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MICROBIOLOGICAL PROFILE OF ANTIMICROBIAL SENSITIVITY AND RESISTANCE IN A GENERAL HOSPITAL IN THE PERUVIAN JUNGLE, 2021

PERFIL MICROBIOLÓGICO DE SENSIBILIDAD Y RESISTENCIA ANTIMICROBIANA EN UN HOSPITAL GENERAL DE LA SELVA PERUANA 2021

Javier Achong-Sánchez [1,2,a], Ruth Lazo-Paredes [3,b], José Amado-Tineo [1,4,c]

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ABSTRACT

Introduction: Antimicrobial resistance increases hospital mortality and is a public health problem. **Objective:** to determine the characteristics of microorganisms isolated from hospitalized patients and to detail antimicrobial sensitivity profiles. **Methods:** cross-sectional study Cross-sectional study in a hospital in the Peruvian jungle during 2021. The type of microorganism, antimicrobial sensitivity (VITEK ® 2 bioMérieux), source of isolation, patient age and hospitalization service were identified. **Results:** 477 positive cultures were included in 453 patients. The samples came from bronchial secretion 54.9%, blood 35.2%, urine 6.5% and others 3.4%. The hospital services of origin were emergency 49.9%, intensive care unit 40.0%, medicine 9.6% and surgery 0.5%. Gram negative bacteria (74.6%), Gram positive bacteria (16.4%) and fungi (9%) were isolated. The most frequently isolated microorganisms were Acinetobacter baumannii complex (32.7%), Klebsiella pneumoniae ssp. (16.8%) and Pseudomonas aeruginosa (13.4%). Antimicrobial resistance for the most frequently isolated microorganisms was: Acinetobacter baumannii complex, XDR in 88.5%; Klebsiella pneumoniae ssp., MDR in 56.3%; Pseudomonas aeruginosa, XDR in 54.7%; Staphylococcus epidermidis, MDR in 92.3%; and Staphylococcus haemolyticus, MDR in 100%. **Conclusions:** Gram-negative bacteria are the most prevalent, being more affected hospital critical areas, finding a high percentage of antimicrobial resistance.

Keywords: Microbiology; Bacteria; Fungi; Microbial drug resistance. (Source: MESH-NLM)

RESUMEN

Introducción: La resistencia antimicrobiana incrementa la mortalidad hospitalaria y es un problema de salud pública. Objetivo: Determinar las características de microorganismos aislados en pacientes hospitalizados y detallar los perfiles de sensibilidad antimicrobiana. **Métodos:** Estudio transversal en un hospital de la selva peruana durante el año 2021; se identificó el tipo de microorganismo, sensibilidad antimicrobiana (VITEK ® 2 bioMérieux), fuente de aislamiento, edad del paciente y servicio de hospitalización. **Resultados:** 477 cultivos positivos en 453 pacientes. Las muestras procedieron de secreción bronquial: 54.9 %, sangre 35.2 %, orina 6.5 % y otras 3.4 %. Los servicios hospitalarios de procedencia fueron emergencia 49.9 %, unidad de cuidados intensivos 40.0 %, medicina 9.6 % y cirugía 0.5 %. Se aislaron bacterias gramnegativas (74.6 %), bacterias grampositivas (16.4 %) y hongos (9 %). Los microorganismos más frecuentemente aislados fueron Acinetobacter baumannii complex (32.7 %), Klebsiella pneumoniae ssp. (16.8 %) y Pseudomonas aeruginosa (13.4 %). La resistencia antimicrobiana para los microorganismos más frecuentemente aislados fue: Acinetobacter baumannii complex, XDR en 88.5 %; Klebsiella pneumoniae ssp., MDR en 56.3 %; Pseudomonas aeruginosa, XDR en 54.7 %; Staphylococcus epidermidis, MDR en 92.3 %; y Staphylococcus haemolyticus, MDR en 100 %. **Conclusiones:** Las bacterias gramnegativas son las más prevalentes y las más afectadas, las áreas críticas hospitalarias; se encontró un elevado porcentaje de resistencia antimicrobiana.

