

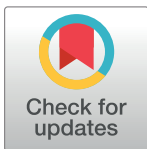
RESEARCH ARTICLE

A one-year prospective study of colonization with antimicrobial-resistant organisms on admission to a Vietnamese intensive care unit

Duong Bich Thuy^{1,2*}, James Campbell^{1,3}, Nguyen Van Minh Hoang¹, Truong Thi Thuy Trinh², Ha Thi Hai Duong², Nguyen Chi Hieu², Nguyen Hoang Anh Duy², Nguyen Van Hao^{2,4}, Stephen Baker^{1,3,5}, Guy E. Thwaites^{1,3}, Nguyen Van Vinh Chau⁶, C. Louise Thwaites^{1,3}

1 Hospital for Tropical Diseases, Wellcome Trust Major Overseas Programmes, Oxford University Clinical Research Unit (OUCRU), Ho Chi Minh City, Vietnam, **2** Adult Intensive Care Unit, Hospital for Tropical Diseases, Ho Chi Minh City, Vietnam, **3** Centre for Tropical Medicine and Global Health, Nuffield Department of Clinical Medicine, Oxford University, Oxford, United Kingdom, **4** Department of Infectious Diseases, University of Medicine and Pharmacy, Ho Chi Minh City, Vietnam, **5** Department of Medicine, Cambridge University, Cambridge, United Kingdom, **6** Board of Directors, Hospital for Tropical Diseases, Ho Chi Minh City, Vietnam

* duongthuyicu@gmail.com



OPEN ACCESS

Citation: Thuy DB, Campbell J, Hoang NVM, Trinh TTT, Duong HTH, Hieu NC, et al. (2017) A one-year prospective study of colonization with antimicrobial-resistant organisms on admission to a Vietnamese intensive care unit. PLoS ONE 12(9): e0184847. <https://doi.org/10.1371/journal.pone.0184847>

Editor: Binh An Diep, University of California San Francisco, UNITED STATES

Received: June 13, 2017

Accepted: August 31, 2017

Published: September 14, 2017

Copyright: © 2017 Thuy et al. This is an open access article distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Data Availability Statement: All relevant data are within the paper.

Funding: This study is funded by Oxford University Clinical Research Unit based in Vietnam (OUCRU—VN). The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing interests: The authors have declared that no competing interests exist.

Abstract

There is a paucity of data regarding initial bacterial colonization on admission to Intensive Care Units (ICUs) in low and middle-income countries (LMICs). Patients admitted to ICUs in LMICs are at high-risk of subsequent infection with antimicrobial-resistant organisms (AROs). We conducted a prospective, observational study at the Hospital for Tropical Diseases in Ho Chi Minh City, Vietnam from November 2014 to January 2016 to assess the colonization and antimicrobial susceptibility of *Staphylococcus aureus*, *Escherichia coli*, *Klebsiella* spp., *Pseudomonas* spp. and *Acinetobacter* spp. among adult patients within 48 hours of ICU admission. We found the admission colonization prevalence (with at least one of the identified organisms) was 93.7% (785/838) and that of AROs was 63.1% (529/838). The colonization frequency with AROs among patients admitted from the community was comparable to those transferred from other hospitals (62.2% vs 63.8%). *Staphylococcus aureus* was the most commonly isolated bacteria from nasal swabs (13.1%, 110/838) and the methicillin-resistant *Staphylococcus aureus* nasal colonization prevalence was 8.6% (72/838). We isolated *Escherichia coli* from rectal swabs from almost all enrolled patients (88.3%, 740/838) and 52.1% (437/838) of patients were colonized by extended spectrum β -lactamase producing *Escherichia coli*. Notably, *Klebsiella pneumoniae* was the most frequently isolated bacteria from the tracheal swabs (11.8%, 18/153). Vietnamese ICU patients have a high rate of colonization with AROs and are thus at risk of subsequent infections with these organisms if good infection control practices are not in place.

Introduction

Leaders in world health have described antimicrobial-resistant organisms (AROs) as “nightmare bacteria” that account for a substantial number of excess deaths, and catastrophic health-care spending [1]. The impact of AROs is suggested to be far more serious in low and middle-income countries (LMICs) than in well-resourced countries, where unregulated antimicrobial use, and poor infection control practices may result in increased numbers of infections related to AROs [2].

