Conclusion. GBS patients with evidence of ZIKV infection were clinically similar to those without evidence of ZIKV infection, but more likely to have facial weakness and paresthesia during acute neurologic illness and report abnormal tear production at 6 months post neurologic onset. Pathophysiologic investigations should examine potential ZIKV autoimmune response preferential effect of cranial nerves among GBS patients.

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314. Six Months Follow-up of Patients with Guillain–Barré Associated to Zika Virus Infection

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Background. Increasing data has shown the relationship between Zika Virus (ZIKV) and neurological complications. However, there are still uncertainties about the prognosis of these complications. The aim of this study is to show the neurological characteristics of patients six months after a Guillain–Barré episode related to ZIV infection.

Methods. Patients with a Guillain–Barré episode were identified prospectively at five intensive care units in an endemic zone in Colombia (Valledupar, near the Caribbean coast of Colombia). Brighton´s criteria for Guillain–Barré case definition were used to classify the patients. Clinical data from the clinical records was used. Patients with a positive Zika serology were followed after 6 months.

Results. Of 25 patients with a diagnosis of Guillain–Barré, 20 had a serological study for ZIKV and it was positive in 19 patients (95%). Seventy-five percent of the cases were men, the median age was 45 years old and they had a median length of stay of 25 days. 68% had a febrile syndrome in the 7–14 days prior to hospitalization. Median time between fever and neurological symptoms was 9 days. Incapacity to walk was found in 100%, dysphagia in 55%, and respiratory insufficiency in 55%. Patients were treated with immunoglobulin or plasmapheresis. Median time to follow-up was 193 days in 15 patients. Cuadriparesia was found in 44%, difficulty to walk in 31%, unilateral facial palsy in 19%, and bilateral in 6%. Dysphagia or respiratory distress was not found. Eighty-seven percent of the patients were independent for basic and daily activities.

Conclusion. Guillain– Barré syndrome related to ZKV infection is a severe disease with a high grade of disabilty at 6 months after the episode.

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315. Clinical Manifestations, Hematology, and Chemistry Profiles of the Six Most Common Etiologies from an Observational Study of Acute Febrile Illness in Indonesia

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Background. Infectious diseases remain a significant healthcare burden in the developing world. In Indonesia, clinicians often manage and treat patients solely based on clinical presentations since the diagnostic testing capacities of hospitals are limited. Unfortunately, the most common infections in this tropical environment share highly similar manifestations, complicating the identification of etiologies and leading to the misdiagnosis of illness. When pathogen-specific testing is available, generally at top-tier specialist hospitals, the limited range of tests and slow turnaround times may never lead to a definitive diagnosis or improved patient outcomes.

Methods. To identify clinical parameters that can be used for differentiating the most common causes of fever in Indonesia, we evaluated clinical data from 1,486 acute febrile patients enrolled in a multi-site observational cohort study during 2013 to 2016.

Results. From the 66% of subjects with confirmed etiologies, the six most common infections were dengue virus (455), *Salmonella* spp. (124), *Rickettsia* spp. (109), influenza virus (64), *Leptospira* spp. (53), and chikungunya virus (37). The accompanying figure shows the clinical signs and symptoms (A) and hematology and blood chemistry results (B) for the color-coded pathogens. Comparing the profiles of all infected subjects reveals parameters that are uniquely associated with particular pathogens, such as leukopenia with dengue virus.

Conclusion. These observations will assist clinicians in healthcare systems with limited diagnostic testing capacities and may be useful in formulating diagnostic algorithms for Indonesia and other developing countries.

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316. Characteristics of *Streptococcus pneumoniae* Serotype 19A Isolates from Children in the Pre- and Post-Conjugate Vaccine Era

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Background. The aim of the present study was to assess the prevalence and characteristics of *S. pneumoniae serotype* 19A isolates from invasive and non-invasive pneumococcal disease (IPD) in children, before and after the introduction of pneumococcal conjugate vaccines (PCVs) in Greece.

Methods. All *S. pneumoniae* isolates collected between 1986 and 2015 were re-cultured for further testing. Serotyping was performed using the quellung reaction and antibiotic susceptibilities were determined by E-test. The altered *pbp* genes (*pbp2b*, *pbp2x*, and *pbp1a*) conferring resistance to penicillin and the macrolide-resistant genes [mef(A), mef(E), and erm(B)] were detected by polymerase chain reaction (PCR) using specific primers. The sequence types (ST) and clonal complexes were determined by multilocus sequence typing (MLST).