Palabras clave: Microbiología; Bacterias; Hongos; Farmacorresistencia microbiana. (Fuente: DeCS- BIREME)

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[1] Faculty of Medicine, Universidad Nacional Mayor de San Marcos. Lima, Peru.
[2] Emergency Department. Hospital EsSalud III. Iquitos, Peru.
[3] CAP II EsSalud Nauta. Loreto, Peru.
[4] Emergency Department. Hospital Edgardo Rebagliati EsSalud. Lima, Peru.
[a] MD, Infectious Disease Specialist.
[b] Licensed Nurse.
[c] MD, Internal Medicine Specialist.

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INTRODUCTION

Bacterial resistance to antimicrobials has a genetic basis that can be intrinsic and/or extrinsic to the microorganism. In recent years, it has gained importance due to the increase in in-hospital mortality, largely because of the irrational use of antimicrobials, which has led it to be declared one of the top 10 threats to public health (1). Additionally, healthcare costs have risen due to the use of expensive antibiotics, longer hospital stays, and a social impact on the wages and productivity of the affected patient (2).

It is known that the spectrum of antimicrobial resistance is variable, thus microorganisms are classified as multidrug-resistant (MDR) when they show no sensitivity to at least one agent in three or more antimicrobial categories; extensively drug-resistant (XDR) when they show no sensitivity to at least one agent in all categories except one or two, that is, bacterial isolates remain sensitive to only one or two families; and pandrug-resistant (PDR) microorganisms when they show no sensitivity to any agents in all categories of antimicrobials, meaning that no tested agents are effective for that organism (3).

The microbiological map is a document that provides information about the microorganisms circulating in different hospital departments, evaluates the sensitivity of these microorganisms to the antimicrobials in use, thus contributing to the initiation of an effective and timely empirical treatment in patients with infections, reducing hospital stay, and decreasing healthcare costs (4). In some hospitals in Peru, such as in Lima, Arequipa, or Trujillo, microbiological maps have been developed, but in many other regions of the country, this information is lacking. It is important to mention that after the COVID-19 pandemic, the irrational use of antimicrobials for the treatment of SARS-CoV-2 pneumonia significantly contributed to the advance of antimicrobial resistance (2,5). Due to the lack of a local microbiological map and the high number of reported infections by multidrug-resistant pathogens, this study aims to identify the microorganisms and their antimicrobial resistance profiles in infections developed in clinical and surgical services.