Infection with AROs is a major problem faced by Intensive Care Units (ICUs) located in LMICs. Progression from colonization to infection has been well established for ICU patients in well-resourced settings with comparably low rates of AROs [3–9]. However, little is known about initial bacterial colonization on admission to ICUs and subsequent infections in LMICs. The reason behind this lack of data is multifactorial but is partly associated with a lack of routine screening, which is rarely available or affordable. However, in such locations routine screening is vital due to the circulation of AROs in the community and increased likelihood of transmission within the ICUs due to poor infection control. To address this knowledge gap in bacterial colonization on a ICU in a LMIC, we conducted a one-year prospective study to assess the initial colonization and antimicrobial susceptibility profiles of *Staphylococcus aureus* (*S. aureus*), *Escherichia coli* (*E. coli*), *Klebsiella* spp. (including *K. pneumoniae*), *Pseudomonas* spp. (including *P. aeruginosa*) and *Acinetobacter* spp. (including *A. baumannii*) on admission to the Adult ICU at the Hospital for Tropical Diseases (HTD) in Ho Chi Minh City (HCMC), Vietnam.

Materials and methods

Setting

This prospective, observational study was conducted in the 20-bed Adult ICU of the HTD in HCMC, Vietnam. HTD is a tertiary referral hospital for infectious diseases serving Southern Vietnam. The study was reviewed and approved by the Ethics Committee of the Hospital for Tropical Diseases in Ho Chi Minh City, Vietnam and the Oxford Tropical Research Ethics Committee (OxTREC), United Kingdom.

Study population and procedure

All patients aged ≥ 15 years admitted to the Adult ICU between 10th November 2014 and 14th January 2016 were eligible for entry to the study. Written informed consent were obtained from the participants or their representatives. All patients whom were readmitted to Adult ICU of the HTD within 90 days from discharge were excluded. All eligible patients had nasal swab, rectal swab, and/or endotracheal aspirate (ETA, in case of intubation or tracheostomy) taken within 48 hours of ICU admission for screening *S. aureus*, *E. coli*, *Klebsiella* spp., *Pseudomonas* spp. and *Acinetobacter* spp..

Microbiological methods

Nasal and endotracheal specimens were cultured on Blood agar (BioMerioux) and MacConkey (BioMerioux) to specifically isolate *S. aureus*, *E. coli*, *Klebsiella* spp., *Pseudomonas* spp. and *Acinetobacter* spp.. An experienced microbiologist selected probable Staphylococcal colonies from blood agar plates inoculated with the patient swabs, and checked for catalase and coagulase, then cultured on CHROMagar plus checked for methicillin resistance using cefotaxime and oxacillin disc diffusion, and re-checked on the matrix assisted laser desorption/ionization time-of-flight mass spectrometry (MALDITOF, Bruker).

Xylose Lysine Deoxcholate agar (BioMerioux) and MacConkey agar (BioMerioux) were used to culture rectal swabs for Gram negative bacteria, and identification of *E. coli*, *Klebsiella* spp., *Pseudomonas* spp. and *Acinetobacter* spp. was confirmed by MALDITOF. Antimicrobial susceptibility testing was conducted by the Kirby/Bauer disc diffusion method and interpreted using the Clinical and Laboratory Standards Institute (CLSI) guidelines 2015. Appropriate organisms were screened for specific antimicrobial-resistant activity including extended spectrum β -lactamase (ESBL) using CHROMagar ESBL, and the double disc diffusion test, AmpC β -lactamase (AmpC) using CHROMagar AmpC, and carbapenemases using CHROMagar KPC.

Definition of colonization

For the purposes of this investigation, admission colonization was assessed as a positive nasal, rectal and/or endotracheal sample for *S. aureus*, *E. coli*, *Klebsiella* spp., *Pseudomonas* spp. and/or *Acinetobacter* spp. within 48 hours of ICU admission. AROs colonization was assessed as a positive culture from nasal, rectal and/or endotracheal sample of MRSA, 3rd-generation cephalosporin (3rd CPS)-resistant *E. coli*, 3rd CPS-resistant *Klebsiella* spp., ceftazidime-resistant *Pseudomonas* spp., carbapenem-resistant *E. coli*, carbapenem-resistant *Klebsiella* spp., carbapenem-resistant *Pseudomonas* spp. and/or carbapenem-resistant *Acinetobacter* spp..

