Bloodstream Infection at Children in Belarus

Serhiyenka E.N, Romanova O.N, Lazarev A.V and Klyuyko N. L

Belarusian State Medical University, Minsk, Belarus

Children's Infectious Diseases Clinical Hospital, Minsk, Belarus

Background

Bloodstream infections due to bacterial pathogens are a major cause of morbidity and mortality in world. In different countries, most patients are treated empirically based on their clinical symptoms. Hence, up-to date etiological data for major pathogens that cause bloodstream infections can play a positive role in better management of healthcare.

The aim of this study was to identify the bacterial pathogens causing major bloodstream infections in Minsk, Belarus.

Methods

From January 2009 to December 2018, a total of 656 blood samples were collected from hospitalized patients in Children's infectious diseases hospital, Minsk, Belarus. Using a BACT / Alert blood culture machine all the blood samples were processed for culture.

Results

Gram-positive (59.5%) bacteria were predominant throughout the study period. Staphylococci were the most frequently isolated blood-borne bacterial pathogen in this study, accounting for 45.4% of the total isolates. Other frequently isolated pathogens included non-fermenter Gram-negative bacteria (17.7%), bacteria of Enterobacteriacae family (15.2%) and Streptococcus species(11.1%)

Conclusion

This study identified the major bacterial pathogens involved with Bloodstream infections at Children's infectious diseases clinical hospital, Minsk, Belarus. We expect our findings to help healthcare professionals to make informed decisions and provide better care for their patients.

Etiology of bloodstream infection in Belarus

Bloodstream infections are serious problems that require immediate attention and treatment as it can lead to severe disease and death, especially if they are caused by multidrug-resistant bacteria [1, 2, 3]. Depending on the age, severity of infection and other risk factors, the mortality rate for bloodstream infections between 20% and 50% [3, 4]. Fever, as one of the important symptoms of bloodstream infections, is the most common cause of hospitalization. Most patients with febrile fever have self-limiting viral infections, but some may carry a serious bacterial infection that requires timely and adequate antimicrobial therapy [5, 6]. Microbiological examination of blood culture is an effective and reliable method of detection of bacterial and fungal pathogens that have caused a pathological condition. The study of blood culture allows you to identify the pathogen and determine its sensitivity, which helps to establish an accurate diagnosis and prescribe adequate antibiotic therapy. Bacteriological culture to isolate offending pathogen and knowledge about isolate sensitivity pattern remains the pillar of definitive bloodstream infection diagnosis and management. However, blood culture is time-consuming and takes at least 2 to 5 days until the identification of organism one key determinant in the ultimate outcome of a patient with sepsis is an institution of early empirical and appropriate antimicrobial therapy [7, 8].

The aim of this study was to determine the etiological structure of pathogens isolated from blood cultures of febrile pediatric patients in order to update the subsequent approaches to empirical therapy and compare our data with current trends worldwide.

Material And Methods

This study was conducted at Children's infectious diseases hospital (CIDH) in Minsk, Belarus for active treatment with 620 beds, average 25.000 admissions annually and serving as a tertiary center for the whole country. This cross-sectional study was conducted at CIDH from 1st January 2009 to 31st December 2018. Children of both genders who are between the age of one month to 18 years admitted to the pediatric ward with recorded temperature of > 380C and with a History of fever that lasted more than two days and whose blood culture was sent. A total 656 blood cultures during 2009-2018 were tested. The patient's blood cultures were performed in microbiology laboratory according to standard guidelines at hospital. First cultures on admission were taken to avoid confounding with hospital-acquired the infection. The primary researcher was following up on the society. The frequency of organisms grown in the culture was documented. The study omitted all repeated isolates from any given individual.

Both specimens were collected using aseptic technique only in the presence of clinical indications according to the principles of good clinical practice. For aerobic and anaerobic cultivation the volume of blood taken (18-20 ml) was distributed equally in two sets. The cultivation was performed through BacT/ALERT 3D according to the instructions of manufacturer. Gram stained the positive cultures, and subcultivated them using conventional methods. The identification of the isolated pathogens was performed by VITEK 2 Compact (bioMerieux, France).

3rd International Conference on Alzheimers, Dementia and Related Neurodegenerative Diseases
October 12-13, 2020 | Vienna, Austria

2020 | Volume 3, Issue 2

Results

Gram-positive bacteria (59.5%, n=390) were predominant throughout the study period; gram-negative bacteria were isolated in 33.8% (n=222) cases and fungus – in 6.7% (n=44). Figure 1 shows the structure of causative pathogens of bloodstream infections over the years. During the analyzed period, the predominance of gram-positive microorganisms (from 51.9% to 68.9%) in the structure of bacteremia remains; gram-negative bacteria were isolated from 24.4% (2011) to 39.6% (2016), fungi – from 2.2% (2013) to 14.7% (2010).

