

PROFILE OF ANTIBIOTIC RESISTANCE AGAINST INFLUENZA IN ADULT PATIENTS: A CASE STUDY AT CITY HEALTH CENTER IN INDONESIA

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ABSTRACT

Objective: In developing countries, cases of *Haemophilus influenzae* (HI) resistance to levofloxacin, cefixime, and tetracycline have become a serious problem in clinical treatment. This study was conducted to determine the antibiotic resistance profile of HI from adult patient isolates and to provide guidelines for more effective clinical treatment in Indonesia.

Methods: The patient isolate stock was rejuvenated, cultured on growth media and the Kirby-Bauer disc diffusion method was used to test for antibiotic susceptibility. Evaluation was guided by recommendations from the Clinical and Laboratory Standard Institute (CLSI).

Results: A total of 643 isolates obtained from the respiratory tract isolated and identified 73 HI strains. The resistance rates of the HI isolates to tetracycline, cefixime, and levofloxacin were 10.54 %, 4.31%, and 5.67%.

Conclusion: Cefixime showed more effective activity than levofloxacin and tetracycline to treat the HI strain.

Keywords: *Haemophilus influenzae*, Levofloxacin, Cefixime, Tetracycline, Resistance, Clinical isolates

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INTRODUCTION

One of the most prevalent organisms that causes community-acquired pneumonia and otitis media is *Haemophilus influenzae* (HI). Invasive pediatric illnesses, including meningitis and sepsis are also brought on by HI. These illnesses linked to HI pose a major threat to respiratory infections [1-3]. The principal method of colonization is adhering to the mucous membranes of the upper respiratory tract where it obstructs ciliary action. As a result, the respiratory system is the primary method of transmission for this species [4]. Bacteria can be classified into encapsulated and nonencapsulated/nontypeable (NTHi) strains based on a polysaccharide capsule antigen. Additionally, six antigenic serotypes can be used to classify the encapsulated isolates (a-f) [5, 6]. Nearly all of the serious illnesses caused by HI type b (Hib) in children under the age of five. The World Health Organization (WHO) estimated in 2012 that Hib causes 199 000 fatalities annually and accounts for 2% of all causes of child mortality [7, 8].

Amoxicillin, cephalosporin, azithromycin, doxycycline, and fluoroquinolone are significant antibiotics used in the treatment of less severe HI infections. However, broad-spectrum cephalosporins and carbapenems are used to treat serious infections [4, 9]. Rifampin is also the medicine of choice for children with Hib who need antibiotic prophylaxis [9]. However, the WHO recently added ampicillin-resistant HI strains to the list of antibiotic-resistant bacteria and medium priority category, along with penicillin-resistant *Streptococcus pneumoniae* and fluoroquinolone-resistant *Shigella* strains, in terms of the urgent need to develop new antibiotics [10]. As a result, it is crucial to evaluate antimicrobial susceptibility trends and track the HI resistance trend in order to inform local antibiotic prescription and prioritization decisions and lower the likelihood of treatment failure.

The advent of MDR HI has sparked significant alarm among researchers, medical professionals, and government health authorities worldwide. The risk factors, effective management controls, prevention, and underlying mechanisms of acquired MDR activity have all been extensively investigated [11-13]. Despite mounting evidence that MDR HI strains have been identified in

many regions. Cases of resistance to the use of tetracycline antibiotics, cefixime, and levofloxacin against HI strains isolated patients have been reported in several countries [14-16].

This study was performed to determine the antibiotic resistance profiles of HI isolates from adult patients in the city health center in Indonesia during 2017.

MATERIALS AND METHODS

The test sample consisted of a composite stock isolate from previous ARTIs (Acute Respiratory Tract Infections) research, which included 643 specific bacterial strains. The sample was purified and rejuvenated to obtain a single bacterial isolate. In accordance with the recommendations from the CLSI, Mueller Hinton Agar (MHA) (Oxoid) was employed as the bacterial growth medium and had a concentration of 38 g/l [14].

There are several biochemical test substances for identifying bacteria, including lactose (Merck), mannose (Merck), maltose (Merck), peptone (Oxoid), phenol red (Taylor), Kovac's reagent (Bio-Rad), TSIA, methyl red (HiMedia), and α -naphthosol (Merck).

