Artigo original

Perfil de IRAS em um hospital geral do sudoeste do Brasil

Profile of HAI in a General Hospital in Southwestern Brazil

Perfil de IRAS en un hospital general del suroeste de Brasil

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RESUMO

Justificativa e objetivos: Infecção relacionada à serviços de saúde (IRAS) é qualquer infecção adquirida sob cuidados de saúde, caracterizada por detecção durante internação ou após a alta do paciente. O uso inadequado de antibióticos levou a um aumento da resistência antimicrobiana, tornando a infecção difícil de tratar, especialmente para microorganismos multirresistentes. O objetivo deste estudo foi determinar os principais patógenos envolvidos em infecções em um hospital brasileiro e avaliar o padrão de resistência antimicrobiana. **Métodos**: Estudo retrospectivo e documental realizado entre 2008 e 2013. Foram analisados os resultados dos exames de cultura microbiológica, totalizando 6094 amostras biológicas. **Resultados**: O estudo foi constituído por amostras do trato respiratório (38,6%), trato urinário (35,8%), pele e do tecido mole (22,2%), cateter venoso central (2,3%) e sangue (1,1%). Cerca de 75% das amostras apresentaram microorganismos multirresistentes, principalmente em cateter venoso central, onde 93% de todas as bactérias eram resistentes a 4 ou mais antibióticos. Bactérias Gram-negativas foram os mais encontrados (86,4%). **Conclusão**: Nosso estudo apoia dados atuais sobre IRAS e perfil de resistência dos microorganismos mais comuns relacionados a essas infecções. Os resultados mostram a necessidade de conscientização sobre as IRAS e seus altos níveis de resistência.

DESCRITORES: Infecção Hospitalar. Bactérias. Resistência Microbiana a Medicamentos. Resistência a Múltiplos Medicamentos.

ABSTRACT

Background and objectives: Healthcare Associated Infections (HAI) is any infection acquired under health care, characterised by detection during the stay or after the discharge of the inpatient. The inappropriate use of antibiotics, has led to an increase on antimicrobial resistance, making the infection difficult to treat, especially for multidrug resistant organisms. Our study aimed to determine the main pathogens involved in infection in a Brazilian public hospital and evaluate their antimicrobial resistance pattern. **Methods**: Retrospective and documental study realized between 2008 and 2013. We analysed the microbiological culture exams results, a total of 6094 samples. **Results**: The sample was constituted by Respiratory tract (38.6%), Urinary Tract (35.8%), Skin and Soft Tissue (22.2%), Central venous catheter

(2.3%), and Blood stream (1.1%) samples. About 75% of the samples presented multidrug resistant organisms, mostly in central venous catheter infections, where 93% of all bacteria were resistant to 4 or more antibiotics. Gran negative bacteria were the most common organism found (86,4%). **Conclusion**: Our study supports current data about HAI and the resistance profile of the most common organisms related to these infections. Results show the need of awareness upon the growing number of the infections and its high levels of resistance.
KEYWORDS: Cross Infection. Bacteria. Drug Resistance, Microbial. Drug Resistance, Multiple.

RESUMEN

Justificación y objetivos: Infección relacionada a los servicios de salud (IRAS) es cualquier infección adquirida bajo atención de salud, caracterizada por detección durante la internación o después del alta del paciente. El uso inadecuado de antibióticos llevó a un aumento de la resistencia antimicrobiana, haciendo que la infección difícil de tratar, especialmente para microorganismos multirresistentes. El objetivo de este estudio fue determinar los principales patógenos involucrados en infecciones en un hospital brasileño y evaluar el patrón de resistencia antimicrobiana. **Métodos:** Estudio retrospectivo y documental realizado entre 2008 y 2013. Se analizaron los resultados de los exámenes de cultivo microbiológico, totalizando 6094 muestras biológicas. **Resultados:** El estudio fue constituido por muestras del tracto respiratorio (38,6%), tracto urinario (35,8%), piel y tejido blando (22,2%), catéter venoso central (2,3%) y sangre (1,1%). Cerca del 75% de las muestras presentaron microorganismos multirresistentes, principalmente en catéter venoso central, donde el 93% de todas las bacterias eran resistentes a 4 o más antibióticos. Las bacterias Gram negativas fueron las más encontradas (86,4%). **Conclusión:** Nuestro estudio apoya datos actuales sobre IRAS y perfil de resistencia de los microorganismos más comunes relacionados a esas infecciones. Los resultados muestran la necesidad de concientización sobre las IRAS y sus altos niveles de resistencia.
DESCRIPTORES: Infección Hospitalaria. Bacterias. Resistencia Microbiana a Medicamentos. Resistencia a Múltiples Medicamentos.

