IOSR Journal of Dental and Medical Sciences (IOSR-JDMS)
e-ISSN: 2279-0853, p-ISSN: 2279-0861.Volume 21, Issue 4 Ser.12 (April. 2022), PP 41-50
www.iosrjournals.org

Bacterial Ecology of Intensive Care Units, Hassan II Hospital in Fez, Morocco.

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Abstract:
The objective of our study was to analyze the microbiological ecology of intensive care units and its evolution between January 1, 2018 and December 31, 2021. We conducted a monocentric retrospective study in the microbiology laboratory of the CHU HASSAN II of Fez. We analyzed all the microbiological samples for diagnosis carried out over this period (identified germ, sensitivity profile), and collected the demographic characteristics of the associated population (number = 1472). Out of 1154 culture-positive samples, 645 were multidrug-resistant bacteria (56%). The proportions of the different bacterial classes (GNB / CG+) have remained stable over the last 4 years, with a predominance of Acinetobacter baumanii (55%), followed by Klebsiella pneumoniae (20%) and Escherichia coli (18%). The most common sites implicated in nosocomial infection were pneumonia (42%), followed by catheter-related infections (19%) and bacteremia (17%). Bacteria of clinical interest showed increasingly worrying levels of antibiotic resistance to betalactam antibiotics, with the exception of methicillin-resistant Staphylococcus aureus, which remained stable between 2018 and 2021. This work is part of an approach to improve antibiotic prescription practices and analyze the impact of changes in antibiotic therapy protocols on the ecology of the department.

Key Word*: nosocomial infection, bacterial ecology, intensive care, microbiology.*

Date of Submission: 11-04-2022 Date of Acceptance: 28-04-2022

I. Introduction

Nosocomial infections are infections contracted in a health care facility [28]. This definition was revised in 2007 in view of the diversification of care structures and pathways, and the sometimes-late onset of infection after surgery [26]. Nosocomial infection can be caused by germs from the patient, the nursing staff or the hospital environment. These infections increase the morbidity, mortality, and cost of hospital care. In the United States, it is estimated that hospital-acquired infections are responsible for 9,000 deaths per year [30].

Although efforts are being made to strengthen hygiene standards in various hospital departments, hospital-acquired infections continue to persist in intensive care units. The 2017 national prevalence survey in France showed a national prevalence of infected patients of 4.98% [6]. In the ICU the number of infected patients is higher due to the density of care, exposure to various invasive devices and the severity of the patients' pathologies. In the "Réa Raisin 2015" network in France the prevalence of nosocomial infection was 10.62% [11]. In the intensive care unit of the “IBN ROCHD" hospital in Casablanca the prevalence rate of nosocomial infection was 17.9% [15].

In Morocco, nosocomial infection remains a concern in terms of morbidity and mortality, and several studies have been devoted to it, such as that of "F.-M.-R. Maoulainine", carried out in Marrakech, which analyzed the epidemiological characteristics of nosocomial infection in the pediatric setting [15]. The present study, carried out in the microbiology laboratory of the Hassan II hospital in Fez, aims to describe the bacterial ecology of intensive care units and to draw up the antibiotic resistance profile of the most frequently encountered germs, in order to guide the prescription of empirical antibiotic therapy for patients hospitalized in these units.

II. Material And Methods

A. Study type and setting:

It is a retrospective, descriptive, observational study, spread over 1 year from January 1, 2021 to December 31, 2021, conducted at the microbiology laboratory of the CHU HASSAN II of Fez, concerning the microbiological profile of nosocomial infections contracted in the intensive care units of the hospital. Blood cultures, catheter samples, respiratory samples of different types (PSB, sputum, BAL), pus samples, biological fluids samples (lumbar, pleural, articular, pericardial punctures) and urinary samples are processed in the

laboratory. The data collected in this study were compared to data collected in previous years, in order to analyze the evolution of bacterial resistance and to evaluate the impact of different antibiotic protocols on the ecology of the wards.

