473. Impact of Adjunctive Clindamycin in Invasive β-Hemolytic Streptococcal Infections: A Propensity Score-matched Analysis of 1956 β-lactam Treated Patients from 118 US Hospitals

Background. Invasive β-hemolytic streptococcal (iBHS) disease encompasses toxic shock syndrome (TSS) and Staphylococcus scalded skin syndrome (SSSS). Invasive disease is caused by group A streptococci (GAS) bacteremia. Treatment of toxin-mediated diseases such as TSS and SSSS with clindamycin has been advocated in vitro and animal studies. Clinical studies, limited to single-center series published over the last 4 decades, have yielded mixed results. Further, challenges remain in identifying clinically relevant subgroups of patients with iBHS infection who may benefit from clindamycin.

Methods. We compared pathogen susceptibilities, clinical features, and outcomes of patients with toxin-mediated diseases to evaluate the role of adjunctive clindamycin in a contemporary setting.

Results. Of 1,956 inpatients with iBHS infection treated with β-lactams at 118 US hospitals, 32 cases of TSS, 38 cases of SSSS, and 1 case of bullous impetigo were identified. Audioclysmic clindamycin was resistant in 40% of cases.

Conclusion. Adjunctive clindamycin suppresses iBHS in vivo, reduces disease severity, and appears safe. Future studies are needed to identify iBHS subgroups who would most benefit from clindamycin.

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proportion matched pairs of 2:1 match and subgroup analysis on propensity matched pairs of (1) proven bHKS alone (2) probable bHKS alone (3) ICU admission (within 24h of culture sampling) (4) patients receiving vasopressor therapy (within 24h of culture sampling) (5) Group A bHKS alone (6) Non Group A bHKS alone. There was no statistically significant difference in the ORs for in-hospital mortality between clindamycin and propensity-matched non-clindamycin cases in the primary analysis (2) as well as all sensitivity and subgroup (1) analyses.

Figure 3: SOFA Score Trajectory by Survival Status

Abbreviations: B: Non-Clindamycin cases, BC: Clindamycin Cases

Conclusion. Documented IV drug abuse resulted in a significant increase in the length of stay in hospitalized adults with SSTIs requiring IV antibiotics. Exposure to combination therapy and anti-psuedomonal agents did not differ between the groups as would be expected. In the future stewardship initiatives are needed to increase adherence to SSTI guideline recommendations for empiric therapy.

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547. High Rate of Extended-Spectrum β-Lactamase Producing Gram-Negative Infections and Associated Mortality in Ethiopia: A Systematic Review and Meta-Analysis
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Background. Extended-spectrum β-lactamase (ESBL)-producing Gram-negative bacteria is associated with high mortality due to ineffective antibiotic treatment. To date, regular surveillance of multidrug-resistant (MDR) pathogens is lacking in Ethiopia. For this report, published data regarding ESBL-producing bacteria in different regions of Ethiopia were reviewed systemically. To our knowledge, this is the first systematic review from Ethiopia on ESBL-producing infections and associated mortality in the country.

Methods. A literature search was conducted in PubMed, PubMed Central, and Google Scholar from January 1, 1990 to April 28, 2019, using the following search terms: “ESBL-producing Enterobacteriaceae,” “Gram-negative bacterium infection associated mortality,” and “Ethiopia.” Patient mortality associated with infections by ESBL-producing Gram-negative bacteria was recorded.

Results. Fourteen publications qualified for review. Totally, 1,782 Gram-negative bacteria isolated from 5,191 clinical samples were included. The phenotypic pooled rate of ESBL-producing Gram-negatives was estimated to be 52.90% (CI: 50.55% – 55.44%). Among different species, ESBL rates were 65.7% (262/399) Klebsiella spp., 60.6% (203/335) Enterobacter spp., 47.8% (22/46) Citrobacter spp., 47.0% (383/815) (E. coli, 45.7% (85/186) for Salmonella spp., 27.4% (15/54) for Proteus spp., 16.7% (24/24) for P. aeruginosa, 14.3% (3/21) for Acinetobacter spp., and 40.5% (15/37) for others, respectively. ESBL genes were confirmed in three studies. blaCTX-M-1 and blaTEM were the predominately detected genes. Two studies reported mortality associated with Gram-negative infections and 86% (12/14) of the patients infected with ESBL-producing bacteria died.

Conclusion. In this meta-analysis, the pooled phenotypic prevalence of ESBL-producing pathogens is considerably high. Also, the mortality due to ESBL-producing MDRO is high but data are scarce. This highlights the need for establishing and upgrading of clinical microbiology laboratories in the country for routine antibiotic susceptibility testing. The capacity to detect ESBL genes is desirable for continuous surveillance of MDRO.

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546. Risk Factors of Community-Onset Extended-Spectrum β-Lactamase-Producing Klebsiella pneumoniae Bacteremia in South Korea Using National Health Insurance Claims Data
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Background. Antibiotic resistance is a significant threat to public health not only in healthcare setting but also in community because antimicrobial-resistant infections can be transmitted in community. Although it is essential to know whether there are particular reasons that caused antibiotic-resistant infection in community, there is lack of evidence regarding risk factors for community-onset extended-spectrum β-lactamase-producing Klebsiella pneumoniae bloodstream infection (ESBL KP BSI) in South Korea. In the present study, we aimed to reveal risk factors for community-onset ESBL-KP BSI.

Methods. From May 2016 to April 2017, patients with community-onset KP BSI (n = 408) from six sentinel hospitals in South Korea were included. The hospitals are located in different districts throughout South Korea, and a total of 5,194 beds, ranged from 715 to 1,050 beds per hospital. Admission history and previous usage of antibiotics and medical devices before bacteremia were acquired from National Health Insurance claims data. Risk factors of ESBL-KP BSI were analyzed with a multivariable logistic regression model. PCR and sequencing for the identification of genes encoding ESBLs, and multilocus sequence typing were performed.