Results. Among 1,875 isolates examined, 210(11.2%) (belonged to serotype 19A. The proportion of serotype 19A isolates increased from 4.6% (47/1018) in the pre-PCV7 years (1986–2005) to 19.6% (88/449) in the post-PCV7 years (2006–2010) and to 18.4% (75/408) in the post PCV-10 and PCV13 years (2011–2015).The resistance frequencies to penicillin, cefotaxime, erythromycin, clindamycin, and tetracycline increased significantly after 2005 as compared with the preceding period (1986–2005) from 8.5% to 31.9%, 2.1% to 20.8%, 10.6% to 65.6%, 4.2% to 47.7% and 19.1% to 46.0%, respectively ($P < 0.01$). Moreover, 94 (57.7%) of 163 isolates after 2005 exhibited multidrug-resistant (MDR) phenotype, whereas only seven (15.9%) of 47 isolates from period 1986–2005 were MDR ($P < 0.001$). All the penicillin non-susceptible isolates examined ($N = 136$), had altered one or more of the *pbp* genes. Of 112 erythromycin-resistant isolates, 22 contained the *mefE* gene, 39 the *ermB* and 51 both the *mefE* and *ermB* genes. MLST analysis of 31 invasive isolates revealed four clonal complexes (CC); CC172 ($n = 11$), CC199 ($n = 8$), CC320 ($n = 5$), and CC276 ($n = 3$), and four isolates belonged to CC2669, CC177, CC81, and CC63. The CC172 and CC199 were present throughout the study period, whereas the CC320 and CC276 appeared after 2009.

Conclusion. *S. pneumoniae* serotype 19A increased significantly after the introduction of PCV7 and a substantial proportion of these isolates exhibited MDR phenotype. The majority of the examined isolates belonged to limited number of CC.

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317. Ceftolozane-Tazobactam Resistance in Multidrug-Resistant *Pseudomonas aeruginosa* Isolates Not Associated with AmpC Activity

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Background. Ceftolozane-tazobactam (CT) is a newly approved cephalosporin/β-lactamase inhibitor combination with excellent *in vitro* activity against multidrug-resistant (MDR) *P. aeruginosa*. Unfortunately, CT-resistance (CT-R) has already been reported. In this work, we evaluate mutational pathways associated with high level of CT-R and assess the role of AmpC in a clinical strain-pair of MDR *P. aeruginosa*.

Methods. A CT susceptible isolate of *P. aeruginosa* (2365) and its CT-R derivatives (2366 and 2367) were recovered from the infected device of a patient before and after treatment with CT. Minimum inhibitory concentrations (MICs) to CT were determined by Etest. Resistance mediated by AmpC hyperproduction was evaluated

using ceftazidime (CAZ) and meropenem (MER) with and without cloxacillin (CLOX) at concentration of 1 mg/ml. In addition, the β-lactamase hydrolysis activity was determined for crude cell lysate of the isolates using a spectrophotometric assay for nitrocefin degradation. Furthermore, whole genome sequencing of the three strains was performed and compared (2365 vs. 2366 and 2367). Reads from each isolate were mapped against the genome of the reference strain PAO1. Variants identified by GATK, SamTools and CLC Genomics Workbench 8.5 were selected and annotated with SnpEff.

Results. Strain 2365 had a CT MIC of 0.75 mg/ml while 2366 and 2367 have MICs > 256 mg/ml. AmpC hyperproduction test was positive only for the susceptible isolate (2365). In concordance, the hydrolysis assay showed a lack of nitrocefin degradation by CT-R 2366 compared with its CT-susceptible isolate 2365. Notably, the three strains (S and R) exhibited a truncated AmpD. Comparison of the resistant derivatives vs. 2365 and 2367 showed a 7 amino acid deletion in the Ω-loop of the β-lactamase AmpC in both resistant derivatives and mutations in genes predicted to encode a hypothetical protein, an ABC transporter ATP-binding protein and a multidrug resistance operon repressor MexR.