B. Sampling;

Five multidrug-resistant bacteria were targeted in this study: imipenem-resistant Acinetobacter baumanii (IRAB); C3G-resistant Enterobacteriaceae (E-ESBL); carbapenemase-producing Enterobacteria (CPE); ceftazidime- and imipenem-resistant Pseudomonas aeruginosa (CIRPA); and methicillin-resistant Staphylococcus aureus (MRSA). All diagnostic specimens from intensive care units with a positive culture for one of the above-mentioned germs were included in the study. Sampling was performed in a non-redundant design. Samples taken in the context of screening for nasal or digestive carriage of resistant germs were excluded. Also, the sampling was of non-probability convenience, all samples meeting the inclusion criteria were recruited**.**

C. Data Collection Process:

Data collection was carried out by analysis of the bacteriology registers of the different samples. The following information was collected: patient index, age, sex, department from which the sample was taken, type of sample received, culture result and antibiogram result. These data were transcribed on an Excel table and classified according to the date.

D. Analytic phase:

1. Microscopic exam:

The gram stain result is obtained within a short period of time (usually less than one hour after arrival at the laboratory); its positive predictive value is better for specimens from sterile sites, but its sensitivity rarely exceeds 50% for specimens contaminated with flora (respiratory or skin specimens). Microscopic examination after May-Grümwald-Giemsa staining is also performed for sputum to assess the number of epithelial cells and leukocytes per microscopic field at x40 magnification. According to the criteria of Bartlett, Murray, and Washington, an optimal specimen should contain < 10 epithelial cells and more than 25 polynuclear cells per field. A specimen containing more than 25 epithelial cells per field is considered to be contaminated with saliva and is therefore not seeded.

2. Culture:

Inoculation is performed using a 10 µL calibrated loop. Urinary samples are plated by enumeration, respiratory samples by star plating, after fluidization and successive dilutions. Other types of samples are plated by the dial technique. The choice of media depends on the type of sample and the suspected bacteria. Ordinary agars (CLED, BCP), selective agars (Chapman for staphylococcus, EMB for gram-negative bacilli, CNA for streptococci) and enriched agars (chocolate, fresh blood) are available...

3. Bacterial identification:

Bacterial strains identification was based on the study of morphological, cultural and biochemical characteristics (fermentation of sugars, reduction of nitrates, search for enzymes such as oxidase, DNAase, catalasis...). The precise identification of bacteria (genus and species) was carried out by automated method on Phoenix 100 of Becton Dickinson.

4. Antibiotic susceptibility testing:

For each strain, susceptibility was determined by automated susceptibility testing (Phoenix 100) in liquid medium, and by standard susceptibility testing by swabbing using the Mueller-Hinton agar diffusion method. The reading and interpretation criteria are those of the French Microbiology Association (CASFM/EUCAST 2020) [2]. Mueller-Hinton (MH) agar, prepared locally, is used in the agar diffusion method for bacteria other than slow growing ones. MH-F agar supplemented with 5% defibrinated horse blood and 20 mg/L B-NAD, purchased ready-to-use, is used for streptococcus spp, haemophilus spp and other slow growing bacteria.

5. Choice of antibiotics tested:

The choice of antibiotics tested was made by taking into consideration the standard and complementary lists of the CA-SFM / EUCAST 2020 [2].

6. ESBL Character Detection:

ESBL production by a bacterial strain was confirmed by testing for β-lactam resistance using a qualitative method: the synergy test. Under standard antibiotic susceptibility testing conditions, a central disk of amoxicillin + clavulanic acid and a peripheral disk of C3G (Ceftriaxone) placed 3 cm from the central disk were used for the qualitative detection of extended spectrum beta-lactamase production. The presence of synergy between the two discs, detected by the presence of a characteristic "champagne cork" image, confirms the presence of an extended spectrum beta-lactamase.