Clinical isolates are rejuvenated and purified

The process of renewing clinical isolates was done utilizing the scratch plate technique. Rejuvenated clinical isolates from earlier research were cultured at 37 °C for 18 h on fresh MHA growth medium. Different haemolytic and morphological observations of colony morphology, including colony structure, color, and other factors, were made [15].

Identification, biochemical and morphological characterization

Cellular morphology and bacterial classification were determined using the gram stain technique and microscopic observation at a resolution of $\times 100$. The isolated bacteria were classified using a conventional biochemical test after the phenotypic and cell colonies had been identified, in accordance with the biochemical testing technique currently in use [18]. GS for Gram Staining, MT for Motility Test, MR for Methyl Red, SC for Simone Citrate, TSIA for Triple Sugar Iron Agar, OX for Oxidase, UR for Urease Test, XY for

Xylose, CT for Catalase, VP for Voges-Proskauer, carbohydrate fermentation test (LAC=Lactose, MAN=Manose; MAL=Maltose; SAC=Saccharose); and IND for Indole Test are the standard biochemical tests.

Antimicrobial susceptibility testing (AST)

The sensitivity of drugs to bacterial isolates was evaluated using the Kirby-Bauer disc diffusion test [17]. By evaluating the diameter of the

inhibition zone, this test can assess the efficacy of antibiotics that are either already resistant or are still sensitive. This testing method is based on the diffusion concept using antibiotic paper disks. Three times were tested during this experiment. By comparing the diameter of the inhibition zone with the standard diameter of the resistance zone created [14], it was possible to determine how resistant the tested bacteria were to cefixime and tetracycline. Table 1 shows the value for the resistance level category.

Table 1: Categories of antibiotics inhibition zone diameter based on CLSI

Categories	Tetracycline (mm)	Cefixime (mm)	Levofloxacin (mm)
Resistant	≤11	≤17	≤18
Intermediates	12-14	18-20	19-27
Sensitives	≥15	≥21	≥28

RESULTS

Biochemical conventional characterization

643 bacteria were successfully isolated and identified from patient samples who had been diagnosed with acute respiratory tract infections. Bacterial isolates were collected from patients whose cases of respiratory tract infections had been verified by a clinician. According to statistical analysis, the major bacterial genera that made up the isolates

were Staphylococcus (35.5%), Streptococcus (28.5%), Bordetella (15%), Haemophilus (11.5%), and Corynebacterium (9.5%).

Using biochemical characterization, 643 stocks of bacterial isolates classified as Gram-negative, Gram-positive, bacilli (rod-shaped), coccoid (rod-shaped), and coccobacilli were identified. Results of the conventional biochemical tests on bacteria indicated five different bacterial genus: Bordetella, Corynebacterium, Staphylococcus, Streptococcus, and Haemophilus (table 2, fig. 1).

Table 2: Results of biochemical and morphology cell identification

Grouping	Structure	Gram	Genus	Isolates	Biochemical test
1	Round-shaped	Positive	Staphylococcus	228	CT, MR, VP, UR, SC, LAC, MAN, MAL
2	Coccus-capsulated	Positive	Streptococcus	182	LAC, MAL
3	Coccobacillus-capsulated	Negative	Bordetella	95	OX, CT,UR
4	Coccobacilli	Negative	Haemophilus	77	CT, OX, MAL
5	Bacilli-rod shaped	Positive	Corynebacterium	61	MR, CT, TSIA, LAC, MAN, MAL

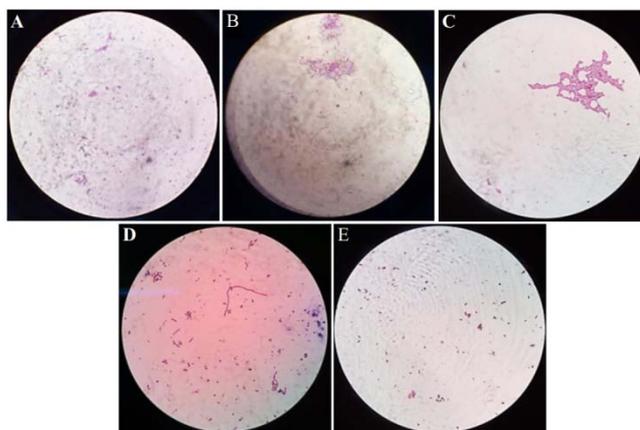


Fig. 1: Gram stain of the bacterial group: (A). Staphylococcus, (B). Streptococcus, (C). Bordetella, (D). Haemophilus, (E). Corynebacterium

