**Original Article**
**J Immunol Clin Microbiol**. 2020;5(4):133-138

*J Immunol Clin Microbiol*

# Microbiological Evaluation of the Clinical Isolated Patients in the General Adult Intensive Care Unit

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## Abstract

**Backround:** In this study; microbiological evaluation of clinical isolates of 490 patients treated in general adult intensive care unit between 2016-2018 was aimed.

**Materials and Methods:** Blood culture samples were evaluated in an automated blood culture system BacT/Alert 3D (BioMerieux, France). Vitek 2 Compact (BioMe´rieux, Marcyl'Etoile, France) automated bacterial identification system was used for determination of biochemical parameters and antibiograms. Statistical Package for the Social Sciences (SPSS) Version 23.0 (SPSS Inc., Chicago, IL, USA) was used to analyze the data.

**Result:** In this study; non-fermentative gram negative microorganisms were found to be 10.816% (n = 53). *Pseudomonas aeroginosa* were detected in 49 patients (10%). Especially in 2018, the total number of microorganisms was found to be higher than the other years, while *P. aeroginosa* strain (n = 41) increased significantly. The major pathogens were *P. aeroginosa*, Non-Fermentative Gr negative bacteria, *Klepsiella spp., Escherichia coli, Candida spp., Proteus spp., Pseudomonas spp.* was determined.

**Conclusion:** In this study; microorganism distribution of patients hospitalized in intensive care unit was determined. Investigating the resistance status of microorganisms will be useful in regulating treatment protocols and preventing resistant pathogenic microorganisms.

**Key words:** *Pathogen, Culture, Adult İntensive Care*

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## Introduction

Nosocomial infections; it is a very important problem in developed or developing countries. These infections cause deaths, long-term treatments and increased treatment costs (1). Patients treated in intensive care units (ICU) are generally at greater risk of hospital-acquired infections than patients treated in other units. The risk of infection increases considerably due to the prolonged treatment of the inpatients, the high number of wounds, and the suppressed immune system of elderly patients (2).

Urinary tract infections, circulatory system infections and pneumonia are the most common infections in ICU patients (3). The use of antibiotics for the treatment of these infections, especially in ICU patients, is quite high. Many bacteria may show multiple antibiotic resistance during treatment. Increased multiple antibiotic resistance poses serious problems in the treatment of bacterial infections (4). For this reason, it is very important to determine the microbiological distribution of the patients hospitalized in the intensive care unit in different culture environments and to apply the correct treatments according to antibiotic resistance profiles. Therefore; In this study, we aimed to make microbiological evaluation of clinical isolates of patients hospitalized in intensive care unit.

## Materials and Methods

In this study; microbiological evaluation of the clinical isolates of 490 patients treated in General Adult Intensive Care Unit between the years of 2016-2018 in the 2nd Stage Health Institution was performed.

Clinical specimens were classified as blood, urine, airway [bronchoalveolar lavage (BAL), tracheal aspirate, sputum], skin and soft tissue (wound, burn, surgical site infection), catheter, cerebrospinal fluid (CSF). Blood culture samples were evaluated in BacT / Alert 3D (bioMerieux, France) automated blood culture system. Samples were incubated on a BacT / Alert 3D instrument for 7 days. Gram dyes were made for the identification of the samples taken from the cultures where growth was detected. Samples were grown on 5% Sheep Blood Agar, Eosin-Methylene Blue agar (EMB) and, if necessary, chocolate and Sabouraud Dextrose Agar (SDA). Samples that did not show any bacteria in gram staining and did not grow in the media were not included in the study.

### *Statistical analysis*

Statistical Package for the Social Sciences (SPSS) Version 23.0 (SPSS Inc., Chicago, IL, USA) was used to analyze the data. Numerical variables, mean ± standard deviation, categorical variables were shown as numbers (n) and percentages (%). Correlation tests according to statistical assumptions were used to compare the groups. $p < 0.05$ and $p < 0.01$ were considered statistically significant.