INTRODUCTION

Healthcare Associated Infections (HAI), as well called Hospital Acquired Infection, can be defined as any infection acquired under health care, characterised by the detection of the infection during the stay or after the discharge of the patient.[1,2] HAI can be developed through induction of commensal microbiota instability, normally caused by an invasive procedure or by the contact with the hospital microbiota.[3] HAI has been considered a serious problem due to the high morbidity and mortality rates associated, leading to an increase in the use of antibiotics and an extent on hospitalization, increasing costs.[1–4] Gram negative bacteria are considered the most common pathogens in HAI, although this data has modified among the years; nowadays, infections due to Gram positive bacteria such Staphylococcus aureus has increased significantly.[2] In Brazil, approximately 15% of the patients are infected by nosocomial pathogen; in global terms, about 17 to 20 million people die every year of infective diseases, 10 million acquire HAI and 3% of them do not survive.[2,3]

The inappropriate use of antibiotics, especially for prophylaxis measures, has led to an increase on antimicrobial resistance, affecting both Gram positive e Gram negative bacteria.[2,5] The resistance is consequence of the bacteria's ability to adapt but it has been forced to increase due to the indiscriminate use of antibiotics; bacteria are developing resistance faster than the pharmaceutical industry is capable of create new antibiotics, making this infection difficult or even impossible to treat, mainly for multidrug resistant organisms (MDROs).[2,6,7] MDROs are commonly defined as being resistant to one or more antibiotics in, at least, three different classes for which the bacteria are not intrinsically resistant.[810] The control of dissemination of MRDOs infections has been considered a worldwide priority, raising awareness of Healthcare Associated Infections Control organizations and health professionals.[79,11]

From this perspective, the purpose of this study was to evaluate the main species as well as the distribution and the antimicrobial susceptibility of the pathogens in patients from a public hospital of Ipatinga, in Minas Gerais state, Brazil, during a six-year period (2008-2013).

METHODOS

Clinical data and biological samples were collected from patients admitted between 2008 and 2013. We analysed the microbiological culture exams results that were realized in the Hospital Municipal Eliane Martins. We collected data such as patient's age and sex, year and site of collection (samples from blood stream, respiratory tract, skin lesions, urinary tract, and central venous catheter sites), identification of the bacteria, and the susceptibility to antimicrobials profile.

The results were expressed as a proportion of the total number of patients or isolates. Differences in proportions were compared by Mann-Whitney U and Kruskal-Wallis test, as appropriate. The inclusion criteria used was: be clinically significant; be present in 5% of the results at least; and have a complete susceptibility profile. All statistical analyses were done using Statistical Package for the Social Sciences (SPSS – IBM®) version 23 for Windows® considering 0.05 as the significance level.

The project was submitted to the Ethics committee of the Centro Universitário do Leste de Minas Gerais, Brazil, receiving authorization under register number 902.843/2014.

RESULTS

During the study period a total of 6094 forms were analysed. From this set, 2683 (44%) presented a valid data, which correspond to the presence of one or more species of bacteria per sample. A total of 3381 positive samples were identified. The samples were organized per the age of the patient, which was grouped in the category elderly, adult, young adult, adolescent, and children. This sample was constituted by 1378 (51.3%) female patients and mean age of 59 years (57 years for males and 61 years for female) and age range from 0 to 100 years. The elderly group represented most the patients (52.9%), followed by adults (36%), young adults (8.8%), children (1.4%), and adolescents (0.9%). Excepting for the adolescent group, infections had increased with age. There was a significant growth of the samples number among the years studied (p=0.002) (Figure 1). From the beginning to the end of the study we had an average increase of 100 samples a year, the year with the major significant growth was 2010, which had 225 more samples than 2010, and there was a decrease on the number of samples in 2009, 24 samples less than 2008.

