cadernos ESP/CE
Revista Científica
Escola de Saúde Pública
do Ceará Paulo Marcelo
Martins Rodrigues
1808-7329 (1809-0893)

HOSPITAL MICROBIOLOGICAL PROFILE BEFORE AND DURING COVID-19

PERFIL MICROBIOLÓGICO HOSPITALAR ANTERIOR E DURANTE A COVID-19

PERFIL MICROBIOLÓGICO ANTES Y DURANTE LA COVID-19 EN UN HOSPITAL

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ABSTRACT

Objective: To compare the microbiological profile of cultures from patients hospitalized in a private hospital in Fortaleza, CE, before (2018/19) and during the COVID-19 pandemic (2020/21). **Methods:** Descriptive and analytical cross-sectional study using secondary data from an antimicrobial stewardship program. Patients aged over 18 years with cultures collected during the study period were included, excluding one case with incomplete data. Data were tabulated in Excel and analyzed using StataSE. **Results:** There was a predominance of male patients aged 19 to 59 years. The microbiological profile showed a reduction in the number of positive cultures, an increase in the number of isolated fungal and an increase antimicrobial resistance during the pandemic. Carbapenem-resistant *Acinetobacter baumannii* isolates increased from 50.88% to 79.83%, and *Klebsiella pneumoniae* from 29.09% to 54.64%. **Conclusion:** The COVID-19 pandemic contributed to an increase in antimicrobial resistance, highlighting the need to intensify microbiological surveillance.

Keywords: *COVID-19; Antimicrobial Stewardship; Drug Resistance, Microbial.*

RESUMO

Objetivo: Comparar o perfil microbiológico de culturas de pacientes internados em hospital privado de Fortaleza/CE antes (2018/19) e durante a pandemia de COVID-19 (2020/21). **Métodos:** Estudo transversal descritivo e analítico com dados secundários de um Programa de Gerenciamento de Antimicrobianos aplicado em hospital privado. Foram incluídos pacientes maiores de 18 anos com culturas coletadas no período do estudo, excluindo um caso com dados incompletos. Os dados foram tabulados no Excel® e analisados no StataSE. **Resultados:** Predomínio de pacientes do sexo masculino de 19 a 59 anos. Durante a pandemia, houve redução no número de culturas com microrganismos isolados, aumento de isolados fúngicos e maior resistência antimicrobiana. O isolamento de *Acinetobacter baumannii* resistentes a carbapenêmicos subiu de 50,88% para 79,83%, e de *Klebsiella pneumoniae*, de 29,09% para 54,64%. **Considerações finais:** A pandemia de COVID-19 contribuiu para o aumento da resistência antimicrobiana, destacando a necessidade de intensificar a vigilância microbiológica.

Descritores: *COVID-19; Gestão de Antimicrobianos; Resistência Microbiana a Medicamentos*.

RESUMEN

Objetivo: Comparar el perfil microbiológico de cultivos de pacientes hospitalizados en un hospital privado de Fortaleza, CE, antes (2018/19) y durante la pandemia de COVID-19 (2020/21). **Métodos:** Transversal descriptivo y analítico con datos secundarios de un programa de gestión de antimicrobianos. Se incluyeron pacientes mayores de 18 años con cultivos recolectados durante el período de estudio, excluyendo un caso con datos incompletos. Los datos fueron tabulados en Excel y analizados con StataSE. **Resultados:** Predominio de pacientes masculinos de entre 19 y 59 años. Durante la pandemia, hubo una reducción en el número de cultivos con microorganismos aislados, un aumento en los aislados fúngicos y mayor resistencia antimicrobiana. Los aislamientos de *Acinetobacter baumannii* resistentes a carbapenémicos aumentaron del 50,88% al 79,83%, y los de *Klebsiella pneumoniae* del 29,09% al 54,64%. **Conclusión:** La pandemia de COVID-19 contribuyó al aumento de la resistencia antimicrobiana, destacando la necesidad de intensificar la vigilancia microbiológica.

Descriptores: *COVID-19; Programas de Optimización del Uso de los Antimicrobianos; Farmacorresistencia Microbiana.*

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INTRODUCTION

Antimicrobial resistance (AMR) is accelerated by the overuse of antimicrobials (ATM) in humans and animals. There are several situations in which this inappropriate use occurs, such as: uninformed diagnosis; the pressure from family members and patients to use the medication; the lack of adequate adherence by the patient to the treatment as prescribed and self-medication through improper purchase at the drugstore without a medical prescription (1). In addition, the inappropriate use of TMJ (e.g., non-isolated pathogen or site of infection where the drug does not penetrate), or inadequate dose and time are other very important factors in the triggering of resistance (2).

