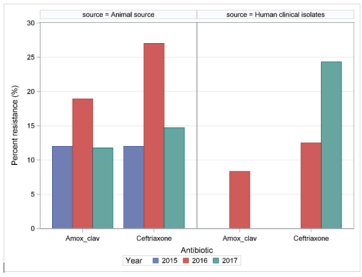

Figure Antimicrobial resistance in Non-typhoidal *Salmonella* isolates from retail meat (n=96) and human (n=109) sources — Pennsylvania, 2015-2017

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

629. Emergence and Clonal Spread of Delafloxacin-Resistant *S. aureus* in Brooklyn, NY

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Background. Delafloxacin is a new anionic fluoroquinolone with enhanced activity against methicillin-resistant *S. aureus* (MRSA). Delafloxacin has become a valuable option in the treatment of skin and soft-tissue infections.

Methods. Unique patient isolates of *S. aureus* were gathered during a surveillance study performed in 2017 involving 7 hospitals in Brooklyn, NY. Isolates underwent susceptibility testing using the agar dilution method; results were interpreted according to CLSI and FDA defined breakpoints. For select isolates, (1) multilocus sequence typing (MLST) was performed using established PCR primers and conditions, (2) mutations involving *grl*A, *grl*B, *gyr*A, and *gyr*B were identified by PCR, and (3) MICs for delafloxacin were performed with and without the addition of 32 µg/mL of the efflux inhibitor 1-(1-naphthyl methyl)-piperazine (NMP).

Results. During the surveillance study, a total of 757 isolates of *S. aureus* were gathered. Susceptibility results are given in the table. Fifteen delafloxacin-resistant isolates underwent MLST, and 14 were found to belong to ST105 and 1 to ST8. ST105 was recovered from all 7 hospitals. In contrast, of 14 delafloxacin-susceptible MRSA, identified ST clades included ST72 (n = 4), ST8 (n = 8), ST5 (n = 1), and ST1181 (n = 1). For 6 delafloxacin-resistant isolates, alterations in (1) GrlA included Ser80Tyr/Phe (5 isolates) and Glu84Gly (4 isolates) and (2) GyrA included Ser84 Leu (6 isolates), Glu88Lys (5 isolates) and Ser85Pro (1 isolate). The addition of the efflux inhibitor NMP did not affect delafloxacin MICs in the 5 isolates tested.

Conclusion. Clonal spread of delafloxacin-resistant isolates of MRSA has been identified in Brooklyn, NY. Alterations in GrlA and GyrA were identified in the delafloxacin-resistant isolates.

	MSSA (n=492)			MRSA (n=265)		
	MIC_{50}/MIC_{90}	range	susceptible	MIC_{50}/MIC_{90}	range	susceptible
	µg/ml		%	µg/ml		%
Ciprofloxacin	0.25/>4	≤ 0.06->4	78	>4/>4	≤ 0.06->4	22
Delafloxacin	≤ 0.06/0.12	≤ 0.06->4	98	0.12/4	≤ 0.06->4	78

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

630. Clinical and Molecular Characteristics of Carbapenem-Resistant *Enterobacteriaceae* in Qatar: A Retrospective and Prospective Observational Study

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Background. There are limited data describing carbapenem-resistant *Enterobacteriaceae* (CRE) from the Arabian Gulf region. Our aims were to describe the clinical, microbiological and molecular characteristics of CRE infections and to characterize the gene displaying resistance to carbapenem.

Methods. Retrospective and prospective review of clinical, microbiological and molecular characteristics of CRE isolated between April 2015 and November 2017 at 7 tertiary hospitals in Qatar. Susceptibility testing was performed and interpreted according to Clinical Laboratory Standards Institute methodology and breakpoints. Carbapenemase genes were identified using PCR. Whole-genome sequencing followed by bioinformatics analysis was performed on a subset of samples for accurate detection of resistant genes. SPSS V.21.0 was used for all statistical analyses.