METHODS

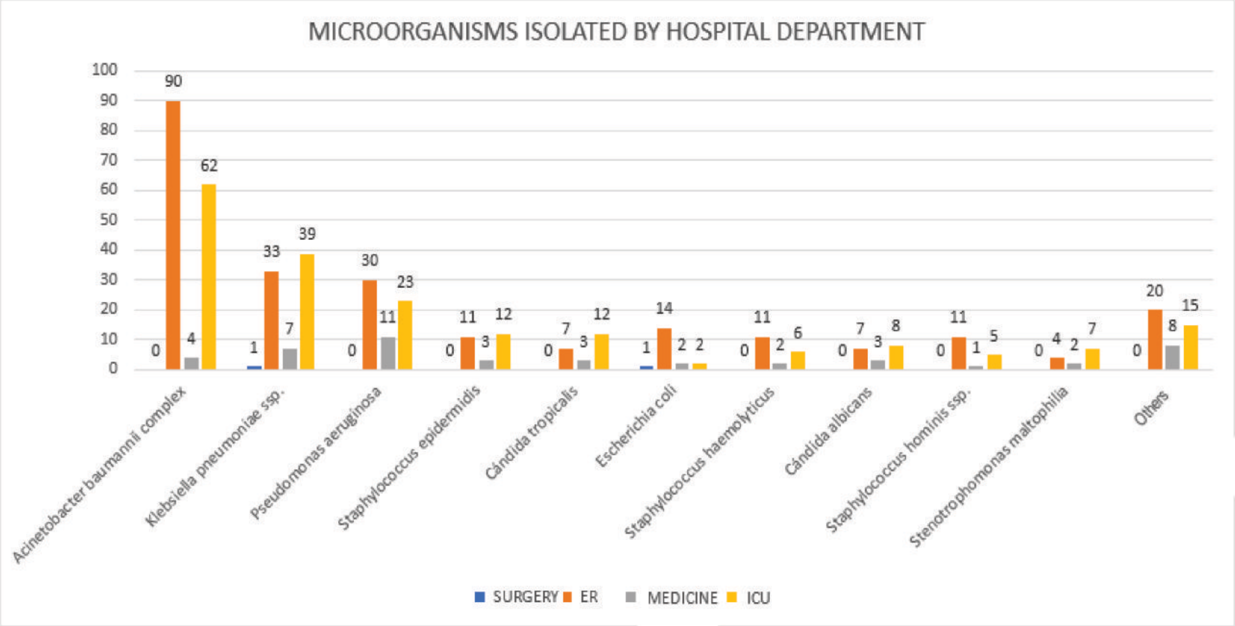
This is a descriptive cross-sectional study that evaluated the results of cultures and antibiograms from clinical samples of patients with suspected infection, who were admitted between January and December 2021 in a hospital located in the Peruvian Jungle. This hospital is one of the main healthcare centers in the Loreto region, with 191 hospital beds, including 56 in the Emergency Department: 42 for adults, 10 for pediatrics, and 4 for obstetrics and gynecology. Additionally, there are 21 beds in the Intensive Care Unit (ICU): 11 for adults, 4 for neonates, and 6 for pediatrics. Other departments include 14 beds in Pediatrics, 26 in Surgery, 19 in Obstetrics and Gynecology, 14 in Traumatology, 29 in Internal Medicine, and 12 in Infectious Diseases. The hospital serves a population of 240,000 people. For microbiological identification, the VITEK® 2 (bioMérieux) system was used, which is an automated spectrophotometric system for assessing microbial (bacteria and fungi) growth and susceptibility to antimicrobials, according to updated cutoff points from the Clinical and Laboratory Standards Institute (CLSI) guidelines.

The type of microorganism, antimicrobial sensitivity, source of isolation, patient's age, and hospital department were identified. The study was approved by the hospital's Ethics Committee. Data were collected in an Excel spreadsheet (version 2016), coded, tabulated, and analyzed using SPSS Statistics version 25.00. Descriptive statistical analysis was performed, including measures of central tendency and frequency distribution.

RESULTS

A total of 477 positive cultures were identified, corresponding to 453 patients. Of these, 262 (54.9%) cultures were from bronchial secretions, 168 (35.2%) from blood cultures, 31 (6.5%) from urine cultures, and five or fewer from wound secretions, laminar drainage, central venous catheter tip, tracheal secretion, cerebrospinal fluid, pleural fluid, and peritoneal fluid.

The age of the patients ranged from one day old to 88 years (median 56 years). The most frequently isolated microorganisms were Acinetobacter baumannii complex and Klebsiella pneumoniae ssp., found more commonly in bronchial secretion cultures in the Emergency Department and Intensive Care Units (Figure 1).



ER: Emergency, ICU: Adult Intensive Care Unit + Neonatal Intensive Care Unit. Others: Citrobacter freundii + Enterobacter aerogenes + Enterobacter cloacae complex + Morganella morganii ssp. + Proteus hauseri + Proteus mirabilis + Providencia stuartii + Pseudomonas stutzeri + Serratia marcescens + Sphingomonas paucimobilis + Enterococcus faecalis + Enterococcus faecium + Kocuria kristinae + Staphylococcus aureus + Staphylococcus capitis + Staphylococcus lugdunensis + Staphylococcus saprophyticus + Staphylococcus warneri + Candida ciferrii + Candida krusei + Candida parapsilosis

Figure 1. Microorganisms isolated by hospital department in a general hospital located in the Peruvian Jungle, 2021.