Research in the European Union and the United Kingdom shows that vancomycin resistance in *Enterococcus faecium infections* almost doubled between 2015 and 2019, in addition to being observed in the classes of carbapenems against *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Acinetobacter spp* (3). In 2019, the World Health Organization (WHO), through the IACG (*Interagency Coordination Group*), published the report *NO TIME TO WAIT,* warning of the emergency problem of AMR as a public health issue. The document predicts up to 10 million deaths annually from resistant bacteria by 2050 and an economic crisis that could push 24 million people into extreme poverty by 2030 in the absence of a response (4). Antimicrobial Stewardship (PGA) programs, microbial culture monitoring, and AMR surveillance are needed to address the problem.

During the COVID-19 pandemic, several public health strategies were undermined and the use of TMJ grew considerably, which worried the community about the effects of AMR. The objectives of this article were to describe and compare the microbiological profile in cultures of patients followed by the PGA of a private hospital in Fortaleza-CE before (2018 and 2019) and during the COVID-19 pandemic (2020 and 2021) in order to assess whether there were changes in the two periods.

METHODS

This is a descriptive and analytical cross-sectional study based on secondary data from the database of a PGA of a health plan operator (OPS), approved by the Ethics Committee (CAAE 20508519.4.0000.5684), updated on April 28, 2022 by the Institute of Health and Hospital Management.

The data were collected at the Unimed Fortaleza Hospital, a private tertiary level hospital, with 260 ward beds, 70 Intensive Care Unit (ICU) beds and its own laboratory. The PGA was conducted by the Pharmaceutical Assistance and Audit (ASSFAR) of PAHO in partnership with the hospital team. The target population included patients over 18 years of age hospitalized in open and closed units, with microbiological cultures collected between January 2018 and December 2021, under PGA monitoring for therapeutic use of antimicrobials, excluding cases of prophylactic use. One patient with incomplete data in 2018 was excluded from the analysis.

The variables were:

1) Demographic Variables: Gender (female and male) and age group (19 to 59 years; 60 to 80 years; over 80 years).

2) Microbiological Variables: Culture results (positive - with microorganism growth or negative - no growth); type of microorganism (bacteria or fungus); microorganism isolated by gender and resistance profile.
3) Antimicrobial resistance was standardized through the antibiogram performed by the Vitek system or with specific enzyme testing (when available):
    (a) ESBL: Gram-negative bacteria resistant to cephalosporins (such as ceftriaxone, ceftazidime, and/or cefepime);
    (b) ERC: Enterobacteria resistant to carbapenems (meropenem and/or ertapenem);
    (c) VRE: *Enterococcus spp.* vancomycin-resistant;
    (d) MRSA: *Oxacillin-resistant* Staphylococcus aureus.

For data analysis, those cultures with bacterial growth and that did not have antimicrobial resistance characteristics mentioned above were classified as bacteria with sensitivity or "sensitive". This standardization was necessary because, over the years, the PGA underwent adjustments, and the laboratory responsible for the hospital underwent changes and modernizations. Since not all laboratories performed the enzyme test, it was decided to classify resistance based on the antibiogram in the absence of this test.

The relative and absolute frequencies of the variables, including the positivity profile of the crops, the growth of bacteria and fungi, the pathogens with the highest prevalence, and the most clinically relevant genera of microorganisms were evaluated to identify changes in microbial growth between the periods analyzed. The resistance profile (*VRE, MRSA, ERC* and *ESBL)* was also investigated. Rectal *swab* samples were excluded, as well as cultures with fungal growth in the resistance analyses, due to the absence of antifungigram.

The data were tabulated in Excel 2016 and analyzed using the statistical program StataSE to perform comparative analyses. The variables analyzed were categorical, so Pearson's Chi-square test was used. A significance of $p < 0.05$ was considered for these analyses. For the comparative analyses, the independent variable (or exposure) was considered the group of years: before the pandemic (2018 and 2019) and during the pandemic (2020 and 2021) since the objective of the comparison is to verify changes in the period before and during a pandemic that had such an impact on health. Therefore, the dependent (or outcome) variables were: Crop results (Positive or Negative); type of microorganism (Fungus or Bacteria); resistance type (Sensitive; ERC; ESBL; VRE; MRSA) and growth of the main genera of fungi and bacteria.

