drug development process needs the assessment of the action of the microbiota.

3.2.2 Antimicrobial function

The gastrointestinal microflora exerts a barrier effect against enteropathogens. Gut microbiota provides its host with a physical barrier to incoming pathogens by competitive exclusion, such as occupation of attachment sites, consumption of nutrient sources, and production of antimicrobial substances. In addition to microbial cells or microbial structural components, microbial metabolites also have the ability to stimulate the host to produce various antimicrobial compounds (Sekirov et al., 2010).

Among the species present in the human intestinal microflora, several reports have emphasized the role of *Bifidobacteria*. A study of Lievin et al., (2000) showed that several *Bifidobacterium* strains from resident infant human gastrointestinal microflora show antimicrobial activity, and they could exert a barrier effect produced by the microflora. *Bifidobacteria* are the predominant intestinal organisms of breast fed infants and it is recognised that the antimicrobial properties of *Bifidobacteria* could contribute to the protection that breast feeding provides against gut infection (Scholtens et al., 2012).

Works have reported that *Lactobacillus* inhibit attachment of pathogens into cultured uroepithelial and intestinal cells, and mucus (Singh et al., 2017). Moreover, reports have shown that *Lactobacillus* in mice can compete with *Escherichia coli* in the stomach and small intestine (Stecher & Hardt, 2011). Other reports show a potential for *Bifidobacteria*, isolated from human adult stools, in inhibiting binding of *Escherichia coli* in an *in vitro* model (Fujiwara et al., 1997). Further studies have shown that some symbiotic bacterial species, i.e. probiotics, may prevent inflammatory disease by not initiating an innate immune response during colonization (Wu et al., 2012).

3.3 Importance of microbiota in food absorption and nutritional contribution

The diet can have a major influence on microbial community composition, which is maintained by action of the metabolism of the host and its immune system. Through the fermentation of undigestible dietary components in the large intestine, the intestinal microbiota can provide nutrients and energy to the host (Flint et al., 2012).

The action of intestinal bacteria on food nutrients allows a better nutritional utilization. This happens through a process of "saving energy", where undigested substrates that arrive in the intestine are fermented by intestinal bacteria and form short-chain fatty acids, which are the main energy source of colonocytes and have trophic effect on the intestinal epithelium. The intestinal flora also helps in normal digestion and assimilation of nutrients and assists in synthesizing various vitamins, especially vitamin K, biotin, B12 and other B-complex vitamins (Ciobârcă et al., 2020).

The probiotic food, which is food supplemented with live microorganisms, plays usual nutritional effects that benefit the host by improving the balance of intestinal microbiota. The most commonly used probiotics are strains of lactic acid producing-bacteria, such as *Lactobacillus* and *Bifidobacterium*, which are included in so called functional foods (milk and some yogurts). They significantly increase the therapeutic and nutritional value of food by increasing the levels of B vitamins and amino acids, the absorption of calcium, iron and magnesium (Coudray et al., 2005; Darfeuille-Michaud et al., 1992). Moreover, prebiotics – that is, non-digestible food ingredients – can also modify the intestinal microflora by changing mainly

the colonic microflora to a healthy microflora, and in particular increasing the level of *Bifidobacteria* (Coudray et al., 2005).

3.4 Diseases associated with gut microbiota

The intestinal microbiota interacts with the gastrointestinal tract of the host to stimulate adequate maturation of mucosal immunity and to provide colonization resistance against pathogens. Enteric infections may occur as a result of the host susceptibility to an opportunistic pathogen or maybe due to a pathological overgrowth of an opportunistic element of intestinal microbial community. To produce a successful infection, the infecting agent has to overcome a number of host defenses, such as mucosal immunity or colonization resistance posed by the normal microbiota (Sekirov et al., 2010).

The gut microbiota is crucial to antigen-presenting cell activation, like dendritic cells. The number of intestinal dendritic cells and macrophages seems to be greater in people with inflammatory bowel disease (IBD). The IBDs represent an important health problem, affecting mainly young people (Rutella & Locatelli, 2011). Several factors may play a role in the development and progression of IBD, including genotype, the host immune imbalance, and the composition of the microbial communities living TGI. So far, it was not possible to reveal a single pathogenic species responsible for IBD. The current view is that, although individual species may play important roles in immunomodulation, side effects for the microbiota, due to its loss or excess, play a key role in the persistence of chronic inflammatory responses (Nagalingam & Lynch, 2012).

3.5 The intestinal microbiota and nosocomial infection

According to Inweregbu et al., (2005), nosocomial infections can be defined as those occurring within 48 hours of hospital admission, 3 days of discharge or 30 days of an operation, and they affect 1 in 10 patients admitted to hospital. It is known that skin, oropharyngeal and intestinal microbiota are important source of bacteria potentially able to cause infections in other sites of the body. Some of those commensal bacteria may cause nosocomial infection if the natural host is compromised.

Translocation of Gram-negative bacteria across the intestinal wall is thought to be a major cause of nosocomial infections (Oliva et al., 2020). The primary reservoir of uropathogenic *Escherichia coli* is believed to be the human intestinal tract and employs diverse repertoire of virulence factors to colonize and infect the urinary tract in an ascending fashion (Inweregbu et al., 2005). *Escherichia coli* cause approximately 85% of cases of urethrocystitis and up to 90 percent of cases of acute pyelonephritis (Guentzel, 1996).