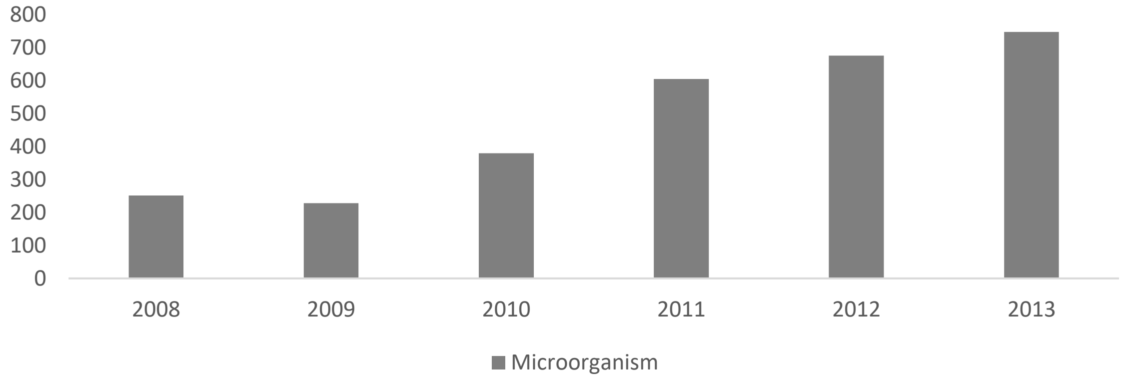

Figure 1 - Distribution of the samples among the years. The left axis presents the absolute number of samples. Except for the year of 2009, where the samples number regressed, the growth was almost linearly.

We found 10 bacterial species that were present in, at least, 5% of the samples, they were: *Enterobacter* spp., *Enterococcus* spp., *Escherichia coli*, *Klebisiella* spp., *Proteus* spp., *Pseudomonas aeruginosa*, *Pseudomonas* spp., *Morganella morganii*, *Staphylococcus aureus*, and *Stenotrophomonas maltophilia*. *Pseudomonas aeruginosa* was considered aside of the *Pseudomonas* group due to its clinical significance and since its relative number was very like the other *Pseudomonas* species altogether.

The samples were collected from diverse sites per the clinician request, there were: respiratory tract infection (RTI), urinary tract infection (UTI), skin and soft tissue infection (SSTI), central venous catheter infection (CVCI), and blood stream infection (BSI) samples (Figure 2). The variation of the samples in each infection site through the years can be seen on table 1.

Among samples collected from RTI, 741 (70.6%) were from male patients with an average age of 60 years old and 64 years for female patients. The most common microorganism found were *S. maltophilia* (18.6%), *Klebisiella* spp. (12.8%), *Pseudomonas* spp. (12.8%) and *Pseudomonas aeruginosa* (10.5%). Regarding difference in the bacterial species among the age group, the variance was considered significant (p=0.036).

UTI samples were mainly colonized by *E. coli* (33.7%), *Klebisiella* spp. (20.7%), and *Enterococcus* spp. (9.5%). The majority of the samples were from female patients (56.2%); the average age was similar for both groups (59 years old for female patients and 60 for male).