7. Carbapenemase detection:

The production of carbapenemase by a bacterial strain was suspected in front of a decrease in sensitivity to Ertapenem (inhibition diameter < 25 mm by diffusion test on agar medium). Any suspected strain was submitted to a genotypic screening by rapid molecular test.

8. MRSA screening:

Cefoxitin resistance was tested using a 30 ug Cefoxitin disc under standard antibiogram conditions.

1. FOX diameter < 22 mm: R
2. FOX diameter > 22 mm: S

Cefoxitin-resistant staphylococcal strains were interpreted as resistant to all beta-lactams.

III. Results

A. Demographic Data:

1472 samples from different patients were included in the study. These patients were predominantly male, 472 men or 65% and 258 women or 35%. The sex ratio was therefore 1.83. The average age of our patients was 42 years with extremes ranging from 0 to 92 years.

B. General microbiology data:

1154 non-redundant bacteria from intensive care units were isolated in 2021. These bacteria are dominated by Acinetobacter baumanii and Enterobacteriaceae. The main representative of gram positive cocci is Staphylococcus aureus. The distribution of these isolates according to bacterial species is shown in Table 1. 58% of them correspond to multi-resistant bacteria (MRB). These MRB are represented by imipenem-resistant Acinetobacter baumanii (IRAB); C3G resistant Enterobacteriaceae by ESBL secretion or derepression; carbapenem-resistant enterobacteria, ceftazidime- or imipenem-resistant Pseudomonas aeruginosa and cefoxitin-resistant staphylococcus aureus. No vancomycin-resistant enterococci were isolated in this series. The proportion of these MRB is shown in Table 2.

Isolated bacteria	Number	%
A. baumanii	367	32%
E. coli	205	18%
K. pneumoniae	229	20%
E. cloacae	53	4%
P. aeruginosa	100	9%
S. aureus	200	17%

Table 1: Distribution of the isolates according to bacterial species.

Isolated bacteria	Number	%
IRAB	356	55%
PAMR	25	4%
C3G R K. pneumoniae	142	22%
C3G R E. cloacae	28	4%
C3G E. R Coli	84	13%
SARM	10	2%

Table 2: Proportion of MRB.

C. MRB and infectious sites:

Nosocomial pneumonia predominated with a rate of 42.01%, followed by catheter-related infections (19.6%) and bacteremia (17.9%). These results are summarized in Table 3.

Isolated bacteria	ABRI	KP	E.Coli	MRPA	MRSA
CBUE	3	16	21	6	0
Pus	19	23	10	5	0
Blood Cultures	65	30	15	0	6
Catheters	69	33	20	5	0
Respiratory Samples	200	40	18	9	4

Table 3: BMR and infectious sites.

D. Bacterial resistance studies to major antibiotics:

1. Resistance profile of A.baumanii to major antibiotics:

Acinetobacter baumannii isolates (n=367) showed increased resistance to the majority of antibiotics tested. The rate of imipenem-resistant *Acinetobacter baumannii* (IRAB) was 97%. The most active antibiotic on these isolates was Colistin. Indeed, MIC measurement by microdilution method did not show any resistance to colistin.

2. Focus on molecular characterization of IRAB strains :

A cross-sectional, descriptive study, carried out in 2018, by the laboratory of microbiology and molecular biology of the faculty of medicine and pharmacy of Fez, in collaboration with the microbiology department of Hasssan II hospital, allowed a molecular characterization of 140 strains of carbapenemase-producing *Acinetobacter baumanii* at the Hassan II University Hospital of Fez [1]. The genes encoding carbapenemases were amplified using conventional PCR, after DNA extraction. The amplification product was then revealed by UV after migration on agarose gel. The bands obtained were then characterized by sequencing using the Sanger method and analyzed by BLAST software.