Results. A total of 144 nonrepeating CRE strains were recovered from 137 individuals over the study period, of which 35 (24.3%) represented colonization. *Klebsiella* spp. (98, 68.1%) and *E. coli* (38, 26.4%) were the most predominant. The most prevalent carbapenemases were NDM (69, 47.9%), OXA-48 (36, 25.0%), and KPC (15, 10.4%). Sixteen (11.1%) strains possessed multiple carbapenemase genes but none were detected in 37 (25.7%) strains. Genomic analysis also detected the presence of NDM-7, NDM-5, NDM1, VIM4, and OXA48-like carbapenemase genes among 34 clinical samples. The majority of the strains were susceptible to tigecycline (124, 86.1%), fosfomycin (122, 84.7%) and amikacin (102, 70.8%). There were 109 CRE infections involving the urinary tract (40, 36.7%), bloodstream (31, 28.4%), and respiratory tract (17, 15.6%). Fifty-seven (52.3%) were males and the median age was 57 years (range 3–97). Baseline comorbidities included diabetes (57, 52.3%), chronic kidney disease (27, 24.8%), and cancer (27, 24.8%) (Table 1). Within the 30 days preceding CRE infection, 38 (34.9%) had received carbapenem therapy, 65 (59.6%) had undergone invasive procedures and 33 (30.3%) had had surgery. All-cause 30-day mortality was 29.4%. The only variable independently associated with mortality was baseline SAPS Score (Table 2).

Conclusion. NDM and OXA-48 are the predominant carbapenemases in Qatar. CRE infections are associated with high overall mortality.

Table 2. Logistic regression for 30-day all-cause mortality.

Variable	Crude Odds Ratios (95% CI)	P value	Adjusted Odds Ratios (95% CI)	P value
Female gender	0.47 (0.2 - 1.1)	0.086	1.4 (0.3 - 6.9)	0.694
Age in years	1.0 (1.0 - 1.1)	0.038	1.0 (0.9 - 1.1)	0.504
Diabetes mellitus	2.0 (0.8 - 4.8)	0.111	-	
Cardiovascular disease	1.3 (0.4 - 3.8)	0.659	-	
Chronic kidney disease	0.8 (0.4 -2.1)	0.729	-	
Chronic liver disease	2.5 (0.6 - 9.8)	0.196	-	
Chronic pulmonary disease	6.4 (1.1 - 37.7)	0.037	1.0 (0.1 - 14.8)	0.998
Solid tumor	3.7 (1.4 - 9.8)	0.01	4.0 (0.8 - 19.4)	0.083
Hematological cancer	1.0 (0.2 - 4.0)	0.956	-	
Intensive care unit	4.7 (1.9 - 11.6)	0.001	0.1 (0.0 - 1.3)	0.083
SAPS Score	1.1 (1.1 - 1.1)	<0.001	1.1 (1.1 - 1.2)	0.001
Systolic blood pressure	0.9 (0.9 - 1.0)	0.01	0.9 (0.9 - 1.0)	0.355
Heart rate	1.0 (1.0 - 1.1)	0.006	1.0 (0.9 - 1.0)	0.356
White blood cell count	1.1 (1.0 - 1.2)	0.002	1.1 (0.9 - 1.2)	0.68
NDM	1.3 (0.6 - 2.8)	0.481	-	
KPC	0.2 (0.0 - 1.6)	0.133	-	
OXA-48	1.0 (0.4 - 2.7)	0.969	-	
Appropriate empiric therapy	3.3 (1.2 - 9.6)	0.025	1.2 (0.2 - 8.4)	0.859
Appropriate targeted therapy	1.2 (0.4 - 3.8)	0.747	-	

Table 1. Baseline characteristics of 109 patients with CRE infections.

Variable	Result
Female gender*	50 (45.9%)
Age in years†	57 (3 - 97)
Diabetes mellitus*	57 (52.3%)
Cardiovascular disease*	17 (15.6%)
Chronic kidney disease*	27 (24.8%)
Chronic liver disease*	5 (4.6%)
Chronic pulmonary disease*	5 (4.6%)
Solid tumor*	17 (15.6%)
Hematological cancer*	10 (9.2%)
Intensive care unit*	31 (28.4%)
Simplified Acute Physiology Score (SAPS)†	31.3 (0 - 95)
Systolic blood pressure †	115.5 (49 - 190)
Heart rate†	88 (50 - 153)
White blood cell count†	10.5 (0 - 41)
Urinary tract infection*	40 (36.7%)
Blood stream infection*	31 (28.4%)
Respiratory tract infection*	17 (15.6%)
Skin and soft tissue infection*	14 (12.8%)
Intra-abdominal infection*	4 (3.7%)
Other sites of infection*	4 (3.7%)
NDM*	52 (47.7%)
KPC*	11 (10.1%)
OXA-48*	24 (22.0%)
Appropriate empiric therapy*	18 (16.5%)
Appropriate targeted therapy*	64 (58.7%)

