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Session: Bacterial Infections

Date: Friday, June 15, 2012

Time: 12:45-14:15

Room: Poster & Exhibition Area

Extraintestinal non-typhoidal Salmonella infection in infants and children at Siriraj hospital, Thailand, 2006-2011

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Background: Non-typhoidal Salmonella (NTS) has been recognized as an important public health problem worldwide. However, there is limited data regarding extraintestinal NTS infections in children in Thailand in the past decade.

The objective was to describe clinical presentations, antimicrobial susceptibility and outcome of children with extraintestinal NTS infections.

Methods: Children less than 15 years of age diagnosed with extra-intestinal NTS infection at Siriraj Hospital, Bangkok, Thailand during July 1, 2006 and June 30, 2011 were retrospectively reviewed for clinical and microbiological data. Multidrug resistant (MDR) NTS was defined as those isolates that were resistant to 3 different classes of antimicrobial agents.

Results: There were 80 children enrolled, with a median age of 12 months (11 days-13.9 years). Forty children (50.0%) were younger than 1 year of age, and 38 (47.5%) children had underlying conditions in which majority were immunosuppressed. The most common clinical presentation was bacteremia (83.7%), followed by skin/soft tissue and internal organ abscesses (6.2%), septic arthritis (3.8%), urinary tract infection (3.8%), and meningitis (2.5%). Forty-three (53.8%) children had concomitant diarrhea. Majority (72.5%) of children with extraintestinal NTS infection had normal or low WBC count and 22 (27.5%) children had thrombocytopenia. Serogroup C (36 cases, 45%) was the most common NTS isolated. Resistance to ampicillin, co-trimoxazole, chloramphenicol, 3rd generation cephalosporin, and ciprofloxacin was found in 76.3%, 25.0%, 50.0%, 34.0% and 4.0%, respectively and 22 (27.5%) isolates were MDR. Two (2.5%) patients developed complications (meningitis with subdural empyema and septicemia with septic shock). Two (2.5%) patients developed recurrent NTS bacteremia. Mortality rates among all and immunocompromised children with extraintestinal NTS infection were 2.5%, and 9.0%, respectively.

Conclusion: Extraintestinal NTS infections caused significant morbidity and mortality in children, particularly among those with immunosuppressed condition. Bacteremia was the most common clinical presentation. High rate of antimicrobial resistance is alarming. More than one-third of extraintestinal NTS isolates were resistant to 3rd generation cephalosporin, and 27.5% were MDR. There was low resistant rate to ciprofloxacin.

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Multi locus sequence type comparison of invasive and commensal Haemophilus influenzae isolates from Delhi

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Background: The most virulent strain is H. influenzae Type b (Hib) responsible for 95% of bloodstream and meningeal Haemophilus infections in children. Hib also constitutes a major portion of nasopharyngeal commensal flora in otherwise healthy individuals. This study was undertaken to analyze if there exist any significant genetic differences between invasive and commensal H. influenzae isolates.

Methods: Isolates causing invasive disease were cultured from sterile body fluid. Commensal isolates were obtained from the nasopharynx of healthy schoolgoing children aged 5-14 years. Isolates with type b serotype from both invasive and commensal isolates were detected through capB polymerase chain reaction and slide agglutination serotyping. In total 15 invasive and 13 commensal isolates were characterized through multi locus sequence typing.

Results: Serotyping revealed that all 15 invasive isolates in this study were of Type b. Seven out of 13 commensal isolates were of serotype b and 6/13 were non-Type b. MLST results showed presence of two sequence types (STs) previously described and five new STs among the Indian invasive H. influenzae isolates tested. Amongst the 13 nasopharyngeal isolates tested through MLST, nine distinct STs were discovered each of which were novel.

Conclusion: In our study of MLST involving Hib of invasive and commensal origin, it was observed that invasive Hib did not demonstrate much variation in their genome. In contrast, genetic diversity among commensal Hib was much more common implying existence of two distinct evolutionary lineages among invasive and commensal Hib.

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