The structure of fungemia (n=44) was dominated by Candida parapsilosis – 29 cases (65.9%), also isolated C. albicans, C. glabrata and fungi of the genus Torulopsis (figure 2). According to the literature data the share of fungemia in the structure of bloodstream infections accounts for up to 20%, and in most studies the predominant species were C. albicans (up to 50-60%) and C. parapsilosis (up to 20%) [9, 10]. Our work revealed the dominance of C. parsapsilosis (65.9%) in the structure of fungemia.

The microbiological landscape of bloodstream infections is table 1. Staphylococci were the most frequently isolated blood-borne bacterial pathogen in this study, accounting for 45.4% of the total isolates. Other frequently isolated pathogens included non-fermenter Gram-negative bacteria (17.7%), bacteria of Enterobacteriacae family (15.2%) and Streptococcus species (11.1%).

Among the 390 isolates of Gram-positive bacteria, the most predominant organisms were Staphylococci spp. accounting up to 278 (71.3%) isolates (CNS was the leading type of Staphylococci (n=234; 60%). Among Staphylococci (n=278) S. epidermidis was dominated – 181 isolates (65.1%). S. aureus was isolated in 15.5% cases among Staphylococci spp. The spectrum of streptococci spp. (n=68) was as follows: Str. viridans (42.7%), Str. pneumonia (27.9%), Str. agalactiae (19.1%) и Str. pyogenes (10.3%). Other isolated Gram-positive pathogens included Enterococci (n=35; 9%) moreover, Enterococcus faecalis and Enterococcus faecium (40% and 37.1% respectively) were isolated with almost the same frequency and Corynebacterium spp. (n=8; 2%). Our findings are fully consistent with current studies from other countries, according to which the most common pathogens of bloodstream infections are coagulase-negative staphylococci (especially epidermal) [2, 3, 11].

Most of the Gram negative isolates in our series were non-fermenter Gram-negative bacteria (n=108; 17.7% of all isolated strains). Among them were dominated Acinetobacter – 50 cases (46.3%, incl. Ac. baumannii – 26 (24.1%); Pseudomonas – 21 cases (19.45%, incl. Ps. aeruginosa – 13 (12.05%), Achromobacter – 13 cases (12.05%) и Stenotrophomonas maltophilia – 9 cases (8.3%). The following gram-negative non-fermenting bacteria were also isolated from the blood: Agrobacterium tumefaciens, Burkholderia spp. (incl. cepacia), Flavobacterium indologenes, Flavobacterium meningosepticum, Ochrobactrum anthropic, Sphingomonas paucimobilis, Sphingobacterium spiritivorum – in 15 cases (13.9%).

The spectrum of gram-negative bacteria of Enterobacteriacae family (n=93) was diverse: Escherichia – 9 cases (9.7%, incl. E. coli 8 cases (8.6%), Salmonella – 6 (6.5%), Shigella – 24 (25.8%), Proteus mirabilis – 1 (1.05%), Providencia stuartii – 1 (1.05%), Serratia – 13 (14%), Klebsiella – 26 (28%, incl. Kl. pneumoniae 22 cases (23.7%), Enterobacter – 11 (11.8%, incl. Enterobacter cloacae – 7 (7.5%) and other – 2 (2.1%).

Table 2 shows the structure of causative pathogens of bloodstream infections in different years. Gram-positive bacteria (from 51.9% to 68.9%) dominated in the structure of bloodstream infections in 2009-2018 due to coagulase-negative staphylococci. The structure of gram-negative flora did not have any regularity: in years (2012-2016) gram-negative non-fermenting bacteria prevailed and in other years - bacteria of Enterobacteriacae family.

Discussion

The empiric therapy of severe infections should be based on up to-date reports of the etiological structure at institutional and national level [12, 13, 14, 15]. In this retrospective study, we aimed to identify the most prevalent pathogenic organisms involved in bloodstream infections over a ten-year period (2009–2018) in patients in Minsk, Belarus.

The analysis of the microorganisms isolated from the blood of patients with bloodstream infections showed:

Staphylococci (45.4%), non-fermentative Gram-negative bacteria (17.7%) and bacteria of the Enterobacteriacae family (15.2%) were dominated among the identified pathogens of bloodstream infections.

Gram-positive bacteria were predominant throughout the study period (n=390; 63.7% from 51.9% to 68.9%); gram-negative bacteria were isolated in 36.3% (from 24.4% to 39.6%). Among the isolates of Gram-positive bacteria, the most predominant organisms were coagulase-negative staphylococci (n=234; 60%), followed by St. aureus (n=43; 11%), Enterococci (n=35; 9%), Str. viridans (n=29; 7.4%) and Str. pneumonia (n=19; 4.9%).