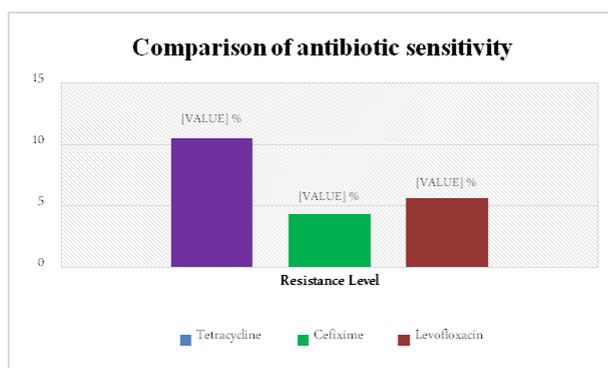


Fig. 2: Test of antibiotics resistance against Haemophilus influenzae

Antimicrobial susceptibility testing (AST)

The primary objective of our study was to determine the incidence of HI bacterial resistance to tetracycline, cefixime, and levofloxacin. The samples were taken from patients who were reported to have respiratory tract illnesses at a medical facility in the urban area of Tasikmalaya, Indonesia.

Our research examined at the degree of antibiotic resistance against bacterial isolates that were positively identified as HI bacteria. The test findings can be used as a guide in selecting the most effective medications to treat infections caused on by HI bacteria. Tetracycline 2-8 µg/ml, cefixime 0.5-2 µg/ml, and levofloxacin 10 µg/ml were the antibiotic disc concentrations utilized in accordance with CLSI recommendations. The susceptibility of categories can be grouped into resistant and non-resistant. The Comparison of Antibiotic Sensitivity is shown in fig. 2.

DISCUSSION

643 bacterial isolates were identified based on biochemical tests and 77 bacterial isolates showed positive results for HI. The oxidase test, catalase test, and carbohydrate (maltose) fermentation assays are biochemical procedures to precisely detect HI. A test for cytochrome oxidase can be used to identify its presence, whereby organisms with cytochrome C as part of their respiratory chain can convert the Kovac oxidase substrate, tetramethyl-p-phenylenediamine dihydrochloride, to a purple molecule [4]. In order to identify HI, this test is important. Catalase, an enzyme that catalyzes the release of oxygen from hydrogen peroxide, is shown to be present in this test (H₂O₂). It is employed to distinguish between bacteria that generate the catalase enzyme. This test makes HI quickly identifiable. A popular technique for identifying microorganisms is based on their capacity to synthesize organic compounds through the metabolism of specific carbohydrates and related substances. Depending on an organism's capacity to ferment carbohydrates added to the basal medium, different fermentation media are employed to separate the organisms. Maltose fermentation was successful with HI. Performing this test is simple, and the findings are obvious.

The widespread use of major respiratory infections that exhibit high rates of antimicrobial resistance has raised substantial questions about the selection of an effective antimicrobial drug for the combination therapy of RTIs. Amoxicillin-clavulanate and oral cephalosporins have been utilized often in Indonesian private-sector hospitals for the management of outpatients with RTIs due to the high prevalence of beta-lactamase in HI.

The study of HI resistance to tetracycline antibiotics showed a relatively low resistance value of 10.5%, when compared to the results of the study in Lebanon (46.7%). The results of the evaluation of HI resistance to cefixime were also relatively low at 4.3%, when compared to the research reported in Iran at 42%. Furthermore, a study in Taiwan regarding the antibiotic resistance of levofloxacin against HI bacteria isolated from the respiratory tract showed a result of 9.2%, which was still higher when compared to the present study, which was 5.6% [8, 17, 18]. This means that the use of tetracycline, cefixime, and levofloxacin for the treatment of HI infection is still reliable. Research concerned with HI resistance in Indonesia is very rare; therefore, this information is important because it can be a guide for the selection of appropriate antibiotics in treating HI infections. The level of AB resistance obtained can provide a reference for health practitioners, especially doctors in prescribing antibiotics. Synergistic coordination between the city health office and health practitioners can be improved in continuously improving patient compliance in taking antibiotics.

In this study, the highest resistance was demonstrated by tetracycline, compared to cefixime and levofloxacin. The resistance mechanism can cause the bacterial cell to be destroyed by adhering to the 30S subunit of the bacterial ribosome and blocking tRNA from binding to either the A or P sites [19, 20]. The tet(B) gene, which is typically found on conjugative plasmids, encodes an efflux mechanism that contributes to tetracycline resistance in HI [21].