Statistical analysis

Descriptive analyses of the endpoints were performed, consisting of frequency (percentage) for categorical data, and median (95% confidence interval— 95% CI or interquartile range— IQR) for continuous data using R statistical software (R Core Team (2013). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria). Comparisons of percentage were performed using χ^2 or Fisher's exact tests. Comparisons of means were performed using Student's t test or nonparametric tests, such as the Kruskal-Wallis test. P-values < 0.05 (two-sided) were considered statistically significant.

Results

General patient characteristics

During the one-year study period, 838 of 873 (96.0%) patients admitted the Adult ICU of the HTD met the inclusion criteria and were enrolled in the study. An additional 35 (4.0%) patients, who were readmitted to the Adult ICU within 90 days and were excluded. Patient characteristics (age, sex, patient origin, history of antimicrobial therapy within 90 days and 24 hours prior to ICU admission) and clinical information (Charlson Comorbidity Index and APACHE II score) were collected using a standardized form on the day of enrollment. The baseline demographic characteristics are shown in [Table 1](#).

Admission colonization status

A total of 1,829 sampling swabs were taken from the 838 enrolled patients within 48 hours of ICU admission: 838 were nasal swabs, 838 were rectal swabs and 153 were ETA samples. The pattern of initial bacterial colonization is presented in [Fig 1](#).

S. aureus was the most commonly isolated organism from nasal swabs, cultured from 110 patients (13.1%): 72/110 (65.5%) of these were MRSA. The rate of nasal methicillin-resistant *Staphylococcus aureus* colonization among patients transferred from other hospitals (9.5%, 48/505) was higher than among those admitted from the community (7.2%, 24/333) but not statistically significant ($p = 0.25$). From the 740 (88.3%) patients from whom we isolated *E. coli*

Table 1. General patient characteristics upon ICU admission.

Characteristics	All patients (N = 838)
Age (yr)—median (IQR)	43 (29–59)
< 60—n (%)	634 (75.7)
≥ 60—n (%)	204 (24.3)
Sex—n (%)	
Male	497 (59.3)
Female	341 (40.7)
Origin of patients—n (%)	
From the community	333 (39.7)
From other hospitals	419 (50.0)
From another general ward at HTD	86 (10.3)
History of previous antimicrobial therapy within 90 days	58 (6.9)
History of previous antimicrobial therapy within 24 hours	181 (21.6)
Charlson Comorbidity Index—median (IQR)	0 (0–1)
No comorbidity (0)—n (%)	512 (61.1)
Mild (1–2)—n (%)	166 (19.8)
Moderate (3–4)—n (%)	108 (12.9)
Severe (≥ 5)—n (%)	52 (6.2)
APACHE II score—median (IQR)	8 (4–14)
Mild (< 5)—n (%)	240 (28.6)
Moderate (5–12)—n (%)	330 (39.4)
Severe (> 12)—n (%)	268 (32.0)

<https://doi.org/10.1371/journal.pone.0184847.t001>

from a rectal swab, 437 (59.1%) were colonized with ESBL-producing *E. coli*, 45 (6.1%) with AmpC-producing *E. coli* and 8 (1.1%) with carbapenemase-producing *E. coli*. *K. pneumoniae* was the most commonly isolated organism from tracheal aspirates, isolated from 11.8% (18/153) of patients.

The overall admission prevalence of bacterial isolation from at least one of the body sampling sites with either *S. aureus*, *E. coli*, *Klebsiella* spp., *Pseudomonas* spp. or *Acinetobacter* spp. was 93.7% (785/838). The prevalence of bacterial isolation was variable between different patient subgroups: 95.8% (319/333) for subjects originated from the community, 77.6% (392/505) for those being transferred to ICU from other hospitals ($p \leq 0.001$, OR = 6.57, 95% CI (3.70–11.67)). The AROs colonization rate at all sites was 63.1% (529/838). 62.2% (207/333) patients admitted from the community were colonized with AROs and that of patients transferred from other hospitals was 63.8% (322/505) ($p = 0.64$).

