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Background. This study investigated the genetic structure of Streptococcus pneumoniae isolates from invasive pneumococcal disease (IPD) in Korean children after national immunization program (NIP) of extended-valency pneumococcal conjugate vaccines (PCVs) in Korea from 2014 to 2017.

Methods. Invasive isolates were collected from 23 hospitals throughout Korea. IPD cases were identified by isolating pneumococci from normally sterile sites. Each isolate was analyzed using standard microbiological techniques, Quellung reaction, multilocus sequence typing, and antimicrobial susceptibility testing. EBURST v3 soft ware was used to estimate the relationships among the isolates and to assign the strains to a clonal complex (CC).

Results. Ninety-two pneumococcal isolates were analyzed. The source of isolates were blood (77), cerebrospinal fluid (7), pleural fluid (2), joint fluid (2), deep tissue abscess (2), and peritoneal fluid (2). A total of 38 STs and 17 singletons were assigned. Ten clonal complexes were identified: CC320, CC81, CC166, CC439, CC358, CC3880, CC3280, CC30935, CC3180, and CC310. New STs were assigned: ST13352, ST13353, ST13354, and ST13602. The serotypes were mostly non-vaccine type (NVTs) (82.6%). The most prevalent STs were ST11189 (17.4%, n = 16, all serotype 10A), ST6945 (10.9%, n = 10, all serotype 12F), ST166 (9.8%, n = 9, serotype 11A [22.2%, n = 2], 13 [22.2%, n = 2], 15B/C [22.2%, n = 2], and 23A [33.3%, n = 3]), and ST10 (10%, n = 5, serotype 19A). Major CCs identified were CC166 (11.9%), CC320 (10.9%), and CC81 (10.9%). Serotypes constituting CC81 and CC166 were all NVTs except 6A (n = 1) and 23F (n = 1) in CC81, CC320 consisted of 19A (n = 9) and 19F (n = 1). The relative proportion of NVTs was 61.3% in major CCs. All major CCs showed multi-drug resistance. No NVTs were identified in group D or C.

Conclusion. The introduction of extended-valency PCVs has resulted in the change of genetic structure of isolates from IPD of Korean children. In particular, two common CCs (CC81 and CC166), which previously contained vaccine types, were replaced with the NVTs while CC320 remains unchanged.

Disclosures. All authors: No reported disclosures.

2339. Perianal Infections in Children With Acute Myeloid Leukemia: A Report From the Canadian Infection in Acute Myeloid Leukemia Research Group

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Background. Little is known about the epidemiology of perianal infection in pediatric cancer patients. Objectives were to describe the characteristics, treatment and outcome of perianal infection and describe features of those with and without definite CCs (CC81 and CC166), which previously contained vaccine types, were assigned. Ten clonal complexes were identified: CC320, CC81, CC166, CC439, CC81, CC166, CC358, CC3880, CC3280, CC30935, CC3180, and CC310. New STs were assigned: ST13352, ST13353, ST13354, and ST13602. The serotypes were mostly non-vaccine type (NVTs) (82.6%). The most prevalent STs were ST11189 (17.4%, n = 16, all serotype 10A), ST6945 (10.9%, n = 10, all serotype 12F), ST166 (9.8%, n = 9, serotype 11A [22.2%, n = 2], 13 [22.2%, n = 2], 15B/C [22.2%, n = 2], and 23A [33.3%, n = 3]), and ST10 (10%, n = 5, serotype 19A). Major CCs identified were CC166 (11.9%), CC320 (10.9%), and CC81 (10.9%). Serotypes constituting CC81 and CC166 were all NVTs except 6A (n = 1) and 23F (n = 1) in CC81, CC320 consisted of 19A (n = 9) and 19F (n = 1). The relative proportion of NVTs was 61.3% in major CCs. All major CCs showed multi-drug resistance. No NVTs were identified in group D or C.

Conclusion. The introduction of extended-valency PCVs has resulted in the change of genetic structure of isolates from IPD of Korean children. In particular, two common CCs (CC81 and CC166), which previously contained vaccine types, were replaced with the NVTs while CC320 remains unchanged.

Disclosures. All authors: No reported disclosures.