Conclusion. Our results suggest that the deletion in the Ω-loop of AmpC in 2366 and 2367 does not contribute to CT-R in these *P. aeruginosa* strains. Further characterization of AmpC and other predicted proteins identified by WGS are needed to determine the mechanism of CT-R.

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

318. Reduced Ertapenem Susceptibility Due to OXA-2 Production in *Klebsiella pneumoniae* ST258

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Background. OXA-2 is a class D β-lactamase which is primarily found in *E. coli* (Ec) and *P. aeruginosa* and confers resistance to penicillins as well as narrow-spectrum cephalosporins. However, recent reports suggest that OXA-2 also possesses carbapenem hydrolyzing activity. We report a case of *K. pneumoniae* that confers reduced susceptibility to ceftazidime and ertapenem due to production of OXA-2.

Methods. *K. pneumoniae* (Kp) strain YDC787 was identified from the BAL culture of an inpatient in December 2016. The strain was initially reported as intermediate to ertapenem. MICs and carbapenemase production were confirmed by Etest and modified Hodge test (MHT) respectively. Ec TOP10 was transformed with purified plasmids followed by selection with ampicillin (TOP10 [pYDC787]), and the carbapenem resistance determinant was cloned into vector pBCSK using partial Sau3AI digestion (TOP10 [pOXA-2]).

Results. Kp YDC787, Ec TOP10 (pYDC787), and Ec TOP10 (pOXA-2) all showed reduced susceptibility to ertapenem and ceftazidime, but not meropenem, imipenem, or cefepime. All isolates were positive for carbapenemase production by MHT. Sanger sequencing of pOXA-2 revealed 2,910-bp partial class 1 integron containing *DaacA4-bla*$_{OXA-2}$*-qacED1-Dsul1*. The presence of *bla*$_{OXA-2}$ was confirmed by PCR in Kp YDC787 and Ec TOP10 (pYDC787).

			MICs (mg/L)				
	MHT	*bla*$_{OXA-2}$	ETP	MEM	IPM	FEP	CAZ
Kp YDC787-3	POS	POS	0.38	0.094	0.38	0.25	4
Ec TOP10 (pYDC787)	POS	POS	0.023	0.032	0.38	0.064	4
Ec TOP10 (pOXA-2)	POS	POS	0.016	0.032	0.38	0.064	4
Ec TOP10	NEG	NEG	0.006	0.023	0.38	0.064	0.25

Conclusion. These findings confirm that OXA-2 functions as carbapenemase and cephalosporinase, significantly reducing susceptibility to ertapenem and ceftazidime, but not to meropenem, imipenem, or cefepime.

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

319. Co-occurrence of NDM-5, OXA-181, and CMY-2 in a Clinical *E. coli* Isolate From a Patient in the United States

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Background. Carbapenem-resistant *Enterobacteriacae* (CRE) are an important public health problem. A mechanism of expansion of the CRE epidemic is transcontinental spread of multidrug-resistant organisms. Here, we present a patient with an intra-abdominal abscess due to *Escherichia coli* with an unusual multidrug resistance phenotype who was admitted to a tertiary hospital in Houston, TX after treatment in a country from the Middle East.

Methods. Identification and antimicrobial susceptibility testing were performed by standard methods. Whole-genome sequencing (WGS) was performed on an Illumina platform, with resistance genes identified by ResFinder 2.1 and plasmids recognized using PlasmidFinder 1.3. ***Results.*** It is confirmed via PCR, S1 pulsed field gel electrophoresis, and Southern blotting. Carbapenemase activity of bacterial lysates was assayed using 50 μM imipenem in the presence of both EDTA and zinc.

Results. The *E. coli* isolate was resistant to all β-lactams, including ceftazidime/avibactam. The organism belonged to ST410 and harbored *bla*$_{NDM-5}$, *bla*$_{OXA-181}$, *bla*$_{CMY-2}$, and *bla*$_{TEM-1B}$. The *bla*$_{OXA-181}$ gene was located on an IncX3 plasmid of ca. 50 Kb in association with the IS*Ecp1* mobile element and the *qnrS21* gene encoding quinolone resistance. The *bla*$_{NDM-5}$ gene was located on an FIA/FIB plasmid of ~100 Kb, in association with ΔIS*Aba125*, and upstream of a putative bleomycin resistance gene, a conserved arrangement among NDM expressing Gram-negative organisms. Cell lysate assays showed decreasing carbapenemase activity with increasing concentrations of EDTA and an increase in activity with the addition of zinc, suggesting the NDM-5 metallo-β-lactamase is largely responsible for the observed carbapenemase activity. Comparison with plasmid sequences available suggested convergence of resistance determinants captured from a wide geographic area.