Antimicrobial susceptibility of colonized bacteria on ICU admission

From all sampling swabs, a total of 1,905 colonizing bacterial isolates were isolated: 143 (7.5%) were *S. aureus*, 1,370 (71.9%) were *E. coli*, 345 (18.1%) were *Klebsiella* spp., 32 (1.7%) were *Pseudomonas* spp. and 15 (0.8%) were *Acinetobacter* spp.. The antimicrobial susceptibility profiles of the isolated organisms are summarized in Table 2. MRSA accounted for 63.6% of all *S. aureus* isolates, vancomycin-resistant *S. aureus* was not detected. The rate of 3rd-generation cephalosporin resistance and ciprofloxacin resistance in *E. coli* was approximately 50%. The rate of 3rd-generation cephalosporin resistance and ciprofloxacin resistance in *Klebsiella* spp. was approximately 20.0% and 12.5%, respectively. Approximately 10% of *Pseudomonas* spp. were ceftazidime-resistant. Markedly, 60% of the isolated *Acinetobacter* spp. were resistant to imipenem or meropenem. We additionally found that a small proportion of *E. coli* and

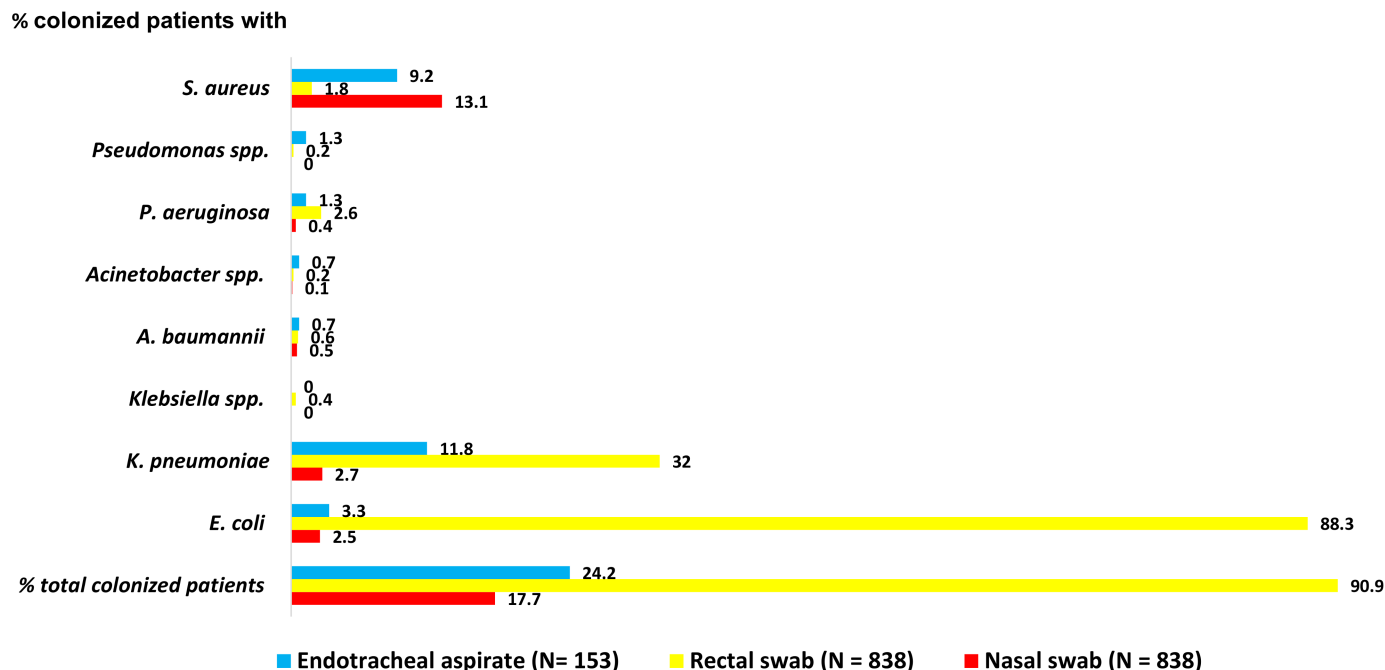


Fig 1. Admission colonization status of 838 enrolled patients.