RESULTS

A total of 8,911 hospitalizations were included: 28.55% (n=2,544) prior to the pandemic (2018 and 2019) and 71.45% (n=6,367) during the COVID-19 pandemic (2020 and 2021).

Before the pandemic, most patients followed were female, aged between 60 and 80 years. During the pandemic, there was a shift to male predominance and the age group between 19 and 59 years old.

During the years 2018 to 2021, 17,548 microbiological cultures were registered, of which 71% (n=12,373) were delivered during the pandemic. It was observed that 32.47% (n=5,698) of the samples were positive, with 36.04% (n=1,865) before the pandemic and 30.98% (n=3,833) during the pandemic. The difference was statistically significant according to Pearson's chi-square test ($p < 0.001$). Of the 5,698 cultures with microbial growth, 86.83% (n=4,948) were evaluated, corresponding to the most clinically relevant microorganisms as shown in Table 1.

Table 1 - Profile of the most clinically relevant microorganisms isolated from the cultures of patients included in the study. Fortaleza, 2018 to 2021.

Variables	General	2018-2019	2020-2021	p
	Total / N (%)	Total / N (%)	Total / N (%)	
Fungi	726 (100%)	198 (100%)	528 (100%)	
Candida albicans	320 (44,07%)	74 (37,37%)	246 (46,59%)	0,026
Candida non-albicans	406 (55,93%)	124 (62,62%)	282 (53,41%)	
Gram positive bactéria	1.429 (100%)	278 (100%)	1.151 (100%)	
Staphylococcus coagulase negative	1.076(75,3%)	133 (47,84%)	943 (81,93%)	<0.001
Enterococcus	173 (12,11%)	57 (20,50%)	116 (10,07%)	
Staphylococcus coagulase positive	142 (9,94%)	68 (24,46%)	74 (6,43%)	
Streptococcus.	38 (2,65%)	20 (7,2%)	18 (1,57%)	
Gram negative bactéria	2.793 (100%)	1.097 (100%)	1.696 (100%)	
Pseudomonas	970 (34,73%)	404 (36,83%)	566 (33,37%)	<0.001
Klebsiella	914 (32,72%)	340 (31,00%)	574 (33,84%)	
Escherichia	495 (17,72%)	290 (26,43%)	205 (12,09%)	
Acinetobacter	414 (14,83%)	63 (5,74%)	351 (20,7%)	

Source: prepared by the authors, 2025.

According to Table 1, among the samples, 726 had fungal isolates, 44.07% (n=320) of *Candida albicans* and 55.93% (n=406) of *Candida albicans*. An increase in *Candida albicans was observed* between the periods analyzed: it represented 37.37% (n=74) before the pandemic and increased to 46.59% (n=246) during the pandemic, a statistically significant difference (p=0.026). The percentages of *non-albicans Candida* remained stable: *Candida tropicalis* (41.13% to 42.55%), *Candida glabrata* (30.65% to 30.85%) and *Candida parapsilosis* (21.77% to 18.09%). During the pandemic, 65.72% (n=347) of the fungal isolates were from ICU samples, and 34.28% (n=181) from wards.

A total of 1,429 cultures with growth of gram-positive bacteria were analyzed. The variation in the profile between the periods was statistically significant ($p < 0.001$), highlighting the increase in the isolation of *coagulase-negative Staphylococcus*, mainly

S. epidermidis (39.87%), *S. haemolyticus* (27.89%), *S. hominis* (17.29%), and *S. capitis* (6.15%) during the pandemic.

Analyzing the growth of gram-negative bacteria, 2,793 were described in Table 1, representing the genera of greatest clinical importance: *Pseudomonas*, *Klebsiella*, *Escherichia* and *Acinetobacter*. Before the pandemic, *Klebsiella* represented 31% (n=340) of the total of these crops and during the pandemic, this microorganism represented 33.84% (n=574). The genus *Acinetobacter* represented 5.74% (n=63) delivered before the pandemic, changing to 20.70% (n=351) of the crops in the period during the pandemic. The growth differences in the two periods between gram-negative bacteria were statistically significant (p<0.001).