*number (%); †median (range); SAPS,

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631. Laboratory Surveillance of Carbapenem-Resistant Enterobacteriaceae in an Endemic Country, Greece, 2015–2018

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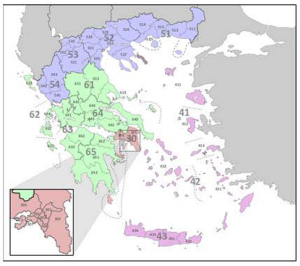
Background. Greece is facing an endemic situation with carbapenem-resistant pathogens in the hospital sector. The Central Public Health Laboratory (CPHL) is the main laboratory for the surveillance of the carbapenem resistance mechanisms, accepting resistant isolates from hospitals on a voluntary basis. The aim of the present study is to evaluate the epidemiology of carbapenem-resistant Enterobacteriaceae (CRE) isolated in Greek hospitals the period 2014–2018 and their susceptibility to other antibiotic classes.

Methods. A total of 843 CRE isolates (741 *Klebsiella* spp., 47 *Enterobacter* spp., 35 *Escherichia coli*, and 20 others) have been submitted from 36 hospitals throughout the country (Figure 1) to the CPHL. They originated from different clinical specimens (295 urine, 157 blood, and 107 other) or surveillance cultures (185 rectal and 23 pharyngeal swabs) or unknown (n = 76). Carbapenemase genes were detected by PCR targeting bla_{KPC}, bla_{NDM}, bla_{VIM}, and bla_{OXA-48}. Resistance to aminoglycosides and fluoroquinolones was tested with the disk diffusion method according to EUCAST guidelines.

Results. The isolates were found positive for several carbapenemase genes (Table 1). Overall, KPC-2 (36%) was the predominant carbapenemase, followed by the metalloenzymes NDM (28%) and VIM (18%) while OXA-48 ranked fourth (7%). KPC enzyme was predominant among *Klebsiella* spp isolates followed by NDM, whereas among *Enterobacter*, *E.coli*, and other species, the VIM metalloenzyme predominated. Simultaneous detection of two carbapenemase genes was found in 30 (4%) isolates: 14 bla_{KPC}/bla_{VIM}, 4 bla_{KPC}/bla_{NDM}, 1 bla_{KPC}/bla_{OXA-48}, 5 bla_{NDM}/bla_{VIM}, 5 bla_{NDM}/bla_{OXA-48}, and 1 bla_{VIM}/bla_{OXA-48}. In 63 isolates (7%), the carbapenem resistance was attributed to other mechanisms, mainly production of ESBL or AmpC plus porin loss. In total, 590 (70%) CRE isolates exhibited a multidrug-resistant phenotype being simultaneously resistant to aminoglycosides and fluoroquinolones.

Conclusion. The CRE isolates' diversity, regarding bacterial species, carbapenemase types and combinations and their temporal and spatial distribution mandate a more structured, continuous laboratory surveillance to monitor the ongoing carbapenem and multidrug resistance evolution and inform infection control and public health actions.



source:wikipedia

NUTS-1_Greece		Participating hospitals
EL3	Attica	17
EL4	Aegean Islands and Crete	2
EL5	Northern Greece	10
EL6	Central Greece	7
	Total	36

Figure1. Number of participating hospitals per first-level Nomenclature of territorial units for statistics (NUTS-1) regions of Greece

Table 1. Carbapenem resistant Enterobacteriaceae (CRE) isolates submitted by the participating hospitals, number and type of confirmed carbapenemases by bacterial genus/species, Greece, 2015-2018.

Submitted CRE isolates (n)	Confirmed carbapenemase type										Other mechanisms of carbapenem resistance		Total number of CRE
	KPC-2		NDM		VIM		OXA-48		Dual combinations				
	n	%	n	%	n	%	n	%	n	%	n	%	n
***Klebsiella* spp**	291	39	236	32	88	12	52	7	25	3	49	7	**741**
Enterobacter spp	2	4	3	6	34	72	3	6	0	0	5	11	**47**
E.coli	12	34	1	3	14	40	1	3	5	14	2	6	**35**
Other	1	5	0	0	12	60	0	0	0	0	7	35	**20**
Total	**306**	**36**	**240**	**28**	**148**	**18**	**56**	**7**	**30**	**4**	**63**	**7**	**843**

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

632. Genetic Diversity of Carbapenem-Resistant *Klebsiella pneumoniae* Causing Late-Onset Neonatal Sepsis in Intensive Care Unit of Caro University Hospital, Cairo, Egypt

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Background. Neonatal sepsis poses a great challenge for clinicians and infection control practitioners. Carbapenem-resistant *Klebsiella pneumoniae* (CRKP) is rapidly increasing and poses a major threat to neonates. Our research aim was to examine the phenotypes, genotypes, and genetic relatedness of CRKP in late-onset neonatal sepsis in the neonatal intensive care unit (NICU) at Cairo University Hospital.