Furthermore, resistance to levofloxacin has been reported in several countries and the main mechanism has been investigated [22, 23].

The main resistance occurs by the mechanism Amino acid alterations in the topoisomerase II and I genes quinolone resistance-determining region (QRDR) are the main cause of fluoroquinolone resistance in HI. Although it hasn't been documented in HI, mutations that cause permeability abnormalities and the overexpression of efflux pumps can likewise impair quinolone susceptibility [24].

Similarly, it has been reported that cases of antibiotic resistance against cephalosporins occur in a number of European countries. Resistance mechanisms have been identified and are related to the TEM-1 and ROB-1 varieties of plasmid-mediated β-lactamases [25, 26]. Penicillin-binding protein 3 (PBP3) alteration, which results in decreased affinity to penicillins and cephalosporins, is the most significant β-lactam resistance mechanism in β-lactamase-negative ampicillin-resistant isolates (BLNAR). This is because ftsI gene mutations cause amino acid substitutions in the transpeptidase domain of PBP3 [27, 28].

Cases of the high prevalence of bacteria resistant to some antibiotics, caused by overuse of antibiotics and the outcome of patient non-compliance with taking antibiotics, occurred in Taiwan [29-31]. Medical staff members, especially doctors and pharmacists, conduct extensive outreach initiatives to assist patients in taking their medicines as prescribed. Coordination between medical actors and health policymakers has implications for monitoring the use of antibiotics properly and encouraging public awareness of antibiotic adherence. The implementation of policies and monitoring of sustainable use of antibiotics in city health centers greatly supports the success of government programs in the regions. Although this study has a relatively large number of bacterial isolates, it has limitations from serotyping data for the isolates. Research in several health centers in cities in Indonesia is needed to determine the resistance profile of HI bacteria more broadly in Indonesia.

Some countries have reported that the vaccines used to treat HI type b (Hib) are ineffective. In comparison to pneumococci, the relative prevalence of non-typeable HI has increased as a result of the use of pediatric pneumococcal conjugated vaccinations [32, 33]. Testing for resistance is indeed required to determine how successful the use of antibiotics is efficient. Furthermore, effective infection management can stop the spread of resistance and minimize HI infection-related mortality [34].

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AUTHORS CONTRIBUTIONS

All the authors have contributed equally.

CONFLICT OF INTERESTS

Declared none

REFERENCES

- Butler DF, Myers AL. Changing epidemiology of *Haemophilus influenzae* in children. *Infect Dis Clin North Am*. 2018;32(1):119-28. doi: 10.1016/j.idc.2017.10.005, PMID 29233576.
- Agrawal A, Murphy TF. *Haemophilus influenzae* infections in the H. influenzae type b conjugate vaccine era. *J Clin Microbiol*. 2011;49(11):3728-32. doi: 10.1128/JCM.05476-11, PMID 21900515.
- Soeters HM, Blain A, Pondo T, Doman B, Farley MM, Harrison LH. Current epidemiology and trends in invasive haemophilus influenzae disease-united states, 2009-2015. *Clin Infect Dis*. 2018;67(6):881-9. doi: 10.1093/cid/ciy187, PMID 29509834.
- Carroll KC, Butel JS, Morse SA. *Jawetz melnick and adelbergs medical microbiology*. 27th ed. McGraw-Hill Professional; 2016. p. 263-6.
- Ladhani S, Neely F, Heath PT, Nazareth B, Roberts R, Slack MP. Recommendations for the prevention of secondary *Haemophilus influenzae* type b (Hib) disease. *J Infect*. 2009;58(1):3-14. doi: 10.1016/j.jinf.2008.10.007, PMID 19152980.