The antimicrobial resistance analysis included only bacterial cultures. In total, 60.52% (n=2,998) of the cultures were sensitive, while 22.89% (n=1,134) were ERC; 15.64% (n=775) ESBL; 0.75% (n=37) MRSA and 0.20% (n=10) VRE, in the period from 2018 to 2021. Comparing the two periods, it was observed that there was an increase in ERC isolates (from 14.67% to 27.04%) and VRE (from 0.18% to 0.21%) during the pandemic with a statistically significant difference (p < 0.001).

When we delve into the main resistance profiles and their expressive microorganisms, 244 ERC-type bacteria were isolated prior to the pandemic, most of which were of the genera *Klebsiella* (40.57%); followed by *Pseudomonas* (37.30%) and *Acinetobacter* (11.89%). During the pandemic, the genus *Klebsiella* was the most predominant, but there was a significant growth of *Acinetobacter* with ERC-type resistance, as described in Table 2.

Table 2 - Antimicrobial resistance profile of the ERC (Carbapenem-resistant Enterobacteria) and ESBL (Extended Spectrum β-lactamases) type and their expressive microorganisms in the cultures of patients included in the study. Fortaleza, 2018 to 2021.

Variables	2018-2019	2020-2021
	N (%)	N (%)
Resistance Type: ERC	244 (100%)	890 (100%)
Klebsiella	99 (40,57%)	320 (35,96%)
Pseudomonas	91 (37,30%)	215 (24,16%)
Acinetobacter	29 (11,89%)	278 (31,24%)
Another	25 (10,24%)	77 (8,65%)
Resistance Type: ESBL	370 (100%)	405 (100%)
Escherichia	118 (31,89%)	84 (20,74%)
Klebsiella	110 (29,73%)	98 (24,20%)
Pseudomonas	85 (22,97%)	180 (44,44%)
Another	57 (15,41%)	43 (10,62%)

Source: prepared by the authors, 2025.

Analyzing the profile of ESBL bacteria, before the pandemic, 370 were isolated with a predominance of *Escherichia* (31.89%); *Klebsiella* (29.73%) and *Pseudomonas*

(22.97%). During the pandemic, there was an inversion, in which the isolation of *Pseudomonas* with ESBL characteristics predominated, as detailed in Table 2.

Before the pandemic, *Klebsiella pneumoniae* was isolated in 330 cultures, of which 29.09% (n=96) were resistant to carbapenems (ERC). During the pandemic, this percentage increased to 54.64%, with 300 of the 549 crops showing resistance. For *Acinetobacter baumannii*, resistance to carbapenems was 50.88% (29 out of 57 crops) before the pandemic, rising to 79.83% (277 out of 347 crops) during the pandemic.

DISCUSSION

Most hospitalizations occurred during the COVID-19 pandemic, reflecting the high use of antimicrobials due to fears of bacterial coinfection and empirical initiation of treatment. A systematic review (2020–2021) showed bacterial co-infection in 5.62% (95% CI 2.26–10.31) of cases and antimicrobial use in 61.77% (CI 50.95–70.90), indicating low prevalence of infection and high drug consumption (5). There was a change in the gender and age profile of the patients, with a reduction in the age group, attributed to the impact of vaccination on the priority population, according to a study (6).

During the pandemic, most cultures showed no microbial growth, in line with the WHO report on the low incidence of bacterial lung coinfection (7). All cultures were from patients using antimicrobials, which allows us to infer that most treatments were performed empirically. Comparatively, a private hospital in Rio Grande do Norte recorded a positivity of 14.14% between 2019 and 2021, differing from this study, but with 85% bacterial isolates and 15% fungal, more similar results (8).

The study's findings, with diagnostic limitations for fungal diseases, indicate that most of the fungi isolated during the pandemic were from ICU cultures. This is due to the vulnerability of patients in the ICU to the use of invasive devices, such as mechanical ventilation (9). Toledo (2022) showed a higher frequency of *Candida albicans*, *Candida parapsilosis,* and *Candida glabrata* in patients with COVID-19, unlike this article, which presented *Candida tropicalis* and *Candida glabrata* as more frequent (10). Coagulase-negative *Staphylococcus* was the most frequent gram-positive bacteria, followed by *Enterococcus* and *Staphylococcus aureus*. Increased coagulase-negative *Staphylococcus* may indicate contamination from the collection or secondary infection. Studies on Healthcare-Associated Infections also indicate coagulase-negative *Staphylococcus* as prevalent, followed by *Pseudomonas aeruginosa* and *Staphylococcus aureus* (11).