Conclusion. Plasmid-mediated spread of β-lactamases among *Enterobacteriaceae* is a rapidly evolving threat, with the introduction of NDM-5 and OXA-181 in the United States being a particularly disturbing development. Introduction of multidrug-resistant organisms from areas of high prevalence of resistance may change the landscape of antimicrobial resistance in the United States.

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

320. Characterization of *Enterobacter* and *Citrobacter* spp. Isolates from United States Hospitals by Whole-Genome Sequencing Analysis and Activity of Ceftazidime-Avibactam and Comparator Agents

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Background. *Enterobacter* spp. and *Citrobacter* spp. are common pathogens in a variety of clinical infections. These organisms can overexpress the chromosomal AmpC that encodes resistance to several β-lactams. Additionally, these isolates may carry acquired BL genes. We evaluated the presence of BL and the activity of ceftazidime-avibactam (CAZ-AVI) among 410 isolates collected in US hospitals during 2016.

Methods. In total, 258 *E. cloacae* (ECL), 81 *E. aerogenes*, 70 *C. freundii*, and 1 *C. koseri* displaying MIC values ≥16 μg/ml for CAZ and/or ≥2 μg/ml for cefepime were submitted to WGS, *de novo* assembly and screening for BL genes using an in-house-developed pipeline.

Results. The most common acquired BL gene was *bla*$_{CTX-M}$ (25 isolates, 20 ECL) and included *bla*$_{CTX-M-15}$ (19 isolates) and six other variants. ESBL *bla*$_{SHV}$ (six variants) was noted among 39 isolates and *bla*$_{SHV-12}$ (23 positive results) was the most frequent variant. Other ESBL genes (*bla*$_{OXA-1/30}$ [20 isolates] and *bla*$_{TEM-10}$ [3]) were also noted. Transferrable AmpCs were detected among 8 isolates (5 *bla*$_{DHA-1}$, 2 *bla*$_{FOX-5}$, and 1 *bla*$_{CMY-2}$ in ECL). Carbapenemase-encoding genes detected (19 isolates) included five *bla*$_{KPC-2}$, 11 *bla*$_{KPC-3}$, and one each of *bla*$_{KPC-4}$, *bla*$_{KPC-6}$, and *bla*$_{NDM-1}$. Isolates carrying these genes were five *C. freundii*, one *E. aerogenes*, and 13 ECL. The *bla*$_{KPC-6}$-carrying ECL exhibited meropenem, doripenem, and imipenem MIC values of 0.06, 0.12, and 0.5 μg/ml, respectively. The majority of the *E. aerogenes* isolates did not carry acquired BL and the only *C. koseri* carried *bla*$_{SHV-5}$. CAZ-AVI was active against 99.5% (408/410) of the isolates, and two isolates were resistant to CAZ-AVI: one ECL carrying *bla*$_{NDM}$-1 (MIC, >32 μg/ml) and one isolate carrying *bla*$_{KPC-4}$ and porin alterations (MIC, 16 μg/ml). Susceptibility (S) rates were 1.0, 1.2, and 72.9% for ceftriaxone, ceftazidime, and cefepime, respectively, and 22.0% for piperacillin-tazobactam. Carbapenems were 92.9–93.7% active against these isolates.

Conclusion. Acquired BL were more frequent among ECL and were mostly *bla*$_{CTX-M}$ or *bla*$_{SHV}$. Carbapenemases were also detected. Cephalosporin resistance is likely due to overexpression of AmpC among *E. aerogenes*. CAZ-AVI was very active against these isolates, including most (17/19) carbapenemase producers.

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321. Frequency and Mechanisms of Spontaneous Fosfomycin Non-susceptibility Observed upon Disk Diffusion Testing of *Escherichia coli*

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Background. *Escherichia coli*, the most common cause of urinary tract infections has become increasingly resistant to commonly used oral antibiotics. Fosfomycin maintains excellent activity against most *E. coli* clinical isolates. The growth of *E. coli*