6. Skoczynska A, Kadłubowski M, Empel J, Hryniewicz W. Characteristics of *Haemophilus influenzae* type b responsible for meningitis in Poland from 1997 to 2004. *J Clin Microbiol*. 2005;43(11):5665-9. doi: 10.1128/JCM.43.11.5665-5669.2005, PMID 16272502.
7. World Health Organization. Estimated Hib and pneumococcal deaths for children under 5 y of age; 2008. Available from: http://www.who.int/immunization/monitoring_surveillance/burden/esti_mates/Pneumo_hib/en. [Last accessed on 02 Dec 2022]
8. Tristram S, Jacobs MR, Appelbaum PC. Antimicrobial resistance in *Haemophilus influenzae*. *Clin Microbiol Rev*. 2007;20(2):368-89. doi: 10.1128/CMR.00040-06, PMID 17428889.
9. Murray PR, Rosenthal KS, Pfaller MA. *Medical microbiology*. 8th ed. Elsevier Health Sciences; 2015. p. 243-8.
10. World Health Organization. WHO publishes list of bacteria for which new antibiotics are urgently needed. Geneva, Switzerland: WHO; 2017.
11. Campos J, Chanyangam M, deGroot R, Smith AL, Tenover FC, Reig R. Genetic relatedness of antibiotic resistance determinants in multiply resistant *Haemophilus influenzae*. *J Infect Dis*. 1989;160(5):810-7. doi: 10.1093/infdis/160.5.810, PMID 2809256.
12. Dimopoulou ID, Kraak WA, Anderson EC, Nichols WW, Slack MP, Crook DW. Molecular epidemiology of unrelated clusters of multiresistant strains of *Haemophilus influenzae*. *J Infect Dis*. 1992;165(6):1069-75. doi: 10.1093/infdis/165.6.1069, PMID 1583325.
13. Levy J, Verhaegen G, De Mol P, Couturier M, Dekegel D, Butzler JP. Molecular characterization of resistance plasmids in epidemiologically unrelated strains of multiresistant *Haemophilus influenzae*. *J Infect Dis*. 1993;168(1):177-87. doi: 10.1093/infdis/168.1.177, PMID 8099940.
14. Bae S, Lee J, Lee J, Kim E, Lee S, Yu J. Antimicrobial resistance in *Haemophilus influenzae* respiratory tract isolates in Korea: results of a nationwide acute respiratory infections surveillance. *Antimicrob Agents Chemother*. 2010;54(1):65-71. doi: 10.1128/AAC.00966-09, PMID 19884366.
15. Vaez H, Sahebkar A, Pourfarzi F, Yousefi Avaryand A, Khademi F. Prevalence of antibiotic resistance of *Haemophilus influenzae* in Iran-a meta-analysis. *Iran J Otorhinolaryngol*. 2019;31(107):349-57. doi: 10.22038/ijorl.2019.34363.2137, PMID 31857979.
16. Karlowsky JA, Thornsberry C, Critchley IA, Jones ME, Evangelista AT, Noel GJ. Susceptibilities to levofloxacin in streptococcus pneumoniae, *Haemophilus influenzae*, and *Moraxella catarrhalis* clinical isolates from children: results from 2000-2001 and 2001-2002 TRUST studies in the United States. *Antimicrob Agents Chemother*. 2003;47(6):1790-7. doi: 10.1128/AAC.47.6.1790-1797.2003, PMID 12760850.
17. Kassaa I, Hamze M, Dabboussi F, Mallat H, Achkar M, Hlais S. Prevalence of type b *Haemophilus influenzae* and antibiotic resistance in 52 clinical isolates in north Lebanon. *East Mediterr Health J*. 2014;19(Suppl 3):S105-10. PMID 24995731.
18. Su PY, Huang AH, Lai CH, Lin HF, Lin TM, Ho CH. Extensively drug-resistant *Haemophilus influenzae* – emergence, epidemiology, risk factors, and regimen. *BMC Microbiol*. 2020;20(1):102. doi: 10.1186/s12866-020-01785-9, PMID 32345232.
19. Chopra I, Roberts M. Tetracycline antibiotics: mode of action, applications, molecular biology, and epidemiology of bacterial resistance. *Microbiol Mol Biol Rev*. 2001;65(2):232-60. doi: 10.1128/MMBR.65.2.232-260.2001, PMID 11381101.
20. Roberts MC. Plasmid-mediated tet m in *Haemophilus ducreyi*. *Antimicrob Agents Chemother*. 1989;33(9):1611-3. doi: 10.1128/AAC.33.9.1611, PMID 2817857.