Among the most prevalent bacteria, those grouped under the acronym ESKAPE (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, *Enterobacter*) were the main isolates and of greatest interest to the WHO due to the high rates of antimicrobial resistance (12). The increase in the genus *Acinetobacter* is worrisome due to the possibility of resistance and deaths, in a study in the ICU of the Santa Casa da Misericórdia Hospital in Ouro Preto, the isolations of *Acinetobacter baumannii* went from eight in 2019 to eighteen during the pandemic (13). In this work, a significant number of *Acinetobacter baumannii samples* showed resistance to carbapenems during the pandemic. In another study carried out in a private hospital in Fortaleza, he attributed the high rate of resistance to the use of multiple consecutive antimicrobials during the pandemic. This study evaluated cultures from 2021 and found 94.7% resistance of *Acinetobacter baumanni* to meropenem; in *Pseudomonas aeruginosa*, resistance was 63% and in *Klebsiella pneumoniae*, 85.80% (14). Another study with similar resistance was found at the Wuhan Union hospital, patients with infections secondary to COVID-19 had isolation rates of carbapenem-resistant *Acinetobacter baumanni* and *Klebsiella pneumoniae* of 91.2% and 75.5%, respectively (15).

Huttner et al. (2020) highlighted the difficulty in differentiating COVID-19 from bacterial pneumonia and treats antimicrobials as a strategy for empirical treatment of critically ill patients. The authors emphasize the moderate and responsible use of these medications, considering the importance of supply to avoid unavailability, the increase in nursing workload, and the long-term consequences of excessive use, which can increase morbidity and mortality in the future (16).

The present study demonstrated that PGA is essential for microbiological surveillance, allowing more effective strategies in the use of TMJ. A study carried out in a public hospital in Fortaleza, Ceará, showed some implications of the PGA in the institution, concluding that there were positive results in both clinical and financial results (17).

FINAL CONSIDERATIONS

The study has limitations, such as its cross-sectional nature and the use of secondary data, which limited the verification of information. In addition, the PGA only followed patients from the Unimed Fortaleza Hospital, excluding other plans and private individuals, but most of those served had a Unimed plan reducing the representativeness bias.

Antimicrobial resistance is a growing public health problem. This study demonstrated that during the years of the COVID-19 pandemic, there was a significant increase in the isolation of microorganisms with an ERC-type resistance profile, especially *Klebsiella* and *Acinetobacter*. These findings underscore the importance of good practices in antimicrobial use and contribute significantly to surveillance data on antimicrobial resistance. Adequate surveillance is crucial to inform and implement effective actions requiring complementary studies and focusing on strategies to optimize Antimicrobial Management Programs and contain antimicrobial resistance, especially in intensive care units.

THANKS

We thank the Pharmaceutical Assistance and Audit team and Unimed Fortaleza for the work carried out and permission to disseminate the data to the scientific community. We thank the CAPES Foundation for the financial support to the main author, allowing dedication to the master's degree and research for essential months.