## Results

Clinical isolates of patients treated in general adult intensive care unit were evaluated. In this study, according to the data of three years, a total of 69,272% (n = 167) cases, 40,541% (n = 90) women and 28,731% (n = 77) men were examined in 2016In 2017, a total of 58,038% (n = 140) cases were examined, 33.784% (n = 75) of women and 24.254% (n = 65) of men. In 2018, 25,676% (n = 57) of women and 47,015% (n = 126) of men were found to be 72,691% (n = 183) of the total number (Table 1). When examined in terms of different age groups, it was found that the majority of patients were

in the 81-90 age range. According to the data of 2016, it was found that 35.145% (n = 83) of the patients, 29,662% (n = 71) in 2017 and 30,714% (n = 81) of patients were examined in 2018 (Table 1). Statistical analysis revealed that age distributions were statistically significant between 40-60 and 81-90 years according to spearman's correlation test (p> 0.01). Also, there was a significant correlation between 61-70 age group and total number of patients (p> 0.01).

**Table 1.** Distribution of different age groups by gender

| Years | Gender | | 40-60 | 61-70 | 81-90 | Toplam |
|---|---|---|---|---|---|---|
| 2016 | **Female** | **n** | 6 | 30 | 54 | 90 |
| | | **%** | 2,703 | 13,514 | 24,324 | 40,541 |
| | **Male** | **n** | 12 | 36 | 29 | 77 |
| | | **%** | 4,478 | 13,433 | 10,821 | 28,731 |
| 2017 | **Female** | **n** | 2 | 32 | 41 | 75 |
| | | **%** | 0,901 | 14,414 | 18,468 | 33,784 |
| | **Male** | **n** | 5 | 30 | 30 | 65 |
| | | **%** | 1,866 | 11,194 | 11,194 | 24,254 |
| 2018 | **Female** | **n** | 5 | 36 | 16 | 57 |
| | | **%** | 2,252 | 16,216 | 7,207 | 25,676 |
| | **Male** | **n** | 12 | 51 | 63 | 126 |
| | | % | 4,478 | 19,030 | 23,507 | 47,015 |

When the distribution of cultures by years is examined, in the study, it was determined that sputum isolates (50,010%) were the first, and urine (24,898%) and blood (22,449%) isolates (Table 2).

**Table 2.** Distribution of cultures by years and gender

| Gender | Cultures | 2016 | | 2017 | | 2018 | | Toplam | |
|---|---|---|---|---|---|---|---|---|---|
| | | **n** | **%** | **n** | **%** | **n** | **%** | **n** | **%** |
| Female | **Sputum** | 36 | 7,347 | 39 | 7,959 | 24 | 4,898 | 99 | 20,204 |
| | **Urine** | 22 | 4,490 | 22 | 4,490 | 20 | 4,082 | 64 | 13,061 |
| | **Blood** | 27 | 5,510 | 15 | 3,061 | 10 | 2,041 | 52 | 10,612 |
| | **Other** | 1 | 0,204 | 0 | 0,000 | 4 | 0,816 | 5 | 1,020 |
| Male | **Sputum** | 43 | 8,776 | 40 | 8,163 | 63 | 12,857 | 146 | 29,796 |
| | **Urine** | 14 | 2,857 | 14 | 2,857 | 30 | 6,122 | 58 | 11,837 |
| | **Blood** | 21 | 4,286 | 11 | 2,245 | 26 | 5,306 | 58 | 11,837 |
| | **Other** | 1 | 0,204 | 0 | 0,000 | 7 | 1,429 | 8 | 1,633 |
| | **Total** | 165 | 33,673 | 141 | 28,776 | 184 | 37,551 | 490 | 100 |

When the Pearson correlation coefficients of the cultures in 2016, 2017 and 2018 were examined, it was found that the cultures were statistically significant with each other. It was found to be statistically significant and positive between 2016 and 2018 (p = 0.741), 2017 and 2018 (p = 0.747) (P> 0.05). Between 2016 and 2017, there was a positive correlation between p> 0.01 (p = 0.941) (Table 3).