In the group of Gram-negative bacteria, Acinetobacter baumannii complex showed 53% sensitivity to tigecycline and 97% to colistin, with 97% and 98% resistance to meropenem and imipenem, respectively, being XDR in 88.5% of cases. For Klebsiella pneumoniae ssp., 58% were extended-spectrum beta-lactamase (ESBL) positive, with 10% sensitivity to ceftazidime and 100% resistance to ceftriaxone, as well as resistance to meropenem and imipenem in 44% and 34%, respectively, being MDR in 56.3% of cases. Pseudomonas aeruginosa showed 96% sensitivity to colistin and 70% to amikacin, with resistance to meropenem and imipenem in 85% and 82%, respectively, being XDR in 54.7% of cases. For Escherichia coli, 89% were ESBL-positive, with 6% and 13% sensitivity to ceftazidime and ceftriaxone, respectively (Table 1). For Gram-positive bacteria, all were isolated from blood cultures; Staphylococcus epidermidis was the most common, followed by Staphylococcus haemolyticus, both being methicillin-resistant in 88% and 100% of cases, with no resistance to vancomycin reported for either microorganism. Staphylococcus aureus was methicillin-resistant in 67% of cases, with no vancomycin resistance, and for Enterococcus faecium, the only strain isolated was resistant to ampicillin but sensitive to vancomycin (Table 2). Regarding fungi, they were isolated from a total of 43 samples, of which antifungal susceptibility testing was performed on six. One of these cultures, from a 66-year-old patient, identified Candida parapsilosis resistant to fluconazole and voriconazole (Table 3).

Table 1. Antimicrobial susceptibility of gram-negative bacteria isolated in a general hospital in the Peruvian Jungle, 2021.

ANTIMICROBIAL SUSCEPTIBILITY																											
GRAM-NEGATIVE BACTERIA	ISOLATES	ESBL (+)	AMPICILLIN	AMOXICILLIN/CLAVULANIC ACID	AMPICILLIN/SULBACTAM	PIPERACILLIN/TAZOBACTAM	CEPHALOTHIN	CEFAZOLIN	CEFUROXIME	CEFOTAXIME	CEFTAZIDIME	CEFTRIAXONE	CEFEPIME	ERTAPENEM	IMIPENEM	MEROPENEM	AMIKACIN	GENTAMICIN	TOBRAMYCIN	CIPROFLOXACIN	LEVOFLOXACIN	NORFLOXACIN	FOSFOMYCIN	TIGECYCLINE	COLISTIN	NITROFURANTOIN	TRIMETHOPRIM/SULFAMETHOXAZOLE
Acinetobacter baumannii complex	156	N	N	N	2%	N	N	N	N	N	N	N	1%	N	2%	3%	36%	9%	0%	1%	0%	N	N	53%	97%	N	1%
Klebsiella pneumoniae ssp.	80	58%	N	8%	6%	34%	N	1%	11%	13%	10%	0%	11%	67%	66%	56%	99%	35%	7%	14%	0%	N	N	75%	87%	6%	18%
Pseudomonas aeruginosa	64	N	N	N	N	22%	N	N	N	N	48%	N	51%	N	18%	15%	70%	50%	33%	25%	25%	0%	N	N	96%	N	N
Escherichia coli	19	89%	0%	27%	24%	76%	0%	5%	0%	0%	6%	13%	5%	95%	94%	100%	89%	47%	43%	5%	0%	0%	100%	100%	100%	88%	33%
Stenotrophomonas maltophilia	13	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	100%	N	N	N	N	N	92%
Serratia marcescens	7	N	N	N	0%	43%	N	N	N	14%	14%	N	29%	14%	14%	29%	71%	57%	N	14%	N	N	N	43%	N	N	14%
Enterobacter aerogenes	4	N	N	N	0%	0%	N	N	N	0%	25%	0%	25%	25%	50%	33%	100%	50%	0%	25%	0%	N	N	100%	100%	0%	50%
Sphingomonas paucimobilis	4	N	N	N	N	25%	N	25%	N	50%	25%	0%	25%	N	25%	50%	25%	25%	0%	50%	0	N	N	100%	N	N	50%
Enterobacter cloacae complex	2	N	N	N	0%	100%	N	N	N	50%	100%	N	100%	100%	100%	100%	100%	50%	N	50%	N	N	N	100%	100%	N	100%
Proteus mirabilis	2	N	N	0%	0%	100%	N	N	N	0%	0%	N	100%	0%	N	0%	100%	0%	N	0%	N	N	N	N	N	N	0%
Citrobacter freundii	1	N	N	N	0%	100%	N	N	N	N	100%	0%	100%	100%	100%	N	100%	100%	100%	0%	0%	N	N	N	N	100%	0%
Morganella morganii ssp.	1	N	N	N	0%	100%	N	0%	N	N	100%	100%	100%	100%	0%	N	100%	100%	100%	0%	0%	N	N	N	N	N	0%
Proteus hauseri	1	N	N	100%	100%	100%	N	0%	0%	100%	100%	N	100%	100%	0%	100%	100%	100%	N	100%	N	N	N	N	N	N	0%
Providencia stuartii	1	N	N	N	0%	100%	N	N	N	0%	0%	N	100%	0%	0%	0%	100%	N	N	0%	N	N	N	N	N	N	0%
Pseudomonas stutzeri	1	N	N	N	N	100%	N	N	N	100%	100%	N	100%	N	100%	100%	100%	100%	N	100%	N	N	N	100%	N	N	100%