The search for oxacillinase genes was done by PCR and showed that all strains have the OXA-51 gene and the ISAbA1 insertion sequence. Also, 89% of the strains have the OXA-23 gene. The genes coding for MBL studied by multiplex PCR show a great genetic diversity, notably the presence of the six genes sought NDM, SIM. GIM. IMP and VIM with a dominance of the latter in 56% of the strains. We also note the detection of the SPM gene for the first time in Morocco.

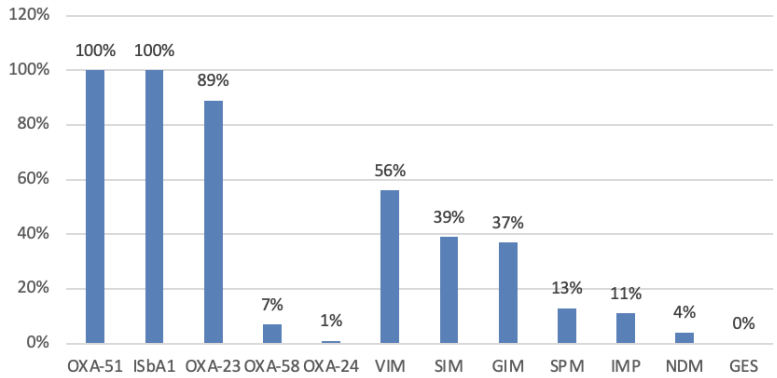

Figure 1: Molecular characterization of IRAB strains.

3. Resistance profile of Pseudomonas aeruginosa to major antibiotics:

Pseudomonas aeruginosa isolates (n=100) expressed a resistance rate of 22% to ceftazidime and 23% to imipenem. The highest rate of resistance was to ciprofloxacin (25%). 2/3 of the strains were susceptible to the combination of Piperacillin-Tazobactam, Ticarcillin and Piperacillin (31% of susceptible strains).

4. Resistance profile of major enterobacteria to key antibiotics:

Of the 487 strains of Enterobacteriaceae isolated, 462 were resistant to aminopenicillins (95%), 339 to amoxicillin-clavulanic acid (70%) and 254 to ceftriaxone (53%). Our strains were mainly sensitive to amikacin (99% sensitivity) and colistin (100%). Plasmid ESBL was detected in 127 strains of enterobacteria and carbapenemase in 11 strains. The distribution of ESBL-producing Enterobacteriaceae according to bacterial species shows a predominance of Klebsiella pneumoniae, representing 64%, followed by Escherichia coli with

23%, then the genus Enterobacter spp which represents 10% and Proteus mirabillis (3%). The distribution of Enterobacteriaceae is shown in Figure 2.

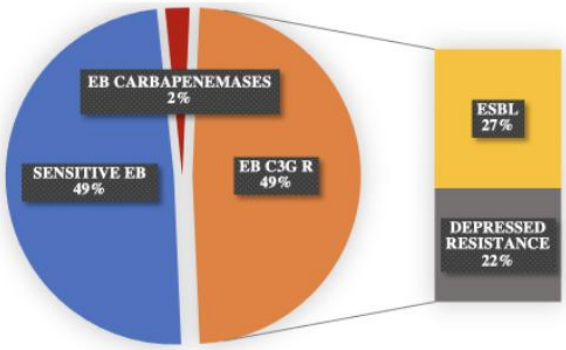

Figure 2: Distribution of Enterobacteria.

5. Molecular characterization of carbapenemases in the ICU:

11 carbapenemase-secreting strains of enterobacteria were identified in 2021. They produced NDM-type enzymes in 8 cases and OXA-48-type enzymes in 2 cases. Only one strain secreted two different types of carbapenemases: OXA-48 and NDM-1.

CPE	Number	%
K. pneumoniae	6	60%
E. coli	2	20%
E. cloacae	1	10%
P. mirabillis	1	10%

Table 3: Molecular characterization of carbapenemasis in the ICU.