**Table 3.** Pearson correlation coefficients of cultures by years

| Years | | 2016 | 2017 | 2018 |
|---|---|---|---|---|
| **2016** | Pearson Correlation | 1 | ,941** | ,741* |
| | Sig. (2-tailed) | | ,000 | ,036 |
| **2017** | Pearson Correlation | ,941** | 1 | ,747* |
| | Sig. (2-tailed) | ,000 | | ,033 |
| **2018** | Pearson Correlation | ,741* | ,747* | 1 |
| | Sig. (2-tailed) | ,036 | ,033 | |

**. Correlation is significant at the 0.01 level (2-tailed)., Correlation is significant at 0.05 level (2 tails).

**Table 4.** Defined microorganisms and distribution by years

| Microorganisms | 2016 | 2017 | 2018 | Total | |
|---|---|---|---|---|---|
| | n | n | n | n | % |
| *Pseudomonas aeruginosa* | 0 | 8 | 41 | 49 | 10.000 |
| Nonfermentative Gr (-) | 37 | 14 | 2 | 53 | 10.816 |
| *Klepsiella* sp. | 14 | 17 | 10 | 41 | 8.367 |
| *Escherichia coli* | 19 | 12 | 12 | 43 | 8.776 |
| *Candida* sp. | 0 | 5 | 26 | 31 | 6.327 |
| *Proteus* sp. | 1 | 0 | 28 | 29 | 5.918 |
| *Pseudomonas* sp. | 19 | 26 | 0 | 45 | 9.184 |
| Methicillin Resistant *Staphylococcus* | 0 | 2 | 21 | 23 | 4.694 |
| *Enterococcus* | 5 | 8 | 7 | 20 | 4.082 |
| *Staphylococcus epidermidis* | 14 | 4 | 5 | 23 | 4.694 |
| Coagulase Negative *Staphylococcus* | 12 | 9 | 1 | 22 | 4.490 |
| *Klebsiella pneumoniae* | 12 | 4 | 2 | 18 | 3.673 |
| Methicillin susceptiple *Staphylococcus* | 0 | 0 | 10 | 10 | 2.041 |
| *Streptococcus pneumoniae* | 7 | 4 | 3 | 14 | 2.857 |
| *Staphylococcus aureus* | 5 | 7 | 2 | 14 | 2.857 |
| Viridans group *Streptococcus* | 0 | 1 | 7 | 8 | 1.633 |
| *Candida albicans* | 3 | 10 | 0 | 13 | 2.653 |
| Yeast | 9 | 4 | 0 | 13 | 2.653 |
| Gram positive | 3 | 4 | 0 | 7 | 1.429 |
| *Proteus mirabilis* | 1 | 0 | 3 | 4 | 0.816 |
| Methicillin Sensitive *Staphylococcus* | 0 | 0 | 2 | 2 | 0.408 |
| *Streptococcus* sp. | 2 | 0 | 1 | 3 | 0.612 |
| *Citrobacter* | 2 | 1 | 0 | 3 | 0.612 |
| *Diplococcus* sp. | 0 | 1 | 0 | 1 | 0.204 |
| Gram negative | 1 | 0 | 0 | 1 | 0.204 |
| **Total** | 166 | 141 | 183 | 490 | 100.000 |

The pathogen microorganisms determined in clinical isolates obtained by years are given in Table 4 as 490. In the study, the rate of non-fermentative gram-negative microorganisms was determined as 10,816% (n = 53) and *P. aeruginosa* was followed by 10% (n = 49) in three years Especially when examined in terms of 2018, it was determined that the total number of microorganisms was higher than other years, while *P. aeruginosa* strain (n = 41) increased significantly. As a result of the study; *P. aeruginosa*, Non-fermentative Gram (-), *Klebsiella sp*, *E. coli*, *Candida spp*, *Proteus spp*, *Pseudomonas spp* were identified as major pathogens. When Pearson correlation coefficients were examined, a statistically significant result was obtained between 2016 and 2017 ($p > 0.01$).