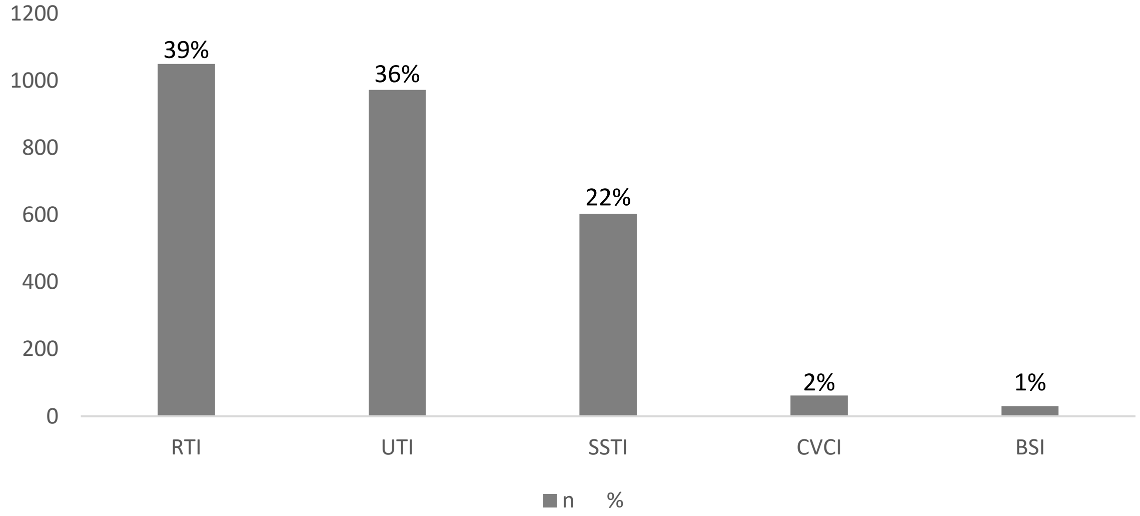

Figure 2 - Distribution of the samples according to the site of infection. The left axis presents the absolute number and the percentage is shown above the columns. This figure was generated by plotting the absolute number of samples in relation of sites of infection: respiratory tract infection (RTI), urinary tract infection (UTI), skin and soft tissue infection (SSTI), central venous catheter infection (CVCI), and blood stream infection (BSI).

Table 1 - Distribution of the samples according to the infection site through the years. CVCI= Central Venous Catheter Infections; SSTI= Skin and Soft Tissue Infections; BSI= Blood Stream Infection; RTI= Respiratory Tract Infection; UTI= Urinary Tract Infection.

INFECTION SITE	CVCI	SSTI	BSI	RTI	UTI
YEAR					
2008	13	52	1	110	127
2009	16	52	6	126	85
2010	30	40	8	221	147
2011	21	155	12	271	248
2012	16	221	22	278	225
2013	29	195	14	352	230

SSTI samples were composed by *E. coli* (15.1%), *S. aureus* (12.0%) and *Proteus* spp. (11.7%), predominantly collected from male patients (53.8%) in average 56 years old while the female patients were some older (62 years old). SSTI presented similar statistical results compared to UTI samples where difference regarding bacterial species was relevant among the age groups analysed (p=0.005).

The most common pathogens found in CVCI samples were *S. maltophilia, S. aureus*, and *Klebisiella* spp. (18.4%, 10.4% and 8.8% respectively) from male patients (48% - average 53 years) and female patients (average 65 years old).

BSI sample were mainly colonized by *S. aureus* (15.6%), *E. coli* (10.9%), and *Klebisiella* spp. (9.4%). Female patients (56,3 %), from which the blood samples came from, were relatively older than male patients (61 and 54 years old on average for female and male patients respectively).

The general resistance profile can be found on table 2 and table 3.

Central venous catheter samples

Bacteria from central venous catheter samples presented higher levels of resistance to ampicillin (92%), clindamycin (89%), and cephalothin (82%). *S. maltophilia, P. aeruginosa,* and *E. coli*, presented the highest levels of resistance among the found species, where, for most of the antibiotics tested, was found an average rate of 74% resistance (p=0.003). *Klebisiella* spp. presented the lowest resistance levels, 46% on average, being highly susceptible to the carbapenems (73%), ticarcillin/clavulanate (82%), and rifampicin (91%). Similar pattern was found for *Enterobacter* spp.

Blood Stream sampling

BSI samples were resistant to clindamycin (85%), monobactams (72%), and to the penicillin’s class (69%). Among the penicillin’s class, high rates were related to ampicillin (87%). S. aureus showed 80% of resistance to benzylpenicillin, 40% was considered Methicillin Resistant *S. aureus* (MRSA) and 10% was Vancomycin Resistant *S. aureus* (VRSA). S. aureus was highly sensible to all the other antibiotics tested except for the monobactam aztreonam (90% resistant). Samples of *Klebisiella* spp. were totally resistant to cefaclor, cephalotin, clindamycin, ampicillin, and to the association ampicillin/sulbactam. *S. maltophilia* showed complete resistance to cephalotin, cefepime, clindamycin, ampicillin and chloramphenicol.