REFERENCES

1. Loureiro RJ, Roque F, Teixeira Rodrigues A, Herdeiro MT, Ramalheira E. O uso de antibióticos e as resistências bacterianas: breves notas sobre a sua evolução. Revista Portuguesa de Saúde Pública [Internet]. 2016 [citado 28 de julho de 2022];34(1):77–84. Disponível em: https://www.sciencedirect.com/science/article/pii/S087090251500067X
2. Monteiro RF dos S, Santos VRR dos, Ferreira AACT, Abreu JRG de. O uso indiscriminado de antimicrobianos para o desenvolvimento de micro-organismos resistentes. REAS [Internet]. 23jul.2020 [citado 28 de julho de 2022] ;(53): e3597. Disponível em: https://acervomais.com.br/index.php/saude/article/view/3597
3. European Centre for Disease Prevention and Control. Antimicrobial resistance and consumption remains high in the EU/EEA and the UK, according to new ECDC data. 2020. [Internet].18nov.2020 [citado 28 de julho de 2022]. Disponível em: https://www.ecdc.europa.eu/en/news-events/antimicrobial-resistance-and-consumption-remains-high-press-release
4. World Health Organization. No time to Wait: Securing the future from drugresistant infections.[Internet] 29april.2019. [citado 28 de julho de 2022]. Disponível em: https://www.who.int/publications/i/item/no-time-to-wait-securing-the-future-from-drug-resistant-infections
5. Alshaikh FS, Godman B, Sindi ON, Seaton RA, Kurdi A. Prevalence of bacterial coinfection and patterns of antibiotics prescribing in patients with COVID-19: A systematic review and meta-analysis. PLOS ONE [Internet]. 2022 [citado 12 de fevereiro de 2024];17(8):e0272375. Disponível em: https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0272375
6. Santos CVB dos, Cavalcante JR, Pungartnik PC, Guimarães RM. Transição da idade de casos, internações e óbitos em internações por Covid-19 no município do Rio de Janeiro. Rev Bras Estud Popul [Internet]. 2022 [citado 12 de fevereiro de 2024];39:e0195. Disponível em: https://www.scielo.br/j/rbepop/a/WNVdGDC8rrD5FNNPm3jDGLP/
7. World Health Organization. Preventing the COVID-19 pandemic from causing an antibiotic resistance catastrophe. 2020 [citado 28 de julho de 2022]. Disponível em: https://www.who.int/europe/news/item/18-11-2020-preventing-the-covid-19-pandemic-from-causing-an-antibiotic-resistance-catastrophe
8. Silva RFD. Impacto da pandemia da COVID-19 no perfil de resistência bacteriana em um hospital da cidade do Natal-RN [Dissertação]. [Rio Grande do Norte]: Programa de Pós-Graduação em Biologia Parasitária da Universidade Federal do Rio Grande do Norte; 2022.
9. Gangneux JP, Bougnoux ME, Dannaoui E, Cornet M, Zahar JR. Invasive fungal diseases during COVID-19: We should be prepared. J Mycol Med [Internet]. 2020 [citado 12 de fevereiro de 2024];30(2):100971. Disponível em: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7136887/
10. Toledo AG. Infecções fúngicas em pacientes internados com COVID-19: uma revisão de literatura. 2022 [citado 30 de setembro de 2023]; Disponível em: http://hdl.handle.net/11449/217172
11. Gomes AAG, Da Silva MR, Garcês TCDCS, Pinto ASB, De Andrade SMO, Saraiva ER, et al. Infecções relacionadas à assistência em saúde em unidades de terapia intensiva no Brasil. Acervo Saúde [Internet]. 2020 [citado 13 de fevereiro de 2024];12(11):e4665. Disponível em: https://acervomais.com.br/index.php/saude/article/view/4665
12. Zhu H, Swierstra J, Wu C, Girard G, Choi YH, van Wamel W, et al. Eliciting antibiotics active against the ESKAPE pathogens in a collection of actinomycetes isolated from mountain soils. Microbiology (Reading). 2014;160(Pt 8):1714–25.
13. Hussar YL. Perfil de utilização de antimicrobianos de uso restrito e resistência bacteriana durante a pandemia de COVID-19 na UTI do Hospital Santa Casa da Misericórdia de Ouro Preto-MG [dissertação]. Ouro Preto: Universidade Federal de Ouro Preto; 2022. Disponível em: http://www.monografias.ufop.br/handle/35400000/5203

14. Mesquita RF, Lima CAL de O, Lima LVA, Aquino BP, Medeiros MS. Rational use of antimicrobials and impact on the microbiological resistance profile in times of pandemic by Covid-19. RSD [Internet]. 2022Jan.16 [cited 2025Jan.25];11(1):e58211125382. Disponível em: https://rsdjournal.org/index.php/rsd/article/view/25382
15. Li J, Wang J, Yang Y, Cai P, Cao J, Cai X, et al. Etiology and antimicrobial resistance of secondary bacterial infections in patients hospitalized with COVID-19 in Wuhan, China: a retrospective analysis. Antimicrob Resist Infect Control. 2020;9(1):153.
16. Huttner BD, Catho G, Pano-Pardo JR, Pulcini C, Schouten J. COVID-19: don’t neglect antimicrobial stewardship principles! Clin Microbiol Infect. 2020;26(7):808–10.
17. Alves Araújo L, Dos Santos LS, Araújo Da Silva FD, Souza Oliveira JV. Implicações do gerenciamento de antimicrobianos em um hospital público. Cadernos ESP [Internet]. 13 de setembro de 2024 [citado 9 de dezembro de 2024];18(1):e1936. Disponível em: https://cadernos.esp.ce.gov.br/index.php/cadernos/article/view/1936