<https://doi.org/10.1371/journal.pone.0184847.g001>

Table 2. Antimicrobial resistance of colonized bacteria on ICU admission.

Antimicrobials n (%)	<i>S. aureus</i> (n = 143)	<i>E. coli</i> (n = 1370)	<i>Klebsiella spp.</i> (n = 345)	<i>Acinetobacter spp.</i> (n = 15)	<i>Pseudomonas spp.</i> (n = 32)
Amoxicillin-clavulanic acid		746 (54.5)	82 (23.8)		
Ceftazidime		702 (51.2)	74 (21.4)	13 (86.7)	3 (9.4)
Ceftriaxone		703 (51.3)	76 (22.0)	13 (86.7)	
Cefepime		639 (46.4)	56 (16.2)	12 (80.0)	3 (9.4)
Ticarcillin-clavulanate		828 (60.4)	87 (25.2)	12 (80.0)	21 (65.6)
Piperacillin-tazobactam		651 (47.5)	51 (14.8)	12 (80.0)	3 (9.4)
Ofloxacin		632 (46.1)	31 (9.0)		
Ciprofloxacin	70 (49.0)	646 (47.2)	43 (12.5)		
Levofloxacin	70 (49.0)			10 (66.7)	3 (9.4)
Sulfamethoxazole-trimethoprim	5 (3.5)	953 (69.6)	106 (30.7)	7 (46.7)	29 (90.6)
Amikacin		26 (1.9)	8 (2.3)	6 (40.0)	2 (6.3)
Gentamycin					2 (6.3)
Ertapenem		29 (2.1)	10 (2.9)		
Imipenem		13 (0.9)	10 (2.9)	9 (60.0)	6 (18.8)
Meropenem		15 (1.1)	10 (2.9)	9 (60.0)	7 (21.9)
Colistin		50 (3.6)	22 (6.4)	0	0
Penicillin	137 (95.8)				
Oxacillin	91 (63.6)				
Vancomycin	0				
Erythromycin	95 (66.4)				
Rifampicin	3 (2.1)				
Clindamycin	89 (62.2)				

<https://doi.org/10.1371/journal.pone.0184847.t002>

Klebsiella spp. (3.6% and 6.4%, respectively) were resistant to colistin, the antimicrobial of last resort for carbapenemase-producing organisms (CPOs).

Discussion

Bacterial colonization of patients on admission to ICUs has been studied in some areas around the world. Data from a cluster-randomized trial in 13 ICUs in 8 European countries (2008–2011) reported a percentage of 13.5% (125/926) of patients colonized with highly resistant *Enterobacteriaceae*, MRSA, and vancomycin-resistant *Enterococcus* (VRE) on admission [10]. In a Turkish ICU, general admission colonization with either MRSA, VRE, ESBL-producing *E. coli*, ESBL-producing *Klebsiella* spp., *P. aeruginosa*, or *Acinetobacter* spp. was observed in 56.8% (54/95) of patients: 60.0% (9/15) for patients from the community and 56.3% (45/80) for those from other health services [11]. Our study noted a rate of colonization with AROs of 62.2% (207/333) among patients admitted from the community which was as high as 63.8% (322/505) for those transferred from other hospitals. Our setting is perhaps unique in that a large proportion of patients are admitted directly from the community and we have shown a similarly increased rate of AROs in those patients compared to those from other hospitals.

In our study, admission *S. aureus* nasal colonization rate was 13.1% which was indeed lower than previously reported in urban and rural northern Vietnam (21.1%, 140/662) [12] and in other countries with rates of between 8.1% and 30.1% [13–16]. However, the prevalence of nasal MRSA colonization of 8.6% (72/838) in this study compared to proportion of MRSA colonization documented in the HTD (2.9% in 2004–2006) [17] and reported in other health-care settings with rates of between 0.3% and 12.9% [14,18–22] may indicate that MRSA is an increasing problem that needs addressing in Vietnam. So, we do not believe that our microbiological approach resulted in significant reduction in the yield of *S. aureus* from the patient's samples.