Respiratory Tract sampling

Bacteria found on respiratory tract sample had considerably elevated levels of resistance to clindamycin (90%), ampicillin (82%), and cephalotin (78%). In general, there were significant difference in the resistance pattern among the age groups (p=0.004). Comparing the different years, the resistance was relatively different (p=0.02), also different comparing the resistance among each bacterial specie (p=0.002). *S. aureus* in RTI presented same pattern that *S. aureus* from BSI samples regarding benzylpenicillin (80%), 27% of the samples were MRSA and 2% VRSA. *Enterococcus* spp. presented 43% resistance to oxacillin and 7% resistance to vancomycin. *E. coli*, *Pseudomonas* spp., and *S. maltophilia* were completely resistant to clindamycin. *S. maltophilia* was also fully resistant to cephalotin. The antibiotics with the lowest levels of resistance were the aminoglycosides (31%) and the carbapenems (24%).

Skin and Soft Tissue sampling

In SSTI samples, the resistance profile for ampicillin, clindamycin and cephalotin was rather high, reaching 90%, 87%, and 73% of the samples respectively. SSTI sample presented similar statistical results compared to UTI samples where the difference among the years studied and among the age groups was considered relevant (p=0.047; p=0.003). *Klebisiella* spp., *P. aeruginosa*, and remaining *Pseudomonas* spp. were altogether resistant to clindamycin. *S. maltophilia* presented full resistance to chloramphenicol. 90% of the *S. aureus* samples were resistant to benzylpenicillin and 15% were MRSA. In average, the level of resistance was 47% among the species.

Urinary Tract sampling

The leading antibiotics for resistance were ampicillin (78%), cephalotin (74%), and cefaclor (70%). Resistance results had a significant variance concerning the years of study, the bacterial species, and the age groups (p=0.005; p=0.002; p=0.001 respectively). *P. aeruginosa* was fully resistant to cefaclor, ampicillin, and ampicillin/sulbactam, while other species of the pseudomonas genus were completely resistant to ampicillin and nitrofurantoin only. MRSA was found in 20% of the *S. aureus* samples were 80% of them were also resistant to benzylpenicillin. Two percent of the *Enterobacter* spp. were vancomycin resistant. The quinolones and nitrofurantoin, highly used to treat UTI, presented an average resistance of 59% and 64% respectively.

Table 2 - Antimicrobial resistance of the main pathogens (Part 1). NT= antibiotic was not tested for the bacterial specie.

Bacteria		***Enterobacter* spp.**	***E. coli***	***Klebisiella* spp.**	***M. morganii***	***P. aeruginosa***
Antimicrobials		**%**	**%**	**%**	**%**	**%**
Aminoglycoside	Amikacin	4	4	7	3	23
	Gentamicin	44	20	53	29	37
Cephalosporin	Cefaclor	53	29	77	83	99
	Cephalotin	89	44	74	89	98
	Cefepime	23	12	49	8	33
	Ceftazidime	30	8	51	5	32
	Ceftriaxone	48	17	64	18	67
Quinolone	Ciprofloxacin	40	49	59	52	39
	Levofloxacin	38	47	58	44	44
	Norfloxacin	40	51	60	50	43
	Ofloxacin	31	48	63	57	44
Penicillin	Ampicillin	91	75	93	84	100
	Piperacillin/ tazobactam	15	8	33	5	26
	Amoxicillin/ Clavulanate	85	24	60	79	99
	Ampicillin/ sulbactam	62	38	67	55	96
Others	Imipenem	2	1	1	0	31
	Clindamycin	97	NT	99	85	99
	Aztreonam	37	12	56	9	19
	Chloramphenicol	49	98	34	53	94
	Sulfamethoxazole/ Trimethoprim	56	63	64	56	91
	Ticarcillin/ clavulanate	43	22	51	9	29
	Tetracycline	61	58	63	79	83

Table 3 - Antimicrobial resistance of the main pathogens (Part 2). NT= antibiotic was not tested for the bacterial specie.

Bacteria		***Proteus* spp.**	***Pseudomonas* spp.**	***S. maltophilia***	***Enterococcus* spp.**	***S. aureus***
Antimicrobials		**%**	**%**	**%**	**%**	**%**
Aminoglycoside	Amikacin	4	25	77	NT	8
	Gentamicin	32	35	72	56	10
Cephalosporin	Cefaclor	56	97	99	NT	25
	Cephalotin	57	98	99	NT	22
	Cefepime	18	36	94	NT	22
	Ceftazidime	4	32	88	NT	20
	Ceftriaxone	26	62	93	NT	21
Quinolone	Ofloxacin	41	47	90	NT	18
	Levofloxacin	36	36	80	69	15
	Norfloxacin	36	39	90	82	22