6. Resistance profile of Staphylococcus aureus to major antibiotics:

Resistance to penicillin by penicillinase production was investigated by agar diffusion method according to CA-SFM 2020 [2]. Penicillinase-producing strains were considered resistant to penicillin G, aminopenicillins, carboxypenicillins, and ureidopenicillins. They are susceptible to betalactamase inhibitors, penicillinase-resistant penicillins (oxacillin), cephalosporins, and carbapenems. In our series, 100% of staphylococcus aureus isolated were penicillinase producers.

Cefoxitin-resistant staphylococci strains were interpreted as resistant to all beta-lactams. In our series, 5% of staphylococcus aureus were resistant to Cefoxitin.

IV. Discussion

At the end of our study on bacterial ecology in the ICU, the objective of which was to establish microbiological documentation of nosocomial infections in the ICU in order to guide the empirical prescription of antibiotics, we found that although nosocomial infections cover a variety of clinical contexts, the bacterial etiologies are just as varied.

A. Distribution of the main germs isolated:

The bacteria responsible for hospital-associated infection in the ICU are dominated by non-fermenting GNB (41% of the bacteria isolated) and by Enterobacteriaceae (42% of the bacteria isolated). Gram-positive cocci are less frequently isolated and represent only 17% of isolated bacteria. GNB are represented by Acinetobacter baumanii (32%), Klebsiella pneumoniae (20%) and Escherichia coli (18%). Among gram positive cocci, Staphylococcus aureus remains the main representative. These data are superposable to those found in other hospitals in the kingdom, and the predominance of Acinetobacter baumanii has also been reported in other national health care centers in Rabat [19], Casablanca [10] and Marrakech [5]. However, these microbiological data contrast with those of European countries where the predominance of Acinetobacter baumanii has not been reported, in favor of enterobacteria and Pseudomonas aeruginosa [14]. According to EPIIC II (European Prevalence of Infection in Intensive Care), which includes 1265 intensive care units in 75 different countries, BGN accounted for 62.2% of all included nosocomial infections [13]. Restrepo and Peterson also underlined

this predominance of BGN in a study that analyzed the germs responsible for nosocomial pneumonia in patients enrolled in 2 large clinical trials in the United States [17].

Figures 3 and 4 illustrate the evolution of the number of Acinetobacter baumanii isolates in the intensive care units of our hospital. These figures show a 250% increase between 2018 and 2021, a very worrying increase that makes Acinetobacter baumanii a serious epidemiological problem, justifying the implementation of a surveillance system of the microbial environment of health care institutions and the strict application of hygiene measures.

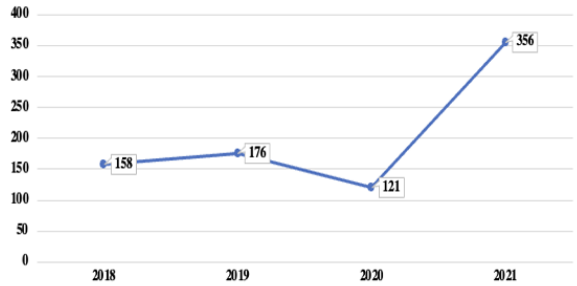

Figure 3: Evolution of the number of IRAB isolates in the ICU.

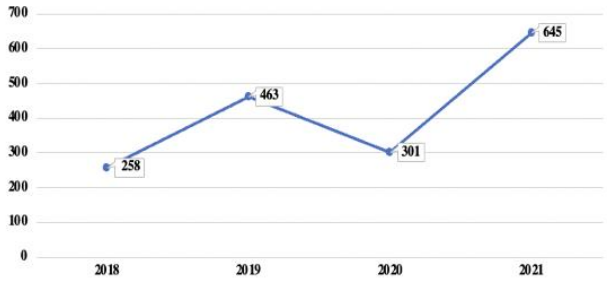

Figure 4: Evolution of the number of C3G-R isolates in the ICU.