N: Sensitivity testing for this antibiotic was not performed

Table 2. Antimicrobial susceptibility of gram-positive bacteria isolated in a general hospital in the Peruvian Jungle, 2021.

GRAM-POSITIVE BACTERIA	ISOLATES	ANTIMICROBIAL SUSCEPTIBILITY																				
		BETA-LACTAMASE (+)	CEFOXITIN DETECTION (+)	BENZYLPENICILLIN	AMPICILLIN	OXACILLIN	GENTAMICIN	STREPTOMYCIN	CIPROFLOXACIN	LEVOFLOXACIN	MOXIFLOXACIN	INDUCED RESISTANCE TO CLINDAMYCIN (+)	ERYTHROMYCIN	CLINDAMYCIN	QUINUPRISTIN/DALFOPRISTIN	LINEZOLID	VANCOMYCIN	TETRACYCLINE	TIGECYCLINE	NITROFURANTOIN	RIFAMPICIN	TRIMETHOPRIM/SULFAMETHOXAZOLE
Staphylococcus epidermidis	26	100%	92%	0%	N	12%	50%	0%	31%	44%	35%	0%	12%	19%	100%	100%	100%	85%	100%	100%	35%	54%
Staphylococcus haemolyticus	19	100%	100%	0%	N	0%	11%	0%	0%	5%	5%	0%	0%	0%	95%	95%	100%	79%	95%	100%	18%	37%
Staphylococcus hominis ssp.	17	100%	71%	0%	N	35%	65%	0%	65%	65%	65%	0%	18%	41%	100%	100%	100%	59%	100%	100%	82%	59%
Enterococcus faecalis	5	40%	N	80%	80%	N	67%	40%	80%	80%	N	0%	25%	N	0%	100%	100%	60%	100%	100%	N	100%
Staphylococcus aureus	3	100%	67%	0%	N	33%	67%	0%	67%	67%	67%	0%	67%	67%	100%	100%	100%	67%	100%	100%	67%	67%
Staphylococcus capitis	2	100%	0%	0%	N	50%	100%	0%	100%	100%	100%	0%	100%	100%	100%	100%	100%	100%	50%	100%	100%	100%
Staphylococcus saprophyticus	2	100%	100%	0%	N	0%	50%	0%	50%	50%	50%	0%	0%	50%	100%	100%	100%	100%	100%	100%	50%	0%
Enterococcus faecium	1	0%	N	0%	0%	N	100%	0%	100%	0%	N	0%	0%	N	100%	100%	100%	0%	100%	0%	N	N
Kocuria kristinae	1	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
Staphylococcus lugdunensis	1	100%	100%	0%	N	0%	100%	0%	0%	0%	0%	100%	0%	0%	100%	100%	100%	100%	100%	100%	100%	100%
Staphylococcus warneri	1	100%	0%	0%	N	100%	100%	0%	100%	100%	100%	0%	0%	0%	100%	100%	100%	100%	100%	100%	100%	100%