	Ciprofloxacin	36	38	87	77	23
Penicillin	Ampicillin	69	98	97	22	85
	Benzylpenicilin	NT	NT	NT	49	83
	Oxacillin	NT	NT	NT	NT	24
	Piperacillin/tazobactam	2	19	87	NT	22
	Amoxicillin Clavulanate	30	94	92	NT	25
	Ampicillin/sulbactam	34	89	70	NT	23
Others	Imipenem	5	28	66	NT	18
	Clindamycin	96	100	100	NT	21
	Aztreonam	9	32	90	NT	90
	Chloramphenicol	64	85	94	NT	10
	Sulfamethoxazole/Trimethop.	61	79	76	NT	11
	Ticarcillin/clavulanate	8	40	77	NT	24
	Tetracycline	90	71	60	60	10
	Vancomycin	NT	NT	NT	3	2

A total of 74% of the samples MDROs. The site they were most commonly found was CVCI, where 93% of all bacteria were resistant to 4 or more antibiotics. CVCI was followed by RTI samples (83%), SSTI samples (76%), UTI samples (72%), and BSI samples (63%), representing on total 78% of the samples. The average resistance among the species in UTI samples was to 7.6 antibiotics, the lowest average between the sites; SSTI samples, SBI samples, RTI samples, and CVCI samples presented average resistance to 8.4, 8.5, 10.6, and 12.8 antibiotics respectively; MDROs were more frequent in the elderly group in all sites but RTI samples, where the highest resistance was found in the Adults group.

Among the all the samples, except for BSI samples, *S. maltophilia* showed resistance to the largest number of antibiotics (UTI: 13.6 antibiotics; SSTI: 16.5; RTI: 15.4; CVCI:17), *P. aeruginosa* presented average resistance to 15.5 antibiotics in BSI, being considered the highest in this group, while *S. aureus* was the lowest resistant in SSTI samples and UTI samples (4.6; 3.9), *E. coli* in BSI and CVCI samples (3.7; 8.0), and *Enterococcus* spp. in RTI samples.

DISCUSSION

In this study, we analysed the pattern of the bacterial infections and its resistance profile to antimicrobials in a general hospital. Our results show a prevalence of RTI and UTI over the other sites, comprehending, together, 72% of the samples (40.4% and 31.6% respectively). Similar pattern of prevalence where found by other authors in Brazil. Analysis performed by Moura *et al* (North region of Brazil), Patzer *et at* (South of Brazil), Damasceno *et al* (Southeast of Brazil), and De Andrade *et al* presented similar patterns of prevalence where RTI and UTI corroborate, altogether, to 76.4%, 42.7%, 58.7%, and 56.1% of the samples respectively.[6,9–11] Other works reported high prevalence for BSI (38.97%), for SSTI (58.5%, 38.46%, 35,7%, and 45%), of RTI and SBI together (56%; 64%; 76%), and the associated prevalence of UTI and SSTI (66.7%).[2,4,12–17]

Our study showed a prevalence of UTI infections in women (56.2%) and mean age of 60 years, corroborating with other studies conducted in the past years.[4,6,14,18–20] The pathogen responsible for most urinary tract infections was *E. coli*, being in accordance with previous studies that also present *Klebisiella* spp. as the subsequent pathogen, as well as other members of the Enterobacteriaceae family, showing the conformance of our study.[6,11,19] Variation in the bacterial profile against other studies is reasonable considering the difference between the population analysed, regarding age, sex, and socio-economic background.

The distribution of agents causing RTI can vary widely per the geographic region analysed. The greater number of studies show a prevalence of infections due to *P. aeruginosa* and *Klebisiella* spp..[6,14,15,17] Our study shows a prevalence of *Pseudomonas genus* (23.3%) but, if considered *P. aeruginosa* alone it takes the forth place (10.5%) after *S. maltophilia* (18.6%), *Klebisiella* spp. (12.8%) and other species of the *Pseudomonas genus* (12.8%). Although Spilker *et al* states that it is crucial the correct identification of the pseudomonas specie to define a correct treatment and define impatient outcome, we did not find significant difference among infection pattern and resistance profile between *P. aeruginosa* and other pseudomonas species.[21] *S. maltophilia* isolated in respiratory tract has been associated to colonization instead of infection, especially when associated to others pathogenic microorganisms such P. aeruginosa, rising concerns about treatment alternatives.[22]