B. MRB and infectious sites:

The proportions of the different types of relative infections in this study seem to fit relatively well with those of the literature: pneumopathies come first, followed by bacteremia and catheter-related infections. Our results are also in line with those of the study carried out by the French RAISIN network in 2015 [11]. In the work carried out in the intensive care unit of the CHU Ibn Rochd, pneumopathies predominate, followed by urinary tract infections, then postoperative peritonitis [27].

C. Antibiotic resistance profile:

1. Non-fermenting GNB :

The results in terms of antibiotic resistance found in our study are alarming. The resistance of Acinetobacter baumannii to ceftazidime (100%), to amikacin (81%), and to imipenem (97%) reached a very high rate. They make it a pioneer bacterium in multidrug resistance. These results are all the more alarming as they are significantly higher than those published by ONEBRA in France in May 2020, which reported much lower rates of beta-lactam resistance, varying between 17 and 35% [3]. A. baumannii resistance to beta-lactams results from several resistance mechanisms: chromosomal cephalosporinase hyperproduction, enzymatic resistance, efflux mechanism or impermeability [14]. Resistance to imipenem is mainly related to the production of oxacillinases, which have carbapenemase activity [24]. The results found in the other hospitals of the kingdom are similar [5 - 4 - 7]. They make Acinetobacter baumanii a recurrent health problem and one whose drug resistance is increasingly threatening, because although colistin remains active on almost all of these strains, it frequently constitutes the last available therapeutic option, at the cost of nephrotoxicity, and gives rise to fears of the emergence of colistin-resistant isolates, and thus an evolution towards pan-resistance in the near future.

Pseudomonas aeruginosa occupies a central position in the problem of nosocomial respiratory infections. This ubiquitous Gram-negative bacillus is responsible for 13% to 15% of all nosocomial infections observed in our study, with a higher frequency reported in certain categories of high-risk patients such as chronic bronchopulmonary pathologies, immunodepression, and burn victims. The analysis of the resistance profile of Pseudomonas aeruginosa strains to the different antibiotics tested shows increasing levels of resistance to the

betalactam antibiotics tested: Ticarcillin + clavulanic acid (31%), piperacillin + tazobactam (31%), Ceftazidime (23%), and Imipenem (25%) (figure 5). The development of resistance in Pseudomonas is due to the production of a broad-spectrum β- lactamase, which rapidly hydrolyzes aminopenicillins (amoxicillins and ampicillin), first and second generation cephalosporins, but affects little when produced at a basal level, ticarcillin (carboxypenicillin), piperacillin (ureidopenicillin), and some third generation cephalosporins, such as Ceftazidime [25 - 21]. As for aminoglycosides, often prescribed in combination with beta-lactams in the treatment of serious Pseudomonas infections, we note that amikacin has the lowest resistance rate in the kingdom, around 2%. Concerning quinolones, the rate of resistance to ciprofloxacin is 25%, while it is about 54% in Tunisia [18], and 24% in France [22]. Thus, despite its multiple resistance mechanisms, in current hospital practice, the combination of anti-Pseudomonas beta-lactam (Ceftazidime or piperacillin + tazobactam) and anti-Pseudomonas aminoglycoside (Amikacin) is still effective on more than 80% of the strains encountered in our intensive care units.

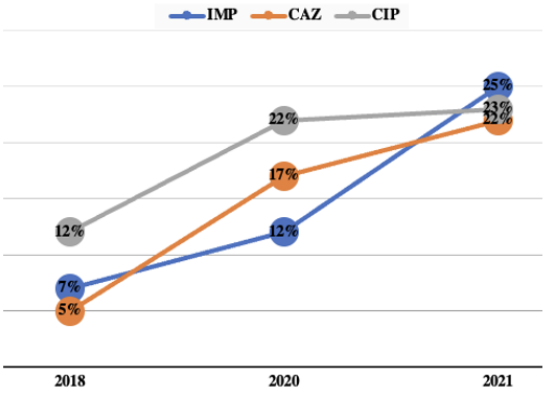

Figure 5: Trends in antibiotic resistance since 2018.