## Discussion

Nosocomial infections in ICUs are an important cause of morbidity and mortality and also increase hospital stay and increase health expenditures. studies on the surveillance and prevention of these infections are important (5-10). The frequency of infection in patients receiving ICU treatment is high. Urinary tract infections, circulatory system infections and pneumonia are the most common infections (3). In our study, pathogen microorganisms from the urinary system and blood cultures, especially sputum cultures, were found.

In a study, the most commonly isolated microorganisms *Pseudomonas* spp., *Staphylococcus aureus* and *Acinetobacter* spp. is specified (11). In another study, coagulase negative staphylococci (CNS) were reported to be the most common microorganisms with 70.8% (9). Also, Coagulase negative *Staphylococci (*194), *Acinetobacter baumannii* (56), *Escherichia coli* (53), *Candida spp* (46) and *S.aureus* (45) were reported as the most commonly isolated agents (12). In our study, the rate of CNS was determined as 4.490%. *E. coli* was the 4th in our study with 8.776%. In recent studies, it has been reported that the incidence of Gram positive bacteria, especially CNS, *S. aureus* and *Enterococcus* species, has increased (12).

In a study conducted in the neurology intensive care unit, the causative agent of ventilator-associated pneumonia (VAP) infections was reported as 46.15% *A. baumannii*, 23.07%, *E. coli* and 15.3% *P. aeruginosa* [13]. In our study, *P. aeruginosa* (10.00%) and *E. coli* (8.776%) were determined in the patients in the general intensive care unit, respectively. In addition, Şahin et al. (2019) found that the most common pathogens from urinary tract infections were *E. coli* and *K. pneumoniae* with 37.5% (13).

Taş and Kahveci (2018), analyzed the 3-year surveillance of the intensive care unit. In this study, *E. coli* was found to be the most common agent in three years. The most common infection was urinary tract infection followed by bloodstream infections (14). In our study, the first place was found to be sputum and then infections from urine and blood cultures. In our study; the microorganism species we analyzed from blood cultures were similar to previous studies isolated from blood cultures in intensive care units (15).

In another study performed in the intensive care unit, 137 microorganisms were isolated from respiratory tract, 87 from blood, 54 from urine and 19 from wound specimens (16). In our study, microorganisms were obtained from sputum (50.010%), urine (24.898%) and blood (22.449%) cultures. Determining the distribution of the microorganisms from the units to the general and examining the resistance statuses and arranging treatment protocols in this direction will be beneficial in the prevention of resistant pathogenic microorganisms.

## Conclusion

In many countries, it is important to determine the prevalence and rational drug use in the fight against pathogens, which have become an important problem both in terms of economic and health. For this reason, it is thought that knowing the characteristics of the pathogens determined in our study will play an important role in determining the direction of the studies to be performed in this field.

**Ethics Committee Approval:** Yes
**Informed Consent:** NA
**Peer-review:** Externally peer-reviewed.
**Conflict of Interest:** No conflict of interest was declared by the author.
**Financial Disclosure:** The author declared that this study has received no financial support.