There are several limitations of this study that warrant further discussion. This was a single-center study, so, the findings may not be representative in other institutions. However, to our knowledge, due to a lack of data at the country level, our study is the first to analyze colonization, especially with AROs on ICU admission in Vietnam. Furthermore, our unique intake of patients also provides an insight into AROs colonization outside of the hospital setting in a resource-limited setting. However, we are not reporting the genetic mechanisms of antimicrobial resistance to better understand current resistance and evaluate potential interventions.

Conclusions

Vietnamese ICU patients have a high rate of colonization with AROs and are thus at risk of subsequent infections with these organisms if good infection control practices are not in place. For many of these organisms, there are limited treatment options available, therefore further research to better understand the relationship between colonization and infection and evaluate new prevention strategies is urgently needed.

Acknowledgments

We would like to thank all doctors, nurses and nursing aids of the Adult ICU of the HTD for data assistance, all staffs working in Microbiology Group of OUCRU—Vietnam for laboratory support, and Mr Bui Thanh Lich for building CliRes Data Management System.

Author Contributions

Data curation: Duong Bich Thuy.

Formal analysis: Duong Bich Thuy, Guy E. Thwaites, C. Louise Thwaites.

Funding acquisition: Guy E. Thwaites.

Investigation: James Campbell, Nguyen Van Minh Hoang, Truong Thi Thuy Trinh, Ha Thi Hai Duong, Nguyen Chi Hieu, Nguyen Hoang Anh Duy.

Methodology: Duong Bich Thuy, Stephen Baker, Guy E. Thwaites, C. Louise Thwaites.

Project administration: Duong Bich Thuy, Nguyen Van Hao, Nguyen Van Vinh Chau.

Resources: James Campbell, Nguyen Van Minh Hoang, Stephen Baker.

Supervision: Stephen Baker, Guy E. Thwaites, C. Louise Thwaites.

Visualization: Duong Bich Thuy, Nguyen Van Vinh Chau.

Writing – original draft: Duong Bich Thuy, Stephen Baker, Guy E. Thwaites, C. Louise Thwaites.

Writing – review & editing: Duong Bich Thuy, Stephen Baker.

References

1. Frieden T. Antibiotic resistance threats. Cdc. 2013; 22–50.
2. Thu TA, Rahman M, Coffin S, Harun-Or-Rashid M, Sakamoto J, Hung NV. Antibiotic use in Vietnamese hospitals: A multicenter point-prevalence study. *Am J Infect Control*. 2012; 40(9):840–4. <https://doi.org/10.1016/j.ajic.2011.10.020> PMID: 22341530
3. Bonten MJ. The role of colonization in the pathogenesis of nosocomial infections. *Infect Control Hosp Epidemiol*. 1996; 17:193–200. PMID: 8708364
4. Boyce MJ. Treatment and control of colonization in the prevention of nosocomial infections. *Infect Control Hosp Epidemiol*. 1996; 17(256–261). PMID: 8935734
5. Greene JN. The microbiology of colonization, including techniques for assessing and measuring colonization. *Infect Control Hosp Epidemiol*. 1996; 17:114–8. PMID: 8835448
6. Jarvis WR. The epidemiology of colonization. *Infect Control Hosp Epidemiol* [Internet]. 1996; 17:47–52. PMID: 8789688
7. Galois-Guibal L, Soubirou JL, Desjeux G, Dusseau JY, Eve O, Escarment J, et al. Screening for multi-drug-resistant bacteria as a predictive test for subsequent onset of nosocomial infection. *Infect Control Hosp Epidemiol*. 2006; 27(11):1233–41. <https://doi.org/10.1086/507277> PMID: 17080382
8. Ren Y, Ma G, Peng L, Ren Y, Zhang F. Active Screening of Multi-Drug Resistant Bacteria Effectively Prevent and Control the Potential Infections. *Cell Biochem Biophys* [Internet]. 2015; 71(2):1235–8. <https://doi.org/10.1007/s12013-014-0333-6> PMID: 25416582
9. Yeşilbaş Z. et al. Is there a relationship between rectal colonization and nosocomial infection of patients in intensive care unit? *Mikrobiyol Bul*. 2015; 49(3):327–39. PMID: 26313275
10. Haverkate MR, Derde LPG, Brun-Buisson C, Bonten MJM, Bootsma MCJ. Duration of colonization with antimicrobial-resistant bacteria after ICU discharge. *Intensive Care Med*. 2014; 40(4):564–71. <https://doi.org/10.1007/s00134-014-3225-8> PMID: 24522879
11. The Colonization and Infection Relationship in Hospitalized Patients at Intensive Care Unit. 2015; (September):568–70.
12. Nguyen VK, Zhang T, Vu NBT, Dao TT, Tran TK, Nguyen DNT, et al. Staphylococcus aureus nasopharyngeal carriage in rural and urban northern Vietnam. *Trans R Soc Trop Med Hyg* [Internet]. 2014; 108(12):783–90. <https://doi.org/10.1093/trstmh/tru132> PMID: 25187670
13. Erdenizmenli M, Yapar N, Senger SS, Özdemir S, Yüce A. Investigation of colonization with methicillin-resistant and methicillin-susceptible Staphylococcus aureus in an outpatient population in Turkey. *Jpn J Infect Dis*. 2004; 57(4):172–5. PMID: 15329450
14. Yan X, Song Y, Yu X, Tao X, Yan J, Luo F, et al. Factors associated with Staphylococcus aureus nasal carriage among healthy people in Northern China. *Clin Microbiol Infect*. 2015; 21(2):157–62. <https://doi.org/10.1016/j.cmi.2014.08.023> PMID: 25658548
15. Cole AM, Tahk S, Orena MI, Yoshioka D, Kim Y, Park A, et al. Determinants of Staphylococcus aureus Nasal Carriage. *Clin Diagn Lab Immunol*. 2001; 8(6):1064–9. <https://doi.org/10.1128/CDLI.8.6.1064-1069.2001> PMID: 11687441