2. Enterobacteria:

In our study, Enterobacteriaceae represent 42% of all isolated bacteria and are therefore the first cause of nosocomial infections in the ICU. They are mainly represented by Klebsiella pneumoniae (20%), Escherichia Coli (18%), Enterobacter cloacae (4%) and Proteus mirabilis (2%). Analysis of the resistance profile of enterobacteria to the antibiotics tested shows a resistance rate of 53% for C3G. This resistance is essentially due to the production of enzymes degrading certain β-lactams (chromosomal derepressed cephalosporinases and extended-spectrum β-lactamases, of plasmid origin). [16]

- ESBL production:

Bacteria resistant to 3rd generation cephalosporins through ESBL production are a major concern in hospitals because of their epidemic spread, their multiresistance to antibiotics and their involvement in the pressure exerted on carbapenems. The control of resistance linked to ESBLs is essential and of particular importance, especially since these enzymes are plasmid-based and therefore transferable from one strain to another. These transfers make their diffusion difficult to control, especially when they concern species responsible for community infections, such as Eschirichia coli [20]. Pseudomonas aeruginosa or Acinetobacter baumanii, although potentially carrying mechanisms of resistance to 3rd generation cephalosporins of the ESBL type, do not justify the same concerns due to a risk of dissemination limited to health care institutions, or even limited to a few hospital sectors with a high potential for transmission (intensive care units, etc.).

According to our study, ESBL-producing Enterobacteriaceae represent 11% of the total bacteria identified, 19.6% of the isolated MRB, and correspond to 26% of the isolated Enterobacteriaceae. These figures are higher than those reported by other Moroccan studies conducted in Rabat and Marrakech in 2016 [9], and remain even higher than those published by the European Bacterial Antibiotic Resistance Surveillance Network in 2020 [2] These results illustrate the continuous progression of E-ESBL in our facility and prompt increased vigilance and measures to prevent cross-transmission in our healthcare facility to reduce the frequency of 3rd generation cephalosporin-resistant Enterobacteriaceae infections. The increase in the incidence of E-ESBL is directly involved in the increase in carbapenem pressure, and thus plays an undeniable role in the outbreak of carbapenemase-active ESBLs observed in our hospital, especially in Klebsiella penumoniae. At Hassan II Hospital, OXA-48 carbapenemases were predominant in 2018. These β-lactamases have a reduced hydrolysis spectrum as they hydrolyze mainly penicillins and carbapenems [23]. Thus, in the absence of co-production of extended-spectrum β-lactamases, oxa-48 strains can remain susceptible to third-generation cephalosporins (cefotaxime, ceftazidime). However, since 2020, NDM-1 metallo-enzyme carbapenemases have become

increasingly prevalent and worrisome. The severity of these NDM-1 strains is due to several factors: near-constant multidrug resistance, the size of the reservoir, particularly the Indian subcontinent, and the community-based nature of the Enterobacteriaceae affected by this resistance [23]. These carbapenemase-producing enterobacterial infections are difficult to treat and can be the source of therapeutic impasses. The introduction of new antibiotics, such as ceftozolane, and new β-lactamase inhibitors, such as Avibactam, has only partially addressed this phenomenon and their use in clinical practice has yet to be defined. In this context, the control of the spread of emerging highly antibiotic resistant bacteria (HRB) must be based on a double strategy of reducing the prescription of antibiotics to limit the selection pressure and preventing the spread from carrier patients.