## References

1. Anderson DJ, Podgorny K, Berríos-Torres SI, Bratzler DW, Dellinger EP, Greene L. Strategies to Prevent Surgical Site Infections in Acute Care Hospitals: 2014 Update. Infection Control and Hospital Epidemiology 2014; 35(6):305-37.
2. D'Agata EM, Thayer V, Schaffner W. An outbreak of Acinetobacter baumannii: the importance of cross-transmission. Infect Control Hosp Epidemiol 2000; 21(9): 588-91.
3. Barış A, Bulut ME, Öncül A, Bayraktar B. Yoğun Bakım Ünitelerinde Yatan Hastalara Ait Klinik İzolatların Tür Dağılımı ve Antibiyotik Duyarlılıkları. Journal of the Turkish Society of Intensive Care 2017;15(1):21-27.
4. Sugeçti S, Koçer F. Antimicrobial Activity Against Clinical Pathogenic Microorganisms of Commercially Important Natural Extract, Anadolu Doğa Bilimleri Dergisi 2015;6 (2): 28-34.
5. Uslu S, Bolat F, Can E, Comert S, Nuhoğlu A. Yenidoğan yoğun bakım ünitelerinde hastane enfeksiyonlarını önleme çalışmaları. Bakırköy Tıp Dergisi 2010; 6(1):1-7.
6. Estripeaut D, Sáez-Llorens X. Perinatal Bacterial Diseases, In: Feigin RD, Cherry JD, Demmler-Harrison GJ, Kaplan SL (Eds): Feigin & Cherry's Textbook of Pediatric Infectious Diseases. 6th edition, Saunders-Elsevier, Philadelphia, USA 2009:979-1020.
7. Edwards MS, Baker CJ. Bacterial Infections in the Neonate, In: Long SS, Pickering LK, Prober CG (Eds): Principles and Practice of Pediatric Infectious Diseases. 3th ed, Elsevier, China 2008:532-9.
8. Clinical and Laboratory Standards Institute. Performance Standards for Antimicrobial Testing. Seventeenth Informational Supplement (M100-S16). Wayne, PA: CLSI, 2007.
9. Banerjee SN, Grohskopf LA, Sinkowitz-Cochran RL, Jarvis WR, Network PP, System NNIS. Incidence of pediatric and neonatal intensive care unit–acquired infections. Infect Control Hosp Epidemiol. 2006;27(6):561-70.
10. Sağlam D, Erçal B. D, Yağmur G, Öz HTH, Akın MA, Berk E. Kayseri Eğitim Araştırma Hastanesi yenidoğan yoğun bakım ünitelerinde kan kültürlerinden izole edilen mikroorganizmaların dağılımı. Abant Tıp Dergisi, 2015;4(3):255-260.
11. İnan D, Saba R, Keskin S, et al. Akdeniz Üniversitesi Hastanesi yoğun bakım ünitelerinde hastane infeksiyonları. Yoğun Bakım Dergisi, 2002;2(2): 129-135.
12. Çetin ES, Kaya S, Pakbaş İ, Demirci M. Yoğun bakım ünitelerinde yatan hastalardan izole edilen mikroorganizmalar ve antibiyotik duyarlılıkları. İnönü Üniversitesi Tıp Fakültesi Dergisi 2007;14(2):69-73.
13. Şahin AR, Yıldız BT, Aktemur A, Topal B, Nazik S, Ateş S. Bir Üniversite Hastanesi Noroloji Yoğun Bakım Ünitesinde Gelişen Enfeksiyonların Değerlendirilmesi. Çağdaş Tıp Dergisi, 2019; 9(1), 43-47.
14. Taş SŞ, Kahveci K. Uzun Süreli Yoğun Bakım Ünitesi ve Palyatif Bakım Merkezinde Hastane Enfeksiyonlarının Sürveyansı; 3 Yıllık Analiz. Çağdaş Tıp Dergisi, 2018; 8(1), 55-59.
15. Taşbent FE, Doğan M. Yoğun Bakım Hastalarında Kan Kültürlerinde Üreyen Mikroorganizmaların Değerlendirilmesi. Journal of Molecular Biology and Biotechnology (MOLBİOTECH) 2018; 2(2), 05-08.
16. Ertürk A, Çopur ÇA, Köksal E, Şentürk KZ, Özyurt S. Yoğun bakım ünitesinde yatan hastaların çeşitli klinik örneklerinden izole edilen mikroorganizmalar ve antibiyotik duyarlılıkları. Ankem Derg, 2012;26(1):1-9.