investigate molecular patterns of GBS strains from mothers and neonates hospitalized in Maayaney Hayeshua.

Methods. During 2017, GBS isolates were collected from asymptomatic pregnant women (280/1,074), neonates with EOD (n = 7), and intrauterine fetal death remains (IUFD) (n = 7). We serotyped isolates from vaginal carriage (n = 203), EOD (n = 7), IUFD (n = 7) and EOD isolates obtained from the Ministry of Health (n = 11). Multilocus sequence typing (MLST) was performed on isolates from asymptomatic pregnant women (n = 14), EOD (n = 7) and IUFD (n = 7). Antibiotic susceptibilities were determined.

Results. GBS carriage rate was 26.1%. In asymptomatic pregnant women the dominant serotype was VI [84 women (41.3%)], followed by III, IV and V in 32 (15.7%), 23 (11.3%) and 21 (10.3%) women, respectively. The dominant serotype in EOD was III [15/18 (83.3%)] and in IUFD VI [5 (71.4%)]. ST-17 was expressed mainly by serotype III, and was associated with EOD. ST-1, expressed mainly by serotype VI, was associated with IUFD. See Tables 1 and 2 and Figure 1. Resistance to erythromycin and clindamycin was 19.3% and 18.2% while resistance in invasive isolates was 45.5% to both antibiotics.

Conclusion. GBS vaginal colonization rate in an OJC was significantly higher than the reported carriage rate of 21.6% reported in Israeli pregnant women. Serotypes VI was dominant in carriage and in cases of IUFD while EOD was exclusively associated with serotype III. Resistance rates to erythromycin clindamycin were high, particularly in invasive disease. These results advocate routine GBS screening in this population and caution against empirical treatment with macrolides or clindamycin in penicillin-allergic women.

Figure 1. Serotype distribution among GBS isolates

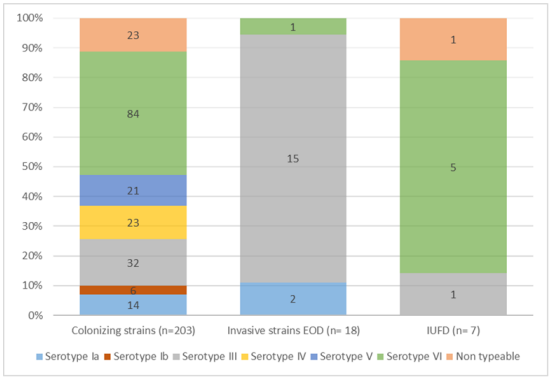

Table 1. Characteristics of GBS isolates according to ST and serotype

ST	Allelic profile*	No. of carried isolates (%)	No. of invasive isolates (%)	No. of invasive IUFD (%)	Total	Serotype (no. of isolates)
1	1,1,2,1,1,2,2	8	0	4	12	VI (12)
17	2,1,1,2,1,1,1	4	7	1	12	III (11),VI(1)
6	9,1,2,1,3,2,2	0	0	1	1	Ib (1)
19	1,1,3,2,2,2,2	1	0	0	1	III (1)
196	1,1,3,1,1,12,2	0	0	1	1	VI (1)
459	1,1,3,1,41,12	1	0	0	1	IV (1)
Total		14	7	7	28	

Correlation between GBS serotypes and ST types of GBS isolates from asymptomatic women, neonates with EOD and IUFD remains. ST types were determined by MLST.

Table 2. Correlation between ST types and clinical state

		EOD	IUFD	Asymptomatic carriage	P value
ST type	ST1	0.0% (0)	57.1% (4)	60.0% (9)	<0.05
	All other ST types	100.0% (7)	42.9% (3)	40.0% (6)	
ST type	ST17	100.0% (7)	14.3% (1)	26.7% (4)	<0.01
	All other ST types	0.0% (0)	85.7% (6)	73.3% (11)	

Calculations were done using Chi square

Disclosures. **All authors:** No reported disclosures.

242. Comprehensive Pathogen Detection for Pediatric Febrile Neutropenia by Metagenomic Next-Generation Sequencing

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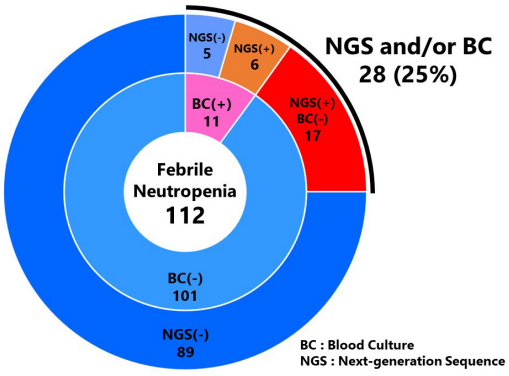
Background. Febrile neutropenia (FN) is a common complication in patients with solid tumors and hematologic malignancies. Identification of the causative microorganisms would contribute to optimization of antimicrobial treatment and thus improve the outcome of FN. However, causative microorganisms are detected in only 10% to 20% of FN patients. Next-generation sequencing (NGS) allows us to comprehensively analyze all microorganisms present in a clinical sample. In this study, we aimed to utilize NGS for the detection of microbial pathogens in infectious diseases and elucidate the infection source in FN.

Methods. FN is defined by two characteristics: (1) neutrophils count < 500/μL, and (2) fever ≥38.0°C. From 2016 to 2018, 112 plasma/serum samples of pediatric FN patients (11 positive blood cultures) were analyzed. Serum samples from 10 neutropenic patients without fever were also analyzed as controls. Shotgun sequencing method was applied for these samples. The metagenomic analyses were performed through the pipeline PATHDET, which has been newly established in our laboratory. Diagnosis based on NGS results was made based on the following criteria: (1) number of reads from all pathogens per million reads (PR) >650, (2) a specific pathogen's reads per million reads (RPM) >200, and (3) diversity index >3.0. The NGS results were compared with those from blood culture.

Results. Sequencing reads of bacteria isolated through blood culture were identified by NGS in all 11 plasma/serum samples leading to the diagnosis of FN. The causative pathogens were diagnosed by NGS using the above criteria in 11 patients. However, the results were consistent with those of blood culture in only 4 samples. Of 101 cases with negative blood culture results, the causative pathogens were detected in 17 cases: *Acinetobacter soli* (2 cases), *Burkholderia cepacian* (1 case), *Klebsiella variicola* (1 case), and *Roseomonas sp.* (1 case) were identified at the species level. In addition, 7 cases (e.g., *Acinetobacter*) were identified at the genus level, and 5 cases (e.g., *Enterobacteriaceae*) were identified at the family level.

Conclusion. Metagenomic NGS technique has great potential for detecting causative pathogens with greater efficiency than the conventional methods.



Disclosures. **All authors:** No reported disclosures.