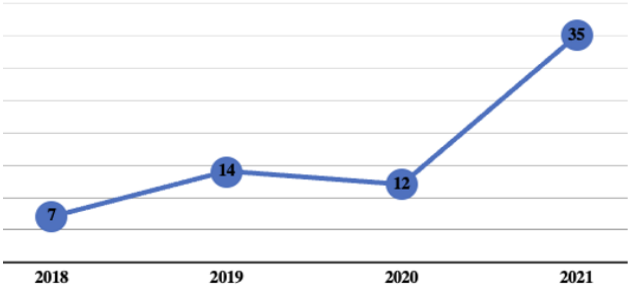

Figure 6: Evolution of number of CPE strains isolated at the UH.

3. Gram positive cocci:

S. aureus plays an important role in nosocomial infections. In our study, 155 isolates (12%) from positive samples correspond to Staphylococcus aureus. The data collected in our study show that 98% of the staphylococcus aureus strains isolated are resistant to penicillin G. The Sheikh Zaid Hospital [30] and the Mohamed V Hospital [18] show similar rates, varying between 87 and 91%. The carrier of this resistance corresponds to a penicillinase encoded by a plasmid transposon that can carry genes for resistance to other antibiotics (aminoglycosides, macrolides). [29 - 8]

- MRSA:

Development of antistaphylococcal penicillins of the meticillin family were then rapidly followed by the emergence of meticillin-resistant staphylococcus aureus (MRSA). In our series, methicillin resistance in S. aureus is about 4%. This rate is much lower than the figures published by other Moroccan hospitals, which show figures varying between 14 and 19%. This resistance to meticillin leads to resistance to all beta-lactam antibiotics [12]. It is determined by the presence of a chromosomal gene (mecA) that codes for an additional PLP, PLP 2a [12]. This additional PLP has less affinity for beta-lactam antibiotics [35]. The therapeutic alternative for these resistant strains remains the use of glycopeptides, whose use is increasing considerably in parallel with the ever-growing emergence of MRSA.

V. Conclusion

Our work was carried out on 1154 culture-positive samples from patients hospitalized in the intensive care unit services of the Hassan II Hospital of Fez between January 2021 and December 2021. It allowed to realize an analysis of the evolution of the bacterial ecology of our services, as well as the analysis of the antibiotic resistance profiles of bacteria isolated in our structures.

The reading and interpretation of the antibiogram of the most represented bacterial species shows that enterobacteria represented 42% of the isolated bacteria and showed resistance rates to aminopenicillins in the presence of clavulanic acid of 70%, a resistance rate to C3G, by production of ESBL or chromosomal cephalosporinase of 53%. With a sensitivity rate of more than 97% to imipenem, carbapenems are still the molecules of choice in the treatment of an ESBL infection, in association with amikacin.

Acinetobacter baumanii represented 32% of positive bacteriological samples. It showed very high resistance rates for ceftazidime (100%), amikacin (81%) and imipenem (97%). These results make Acinetobacter baumanii a recurrent sanitary problem whose drug resistance is increasingly threatening, because if colistin remains active on almost all these strains, it is currently the last available therapeutic option.

The analysis of the resistance profile of Pseudomonas aeruginosa strains to the different antibiotics tested showed increasing levels of resistance to the betalactam antibiotics tested: Ticarcillin + clavulanic acid (31%), piperacillin + tazobactam (31%), Ceftazidime (23%), Imipenem (25%). However, despite its multiple resistance mechanisms, in current hospital practice, the combination of anti-Pseudomonas beta-lactam and anti-

Pseudomonas aminoglycoside (Amikacin) is still effective on more than 80% of the strains encountered in our intensive care units.

The results of this work will therefore help to improve knowledge on bacterial ecology and on the activity of antibiotics against different pathogens in the intensive care units of the Hassan II Hospital of Fez.

Because of the state of health and the altered defenses of the patients in resuscitation we insist on the rigorous respect of the rules of hygiene and of the hands in particular as well as on the sensitization of the personnel to the part that the environment of care can hold in the chain of transmission of these microorganisms.

Finally, we conclude that an efficient fight against these infections requires a global prevention strategy which supposes a close collaboration between epidemiologists, clinicians, bacteriologists, hygienists and the nursing team.

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