16. Mainous A III, Hueston W, Everett CJ, Diaz V. Nasal Carriage of *Staphylococcus aureus* and Methicillin-Resistant *S aureus* in the United States, 2001–2002. *Ann Fam Med*. 2006; 4(2):132–7. <https://doi.org/10.1370/afm.526> PMID: 16569716
17. Schultsz C, Bootsma MCJ, Loan HT, Nga TTT, Thao LTP, Thuy TTD, et al. Effects of infection control measures on acquisition of five antimicrobial drug-resistant microorganisms in a tetanus intensive care unit in Vietnam. *Intensive Care Med*. 2013; 39(4):661–71. <https://doi.org/10.1007/s00134-012-2771-1> PMID: 23306583
18. Tan R, Liu J, Li M, Huang J, Sun J, Qu H. Epidemiology and antimicrobial resistance among commonly encountered bacteria associated with infections and colonization in intensive care units in a university-affiliated hospital in Shanghai. *J Microbiol Immunol Infect [Internet]*. 2014; 47(2):87–94. <https://doi.org/10.1016/j.jmii.2012.11.006> PMID: 23357606
19. Gamblin J, Jefferies JM, Harris S, Ahmad N, Marsh P, Faust SN, et al. Nasal self-swabbing for estimating the prevalence of *Staphylococcus aureus* in the community. *J Med Microbiol*. 2013; 62 (PART3):437–40.
20. George K, Abdulkader JK, Sugumar M, Rajagopal GK. Prevalence of MRSA Nasal Carriage in Patients Admitted to a Tertiary Care Hospital in Southern India. *J Clin Diagn Res [Internet]*. 2016; 10(2):DC11–3. <https://doi.org/10.7860/JCDR/2016/18259.7262> PMID: 27042461
21. Pujol M, Peña C, Pallares R, Ariza J, Ayats J, Dominguez MA, et al. Nosocomial *Staphylococcus aureus* bacteremia among nasal carriers of methicillin-resistant and methicillin-susceptible strains. *Am J Med*. 1996; 100(5):509–16. PMID: 8644762
22. Durmaz G, Sancı O, Öz Y, Güven K, Kiremitçi A, Aksit F. Methicillin-resistant *S. aureus* colonization in intensive care unit patients: Early identification and molecular typing. *J Infect Dev Ctries [Internet]*. 2016; 10(05).