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INCIDENCE OF ENTEROBACTERIACEAE IN NOSOCOMIAL INFECTIONS

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ABSTRACT

This work was carried out in the field of General Microbiology, combining in its contents elements of different biological, medical and technological disciplines.

The special part of this paper included a study at the Tg-Jiu County Emergency Hospital, where we made a statistic during a calendar year on the number of hospitalized patients, detected with different germs on different devices (respiratory, urinary, digestive, etc.) with nosocomial infections.

INTRODUCTION

The study of microorganisms is current, usual and at the same time necessary, which also determines the importance of the topic in question called "Incidence, enterobacteria in nosocomial infections".

Bacteria are unicellular microorganisms with prokarvotic structure - type of organization characterized by lack of intracellular membranes, unlike the eukaryotic type in which the nucleus and some organelles (chloroplasts, mitochondria) possess their own membranes. Genetic material, or bacterial genome, is a chromosome made up of a large molecule of DNA and inherited extrachromosomal units called plasmids, made up of much smaller DNA molecules (about 1% of the chromosome's mass). The bacteria lack mitochondria, Golgi apparatus and endoplasmic reticulum itself. The functions of these structures, characteristic of the eukaryotic cell, are supplemented by other cellular components, especially by the cytoplasmic membrane. Bacteria are metabolically active, having their own enzyme equipment that performs cellular reactions of degradation and biosynthesis. Nutrition is absorptive type, in terms of access of nutrients into the cell and chemotrophic or phototrophic type, according to the way of obtaining the energy necessary for nutritional processes. The main way bacteria multiply is simple binary division or sciziparity. Some bacterial species can exist in nature under two alternative biological forms: the vegetative form, which represents the bacterial cell itself, endowed with all the characteristics characteristic of the species to which it belongs, and the sporulated form, which is a form of resistance and preservation of the species in hostile conditions, unsuitable for life. Unlike the biologically active vegetative cell, bacterial spore is a dormant form, characterized by the absence of multiplication and biosynthetic functions and with a very low intensity of other vital activities. (Moldovan et al. 2015)

MATERIAL AND METHODS

This paper refers to a statistical study that includes a group of patients grouped by sex and age with certain nosocomial germs during 2022. The isolation of these enterobacteria is achieved by seeding the sample on two types of media: siraple media, without inhibitors (agar agar 2%) and media with inhibitors (weak or moderately selective: EMB / Levine, Istrate-Meitert).

These media will be incubated at 37°C, 18-20 hours.

RESULTS AND DISCUSSIONS

Several studies consider *the species Proteus mirabilis* and *P. penneri* to be potentially enteropathogenic.

P. mirabilis is the causative agent of some bacteremias, osteomyelitis and neonatal meningoencephalitis. Involvement of *P. penelli with* bacteremia with subcutaneous femoral abscess in a neutropenic patient with acute lymphocytic leukemia and nosocomial urosepticemia in a diabetic patient. (Chifiuriuc et al. 2015)

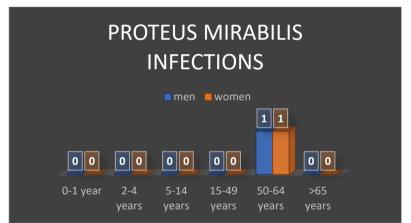


Chart 1. Distribution by age groups and sex of patients with Proteus mirabilis

The genus *Klebsiella* forms colonies with a special appearance, is very vicious, ferments numerous carbohydrates and has a toxic capsular antigen K (77 species) that plays a role in phagocytosis and protection against lethal sera. It contains immobile seeds that it holds as a factor. Encapsulated serotypes K1 and K6 are potentially pathogenic. (Chifiuriuc et al. 2015)



Figure 1. Klebsiella on culture medium



Chart 2. Distribution by age groups and sex of patients with Klebsiella

Serratia is a genus of Gram-negative, facultatively anaerobic, rod-shaped bacteria in the family Yersiniaceae. According to the List of Prokaryotic Names with Permanent Nomenclature (LPSN), there are currently 19 species of Serratia Authoritatively published with exact names as of 2020: S. aquatilis; S. entomophila; S. ficaria; S. fonticola; S. grimesii; S. liquefaciens; S. marcescens; S. microhemolytica; S. myotis; S. nematodiphila; S. odoriferae; S. oryzae; S. plymuthica; S. proteamaculans; S. quinivorans corrig; S. rubidaea; S. symbiotic; S. ureilytica; S. vespertilionis. (https://en.wikipedia.org/wiki/Serratia)



Figure 2. Serratia on culture medium



Chart 3. Age and sex distribution of patients with Serratia

The genus *Salmonella* includes over 1500 species widespread in the animal kingdom. Some are strictly adapted to human species (*S. typhi*, *S. paratyphi A*), while others are strictly adapted to animal species (S. *gallinarum, S. pullorum*) and a significant part parasitizes both humans and animals (*S. enteritidis, S. typhimurium,* etc.). Removed from these hosts, they spread to the external environment (water, soil, food). (Bălașoiu & Turculeanu 2013)

No cases were recorded during 2022.



Figure 3. Salmonella on culture medium

E. coli causes more than 90% of all urinary tract infections, UTIs (urethrocystitis, cystitis, nephritis, and pyelonephritis), and is associated with high rates of bacteremia. Colonization of the urinary tract is initiated by stasis-based invasion of the target mucosa, followed by upward progression of kidney infection against the descending flow of urine. In the kidneys, the infection is preferably localized in the medullary cavity. (Chifiuriuc et al. 2015)



Chart 4. Distribution by age groups and sex of patients with Escherichia coli



Figure 4. Escherichia coli on culture medium

CONCLUSIONS

Over the past two decades, an increasing number of infections acquired from hospital units with enterobacteria have been reported. In these cases, carbapenem treatment was resorted to. As such, resistant strains have emerged and thus an important public health problem. Studying the characteristics of these infections may help identify the correct treatment. The number of infections with antibiotic-resistant enterobacteria is increasing, so it is very important to identify new therapeutic targets. The rapid spread of this type of resistance is due to the fact that coding genes are found on transmissible or movable plasmids. At this point it is important to diminish the social impact of the phenomenon of multiple resistance to antibacterial preparations, through detailed knowledge of the mechanisms of bacterial resistance. The emergence of antibiotic resistance genes in Enterobacteriaceae involved in human infections poses a vital risk and requires familiarity with techniques for identifying these genes in order to institute appropriate treatment and control potential epidemics. Bacteria of the Enterobacteriaceae family have adapted to broad-spectrum antibiotics, as can be seen in the study presented above.

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