N: Sensitivity testing for this antibiotic was not performed

Table 3. Antimicrobial susceptibility of fungi isolated in a general hospital in the Peruvian Jungle, 2021.

FUNGUS	ISOLATES	ISOLATES WITH ANTIMICROBIAL SUSCEPTIBILITY	ANTIMICROBIAL SUSCEPTIBILITY				
			FLUCONAZOL	VORICONAZOL	CASPOFUNGINA	MICAFUNGINA	FLUCITOSINA
Candida albicans	18	3	100%	100%	100%	100%	100%
Candida ciferrii	1	1	N	100%	N	N	N
Candida krusei	1	0	N	N	N	N	N
Candida parapsilosis	1	1	0%	0%	100%	100%	100%
Candida tropicalis	22	1	100%	100%	100%	100%	100%

N: Sensitivity testing for this antibiotic was not performed

DISCUSSION

In our institution, 74.6% of positive cultures were found to be gram-negative bacteria, followed by gram-positive bacteria at 16.4%, and fungi at 9%. There was a high frequency of bronchial secretion cultures from hospitalized patients in the Emergency and Intensive Care Unit services. Similar findings have been described in microbiological maps from other hospitals in Latin America and our country (6*8), primarily related to healthcare-associated infections (HAIs). A very high rate of resistance and multidrug resistance was observed in both gram-negative and gram-positive bacteria.

HAIs are more frequent in the respiratory tract, bloodstream, surgical site, skin-mucous membranes, and urinary tract. During the SARS-CoV-2 pandemic, an increase in HAIs was observed, especially in patients admitted to critical care areas, as noted in the present report, highlighting the importance of performing antimicrobial cultures to specifically identify the associated pathogens (2,9-11).

The pandemic situation allowed greater access to cultures and confirmed the increase in the antimicrobial resistance profile, similar to what was reported in a healthcare institution in Colombia (12). The ICU and Emergency areas reported the highest isolation of microorganisms in the present study, associated with the higher frequency of invasive techniques in patients, which facilitated the entry and subsequent development of infection by these microorganisms. The low frequency of positive cultures in other hospital services is probably due to the lack of resources for sample collection, as critical areas are prioritized, or the lack of awareness among staff about the need to confirm infections (especially HAIs) in non-critical areas of the hospital.

Within the gram-negative bacteria group, Acinetobacter baumannii complex was the most frequently isolated, at 32.7%, with very low sensitivity to imipenem and meropenem, 2% and 3% respectively. This is alarming, as these are reserve drugs typically used empirically for complicated infections, and their low effectiveness is evident in the results shown(13).

In recent years, Acinetobacter baumannii complex has significantly increased its prevalence, along with its resistance mechanisms (14,15). A study conducted between 2012 and 2016 on the microbiological profile and antibiotic susceptibility in two highly complex hospitals of Peru's social health insurance system showed E. coli as the main isolated gram-negative organism (16); in contrast with our study, this highlights the need to continue conducting antimicrobial susceptibility studies to provide an updated overview. Additionally, 47% resistance to tigecycline was observed; although the first reported appearance of tigecycline resistance was in 2007, a recent study on the prevalence of Acinetobacter baumannii complex showed tigecycline resistance to be below 5.5% in Korea, India, and China(17).