Enterobacter cloacae comprises part of the normal flora of the gastrointestinal tract of 40%–80% of the population and is widely distributed in the environment (Foxman, 2010). It is the most commonly isolated member of the Enterobacteriaceae family (Daniel-Hoffmann et al., 2012) and an important nosocomial pathogen capable of causing opportunistic infections among hospitalized or debilitated and immunosuppressed patients. E. cloacae has also emerged as an important pathogen that causes nosocomial infection in neonatal units (Xu et al., 2012).

Proteus, Klebsiella and *Enterobacter* species are among the other organisms most frequently involved in urinary tract infections following intravenous and urinary catheterization and infections complicating burns. These species are also frequent causes of bacteremia and are frequently involved in infections associated with respiratory tract manipulations, such as tracheostomy and procedures using contaminated inhalation therapy equipment. *Proteus* species frequently cause nosocomial infections of the urinary tract, surgical wounds, and lower respiratory tract. *Proteus mirabilis*, is believed to be the most common cause of infection-related kidney stones, one of the most serious complications of unresolved or recurrent bacteriuria (Dalben et al., 2008). *Citrobacter* species cause meningitis, septicemia, and pulmonary infections in neonates and young children. *Citrobacter freundii* and *Citrobacter diversus* have been isolated predominantly as superinfecting agents from urinary and respiratory tract infections (Elbashier et al., 1998). *Klebsiella pneumoniae* is gram-negative bacilli present in the gastrointestinal tract of colonized individuals and it is an important pathogen causing nosocomial infections, especially in

ICUs. Various epidemiological studies revealed that the reservoir for *Klebsiella pneumoniae* strains involved in nosocomial infections is the gastrointestinal tract of the patients (Darfeuille-Michaud et al., 1992). Besides bacterial species, *Candida* is the leading cause of nosocomial vaginal and oral fungal infections in intensive care units.

Antibiotic-resistant bacteria are an increasing problem in hospitalized patients. The increase in the frequency of bacteria belonging to the Enterobacteriaceae family is expressive and this group is the major bacterial species causing hospital-acquired infections. Vancomycin-resistant *Enterococcus faecium* and carbapenem-resistant *Klebsiella pneumoniae* represent some of the major highly resistant organisms that cause infections in hospitalized patients (Ubeda et al., 2010).

Enterococci can survive for long periods on environmental surfaces, including bed rails, door handle or medical equipment. They are tolerant to heat, chlorine and some alcohol preparations, what may help explain why these organisms are widely disseminated in the hospital setting (Ubeda et al., 2010). Meningitis caused by *Enterobacter cloacae* may be the result of a hematogenous spread or a result of multiple foci of infection secondary to high inoculum exposure. Treatment of *Enterobacter cloacae* infection is often difficult considering the resistance of *Enterobacter spp.* to 3rd-generation cephalosporins (Arias & Murray, 2012). *Enterobacter cloacae* are intrinsically resistant to aminopenicillins, cefazolin, and cefoxitin. The resistance rates of *Enterobacter cloacae* for peperacillin, ticarcillin/clavulanic acid, cefoxitin, cefuroxime sodium, trimethoprim/sulfamethoxazole, cefotaxime and ceftriaxone were almost more than 60% (Foxman, 2010). The *Enterococcus spp*. has become prevalent in nosocomial infections of the newborn. The most common source is the mother's gastrointestinal tract, but also objects and surfaces of the contaminated environment. Newborns who remain in the intensive care unit for more than 30 to 60 days, with prolonged use of catheters and exposed to multiple antimicrobials, are particularly susceptible to severe infections by *Enterococcus*, which can include: necrotizing enterocolitis, sepsis, pneumonia, meningitis, endocarditis (Kuo et al., 2010).

A situation with more relevance to the human intestine is the regulation of *Clostridium difficile* populations in the gut. This bacterium is a member of the normal microflora in a small percentage of humans. However, it is also a major cause of nosocomial infection when it settles in the gut of patients treated with antibiotics, resulting in diarrhoea and sometimes pseudomembranous colitis. The use of antimicrobial agents is known to have significant effects on the intestinal microbiota, and can cause several adverse effects on the intestinal microbiota. Resistant bacteria among the microbiota microorganisms, and distribution of resistant genes by transfer of DNA in the microbial community can be responsible to an increased load of potentially pathogenic resistant microorganisms (Mussi-Pinhata & Do Nascimento, 2001).

4. Conclusion

Nosocomial infections designated as healthcare-associated infections are those acquired as a result of healthcare interventions. The occurrence of undesirable complications from healthcare-associated infections has been well recognized for the last several decades. The intestinal microbiota is a complex community of microorganisms and one of the most important functions of the intestinal microbiota is the maintenance of the balance of bacteria and the control of susceptibility to infection with enteropathogenic organisms. Nonpathogenic microorganisms that form the bacterial community in the gastrointestinal tract are protectants against invading pathogenic bacteria, but the commensal bacteria can become a source of infection if occurs an imbalance by the use of antibiotics or if they are transmitted to another site of the body. Thus, in predisposed hosts, the intestinal microbiota may be involved in the nosocomial infection.

Besides the intestinal microbiota, other sources of infectious agents causing healthcare associated infections should be considered such as, medical equipment or devices, the hospital environment, the healthcare personnel, contaminated patient care equipment. Although the intestinal microbiota transmission route is important, the role of the environment should not be ignored and the hospital environment may contribute to the spread of nosocomial infections.

Given what is expressed in this work, the need for more studies that address the correlation between the individual's intestinal microbiota and hospital conditions becomes noticeable, as knowing the opportunistic microorganisms that can become pathogens and information about their resistance profile is fundamental for the prevention and treatment of nosocomial diseases.

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