Among gram-negative bacteria (n=222) were leading non-fermentative bacteria (n=108; 48.6%). Pseudomonas species and Acinetobacter species were the two major non-fermenter bacteria isolated between 2009 and 2018. The following gram-negative non-fermenting bacteria were also isolated from the blood: Agrobacterium tumefaciens, Burkholderia spp. (incl. cepacia), Flavobacterium indologenes, Flavobacterium meningosepticum, Ochrobactrum anthropic, Sphingomonas paucimobilis, Sphingobacterium spiritivorum (13.9%).

Our study showed Klebsiella spp. (28%) and Shigella spp. (25.8%) as leading pathogens of bacteremia caused by gram-negative bacteria of Enterobacteriacae family (n=93).

Blood cultures are vital for recognizing pathogens causing severe infections and in leading appropriate antibiotic therapy. Furthermore, they remain the standard method for identifying bacteremia in the assessment of sick patients inappropriately; blood culture contamination is a common event and may lead to confusion regarding the significance of a positive blood culture.

3rd International Conference on Alzheimers, Dementia and Related Neurodegenerative Diseases
October 12-13, 2020 | Vienna, Austria

2020 | Volume 3, Issue 2

References

1. Ahmed D, Nahid MA, Sami AB, et al. (2017). Bacterial etiology of bloodstream infections and antimicrobial resistance in Dhaka, Bangladesh, 2005–2014. Antimicrobial resistance and infection control. 6(2), doi.org/10.1186/s13756-016-0162-z.

2. Damin Si, Runnegar N, Marquess J. (2016). Characterising health care-associated bloodstream infections in public hospitals in Queensland, 2008–2012. The medical journal of Australia. 204(7), 276e1—276e7.

3. Deen J, Seidlein L, Andersen F, et al. (2012). Community-acquired bacterial blood stream infections in developing countries in south and Southeast Asia: a systematic review. Lancet infectious diseases. 12, 480-487.

4. Bhandari P, Manandhar S, Shrestha B, Dulal N. (2016). Etiology of bloodstream infection and antibiotic susceptibility pattern of the isolates. Asian journal of medical sciences. 7(2), 71-75.

5. Tufail S, Tikmani S, Ali A, et al. (2016). Frequency and etiology of community-acquired bloodstream infection in hospitalized febrile children. Journal of medical diagnostic methods. 5(3), doi.org/10.4172/2168-9784.1000217.

6. Kaur A, Singh V. (2014). Bacterial isolates and their antibiotic sensitivity pattern in clinically suspected case of fever of unknown origin. Science. 16, 105–109.

7. Gergova I, Popivanov G, Dimov V. (2017). Etiological structure and in vitro susceptibility to antimicrobial agents from blood cultures in Bulgarian multiprofile hospital, 2015-2016. Med Microbiol Rep. Available at: https://www.scitechnol.com/peer-review.Accessed March 26, 2019.

8. Laupland KB, Church DL. (2014). Population-based epidemiology and microbiology community-onset bloodstream infections. Clinical microbiology reviews. 27(4), 647–664.

9. Laupland K. (2013). Incidence of bloodstream infections: a review of population-based studies. Clinical microbiological infections. 19, 492-500.

10. Goto M, Al-Hasan M. (2013). Overall burden of bloodstream infection and

bloodstream infection in North America and Europe. Clinical microbiological infections. 19, 501-509.

11. Zhu Q, Yue Y, Zhu L. (2018). Epidemiology and microbiology of Gram-positive bloodstream infections in a tertiary-care hospital in Beijing, China: a 6-year retrospective study. Antimicrobial resistance and infection control. 7(107), doi.org/10.1186/s13756-018-0398.

12. Scerbo MH, Kaplan HB, Dua A. (2016). Beyond blood culture and Gram stain analysis: A review of molecular techniques for the early detection of bacteremia in surgical patients. Surgical infections. 17, 294-302.

13. Basseti M, Righi E. (2015). Development of novel antimicrobial drugs to combat multiple resistant organisms. Langenbeck's archives of surgery. 400, 153-165.

14. Bassetti M, Righi E, Carnelutti A. (2016). Bloodstream infections in the intensive care unit. Virulence. 7(3), 267–279.

15. Bono VD, Giacobbe DR. (2016). Bloodstream infections in internal medicine. Virulence. 7(3), 353–365.

16. Kaur A, Singh V. Bacterial isolates and their antibiotic sensitivity pattern in clinically suspected case of fever of unknown origin. K Science. 2014;16:105

3rd International Conference on Alzheimers, Dementia and Related Neurodegenerative Diseases
October 12-13, 2020 | Vienna, Austria

2020 | Volume 3, Issue 2