Methods. Our study included 88 neonates diagnosed with sepsis; 58 with late-onset sepsis (LOS) and 30 with early-onset sepsis (EOS) admitted to the NICU between November 2015 and April 2016. Laboratory investigations included (vomplete blood count, C-reactive protein, serum interleukin-6 level by ELISA technique and blood culture). bacterial identification and antibiotic susceptibility testing were done by automated VITEK 2 compact system (BioMérieux, France). Detection of carbapenemases (OXA-48, NDM, IMP, KPC, and VIM) by multiplex PCR and pulsed-field gel electrophoresis (PFGE).

Results. K. pneumoniae was the most common encountered pathogen in the LOS group (37.9%) with a mean sepsis score of 6.39 when compared with the 33 EOS group (P < 0.005). The interleukin ratio, C-reactive protein, and interleukin-6 levels were significantly high in the K. group (P < 0.001). The most prevalent 35 carbapenemase gene in the NICU, OXA-48, was identified in 14/23 (60.8%) 36 isolates followed by NDM-1 in 12/23 (52.2%) isolates as detected by multiplex 37 PCR. Coexistence of both carbapenemases was found in 52.2% (12/23). By investigating the genetic relatedness of CRKP by pulsed-field gel electrophoresis, 23 isolates of K. pneumoniae revealed various PFGE patterns, demonstrating that 40 the isolates were nonclonal.

Conclusion. In conclusion, carbapenam-resistant *Klebsiella pneumoniae* remains the most frequent organism detected in neonatal sepsis. Our results revealed that CRKP isolates were not clonal. Extra data are required on the rates of birth asphyxia and microbiology of neonatal infection since reduced records of diseases sets gaps in understanding how to improve existing practices. Infection control actions including antibiotic stewardship programs with continuous surveillance to trace emerging CRKP infections in the early hours as possible particularly in units at risk as NICUs.

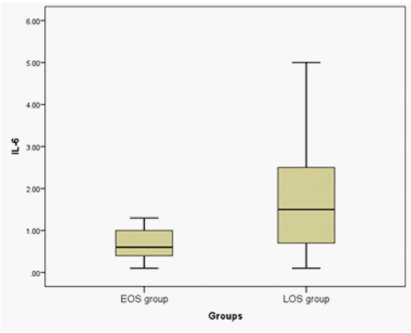

Figure (2): IL6 in early onset sepsis group compared by late onset sepsis group

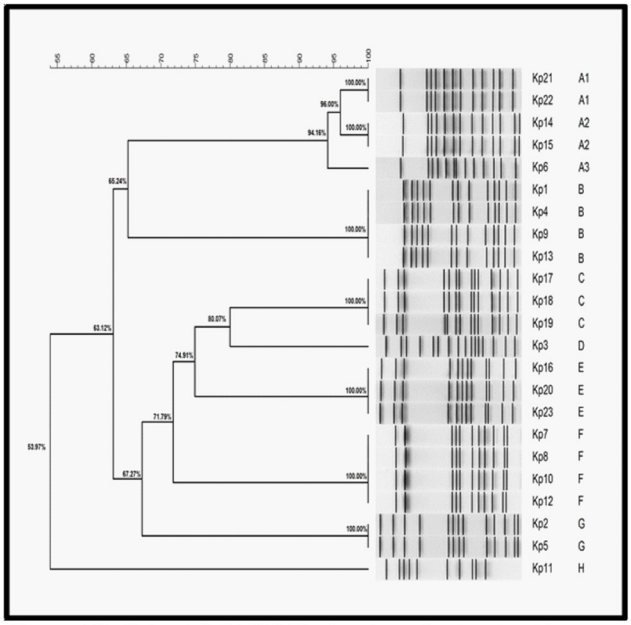

Figure (1): Pulsed-field Gel Electrophoresis showing the presence of multiple pulsotypes of Klebsiella pneumoniae (A1-A3), B, C, D, E, F, G, and H.

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

633. Incidence, Microbial Etiology and Antibiotic Resistance Patterns with Special Reference to Shunt Infections in Neurosurgery at a Tertiary Center in North India

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