Concerns were raised about the utility of this drug for infections associated with Acinetobacter baumannii complex in our region.

The presence of Acinetobacter baumannii complex at such high frequencies suggests that contact isolation measures are inadequate, emphasizing the need for strict adherence to hand hygiene by healthcare personnel as a fundamental part of controlling an endemic situation caused by this pathogen (18). Given the high frequency of resistant microorganisms in the study location, such as Acinetobacter baumannii complex, Klebsiella pneumoniae ssp., and Pseudomonas aeruginosa, empirical therapies should include combinations of reserve antimicrobial agents such as colistin, ampicillin/sulbactam, tigecycline, carbapenems, ceftazidime/avibactam, aztreonam, or aminoglycosides. The main focus should be to isolate and properly characterize the microorganism, and, even more importantly, to implement appropriate preventive measures.

Regarding gram-positive bacteria, Staphylococcus aureus had a low frequency compared to other hospitals (19), likely because few skin lesion isolations were performed in the present study.

Coagulase-negative Staphylococcus (CNS) is often considered the most frequently isolated microorganism in microbiology laboratories (20). In our study, it accounted for 87% of all gram-positive microorganisms, but the clinical significance of these bacteria could not be determined, as they might have been considered contaminants and/or pathogenic microorganisms. Nonetheless, it is suggested to review protocols for proper blood culture collection and emphasize staff training to avoid confusion in the clinical management of patients.

The prevalence of fungi in blood cultures was low, with greater presence in bronchial secretions. The most frequently isolated fungus was Candida albicans (42.9%), as found in a national hospital (21) ¿, and its resistance rate remains low.

In relation to antimicrobial use, it is crucial to optimize therapy in hospitals. In this regard, it is important to mention that in some institutions in the country, there is still a high frequency of unjustified practices related to these drugs, which contributes to an increase in antimicrobial resistance(22,23).

The use of antimicrobials such as aminopenicillins associated with beta-lactamase inhibitors (BLIs), carbapenems, glycylcyclines (tigecycline), and glycopeptides should be monitored by the Antimicrobial Optimization Committee and the Antimicrobial Optimization Program Unit, hospital entities that help optimize the appropriate use of antimicrobials. These entities promote positive changes in prescribing practices and the use of cost-effective treatments, contributing to better clinical outcomes for patients with infections while reducing the selection of resistant microorganisms and the risks to patients from antimicrobial use. As observed, there is a high rate of resistance in both gram-negative and gram-positive bacteria, necessitating appropriate epidemiological surveillance(24,25).

This microbiological map is a passive study based on microbiological samples; as such, it is not possible to determine exactly how many and which of the described microorganisms were colonizers and/or contaminants. Moreover, it was not possible to establish which pathogens caused HAIs or the positivity rate of cultures due to the lack of total culture sample data and the genes involved in resistance. However, despite these limitations, the present study constitutes one of the first local reports, and despite including only one hospital, it is important to understand the situation in our region, providing evidence to continue developing the regional microbiological map, which will offer indispensable information for optimizing antimicrobial therapy in the management of infections. In conclusion, gram-negative bacteria are the most prevalent in the study hospital, and the most affected hospital services are the Emergency Department and Intensive Care Units.

The most involved culture samples were bronchial secretion and blood, with a high percentage of antimicrobial resistance, mainly in Acinetobacter baumannii complex (XDR in 88.5%), Klebsiella pneumoniae ssp. (MDR in 56.3%), Pseudomonas aeruginosa (XDR in 54.7%), Staphylococcus epidermidis (MDR in 92.3%), and Staphylococcus haemolyticus (MDR in 100%).

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Correspondence: *José Amado Tineo.*
Address: *Jr. Belisario Flores 238, Lince, Lima-Perú.*
Telephone: *(+51) 990452547*
Email: ***jamadot@unmsm.edu.pe***

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