BSI were mostly caused by *S. aureus* and *E. coli* in the present study and in previous studies.[5,15] BSI has a similar bacterial profile as SSTI and CVCI, seen that these two infections are the main entry door for microorganisms on the blood stream. CVCI were most commonly caused by *S. aureus*, Enterobacteriaceae and *S. maltophilia*, while SSTI were caused by *E. coli, S. aureus* and *Proteus* spp. mostly. The literature confirms these data associating CVCI and SSTI to S. aureus, Enterobacteriaceae species, and *P. aeruginosa*.[6,13,15,17,23] In the present study, the lower rates for BSI (1.9%) and CVCI (3.7%) can be related to the low use of central venous catheter, commonly substituted for peripheral venous catheter, frequently changed, and the fact that the hospital does not hold an operating room, reducing the invasive procedures and so the risks for BSI; which also could explain the lower taxes of SSTI (21.3%).

In general, it was observed an increase of antibiotic resistance with the age of the inpatient. This can be related to the immune system becoming weaker with the age and can lead to an increase on the extent of the patient and more serious complications.[18] High resistance rates were found for many antibiotics among all microorganism, mostly for lincosimide, tetracycline, monobactams, sulfamethoxazole/trimethoprim, and to 1st and 2nd generation of cephalosporin. Gram negative organisms' resistance profile was in accordance with national studies regarding high levels of resistance to cephalosporin, lincosimide, sulfamethoxazole/trimethoprim, and quinolones, except for *E. coli*, which presented levels higher than those found in the current literature.[9,10,12,15,16,20,23,24]

Gram positive bacteria showed low sensibility to monobactams, lincosimide, benzylpenicillin and sulfamethoxazole/trimethoprim, obtaining similar results to other national data reports.[9,10] However, resistance to Oxacillin was lower in our study than what has been reported on the literature (24% vs 74% on average).[9,10,12,15,16] In addition, must be observed that our data is a local data and, thus, may not be representative of the country due to its continental extension neither may be translated to an international level.[18,25]

Organisms such *S. maltophilia* and *M. morganii* are known for their extensive intrinsic resistance to antibiotics classes like the macrolide, lincosimide, glycopeptides, oxacillin, and ampicillin for *M. morganii*, and β-lactams, sulfamethoxazole/trimethoprim, aminoglycosides, macrolides, lincosimide, chloramphenicol, and tetracycline for *S. maltophilia*. Also, intrinsic resistance is found for the cephalosporin (1st and 2nd generation mostly for *M. morganii* and all generations for *S. maltophilia*), which reduces considerably the treatment options.[24,25]

Recent treatment option for infections by *S. maltophilia* was the use of sulfamethoxazole/trimethoprim, but the resistance to this drug escalated quickly reaching levels of total resistance in some hospital studies. Later, the sulfamethoxazole/trimethoprim was substituted by ticarcillin/clavulanate association which presented better results until the microorganism starts to present resistance. Currently, the synergy between different classes of antibiotics has been used to treat MDROs, including *S. maltophilia* and *M. morganii*. Association between sulfamethoxazole/trimethoprim and either ceftazidime, ciprofloxacin, or tobramycin has shown adequate efficacy to treat infections caused by these organisms.[25]

Healthcare Associated Infections Control centres are essential to monitor the occurrence of infectious diseases, the pathogen involved, and the sensibility profile so that physicians can have a better understanding about the hospital infection profile.[5] If Epidemiological Surveillance Control data was collected reliably worldwide it would allow the comparison of the rates of infection and the resistance profile, providing a better knowledge and allowing a better decision-making about the therapy and the identification of potential risks. [7]

In conclusion, our study supports current data about Healthcare Associated Infections and the resistance profile of the most common organisms related to these infections. The main microorganisms found were from the *Enterobacteriaceae* family and Gram-positive bacteria such *Enterococcus* spp. and *S. aureus*, with sensibility to antimicrobials profile in accordance with the literature. Furthermore, our results show the need of awareness upon the growing number of the infections and its high levels of resistance and concern about the need of control measures for the use of antibiotics for prophylaxis and precise organisms' identification and its sensibility profile to prevent the development and spread of antibiotic resistance.

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