21. Levy J, Verhaegen G, De Mol P, Couturier M, Dekegel D, Butzler JP. Molecular characterization of resistance plasmids in epidemiologically unrelated strains of multiresistant *Haemophilus influenzae*. *J Infect Dis*. 1993;168(1):177-87. doi: 10.1093/infdis/168.1.177, PMID 8099940.
22. Bootsma HJ, Troelstra A, van Veen-Rutgers A, Mooi FR, de Neeling AJ, Overbeek BP. Isolation and characterization of a ciprofloxacin-resistant isolate of *Haemophilus influenzae* from the Netherlands. *J Antimicrob Chemother*. 1997;39(2):292-3. doi: 10.1093/jac/39.2.292, PMID 9069560.
23. Nazir J, Urban C, Mariano N, Burns J, Tommasulo B, Rosenberg C. Quinolone-resistant *Haemophilus influenzae* in a long-term care facility: clinical and molecular epidemiology. *Clin Infect Dis*. 2004;38(11):1564-9. doi: 10.1086/420820, PMID 15156444.
24. Georgiou M, Munoz R, Roman F, Canton R, Gomez Lus R, Campos J. Ciprofloxacin-resistant *Haemophilus influenzae* strains possess mutations in analogous positions of GyrA and ParC. *Antimicrob Agents Chemother*. 1996;40(7):1741-4. doi: 10.1128/AAC.40.7.1741, PMID 8807076.
25. Medeiros AA, O'Brien TF. Ampicillin-resistant *Haemophilus influenzae* type B possessing a TEM-type beta-lactamase but little permeability barrier to ampicillin. *Lancet*. 1975;1(7909):716-9. doi: 10.1016/s0140-6736(75)91630-x, PMID 47483.
26. Rubin LG, Medeiros AA, Yolken RH, Moxon ER. Ampicillin treatment failure of apparently beta-lactamase-negative *Haemophilus influenzae* type b meningitis due to novel beta-lactamase. *Lancet*. 1981;2(8254):1008-10. doi: 10.1016/s0140-6736(81)91214-9, PMID 6118476.
27. Parr TR Jr, Bryan LE. Mechanism of resistance of an ampicillin-resistant, beta-lactamase-negative clinical isolate of *Haemophilus influenzae* type b to beta-lactam antibiotics. *Antimicrob Agents Chemother*. 1984;25(6):747-53. doi: 10.1128/AAC.25.6.747, PMID 6611136.
28. Ubukata K, Shibasaki Y, Yamamoto K, Chiba N, Hasegawa K, Takeuchi Y. Association of amino acid substitutions in penicillin-binding protein 3 with beta-lactam resistance in beta-lactamase-negative ampicillin-resistant *Haemophilus influenzae*. *Antimicrob Agents Chemother*. 2001;45(6):1693-9. doi: 10.1128/AAC.45.6.1693-1699.2001, PMID 11353613.
29. Huang YT, Liao CH, Chen SY, Hsu HS, Teng LJ, Hsueh PR. Emergence of multidrug-resistant sequence type 45 strains among mecA-positive borderline oxacillin-resistant staphylococcus aureus causing bacteraemia in a medical centre in Taiwan. *Int J Antimicrob Agents*. 2018;52(1):70-5. doi: 10.1016/j.ijantimicag.2018.02.014, PMID 29505885.
30. Hsueh PR, Luh KT. Antimicrobial resistance in *Streptococcus pneumoniae*, Taiwan. *Emerg Infect Dis*. 2002;8(12):1487-91. doi: 10.3201/eid0812.020178, PMID 12498668.
31. Hsueh PR, Liu CY, Luh KT. Current status of antimicrobial resistance in Taiwan. *Emerg Infect Dis*. 2002;8(2):132-7. doi: 10.3201/eid0802.010244, PMID 11897063.
32. World Health Organization. *Haemophilus influenzae* type B (HiB). WHO Fact Sheet. 2005;294. <http://www/who.int/mediacentre/factsheets/fs294/en/index.html>.
33. Peltola H. Worldwide *Haemophilus influenzae* type b disease at the beginning of the 21st century: global analysis of the disease burden 25 years after the use of the polysaccharide vaccine and a decade after the advent of conjugates. *Clin Microbiol Rev*. 2000;13(2):302-17. doi: 10.1128/CMR.13.2.302, PMID 10756001.
34. Hasegawa K, Kobayashi R, Takada E, Ono A, Chiba N, Morozumi M. High prevalence of type b {beta}-lactamase-non-producing ampicillin-resistant *Haemophilus influenzae* in meningitis: the situation in Japan where Hib vaccine has not been introduced. *J Antimicrob Chemother*. 2006;57(6):1077-82. doi: 10.1093/jac/dkl142, PMID 16617062.