Conclusion. Invasive GBS infection is a burden for veterans with DM and other high-risk conditions, with some types of infections associated with substantial mortality. Osteomyelitis, the most common type of infection, was associated with lower mortality compared with other invasive GBS infections. DM and chronic lung, kidney and heart disease are common among veterans with invasive GBS infection.

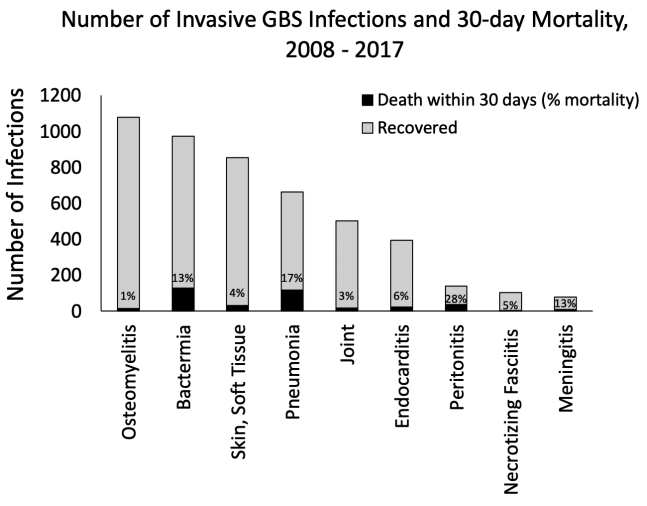

Table. Characteristics and outcome of patients from the US VHA with invasive Group B Streptococcal infection, 2008-2017

Characteristics	All (n = 4780)	Osteomyelitis (n = 1078)	Bacteremia Without Focus (n = 972)	Skin, soft-tissue infection (n = 853)	Pneumonia, Empyema (n = 664)	Joint Infection (n = 501)	Endocarditis (n = 393)	Peritonitis (n = 138)	Necrotizing Fasciitis (n = 103)	Meningitis (n = 78)
Mean Age (±SD)	66.6 (±11.7)	62.7 (±10.1)	69.9 (±12.5)	65.7 (±11)	71.5 (±11.8)	65.1 (±10.3)	67.5 (±11.6)	64 (±10.1)	60.6 (±9.6)	66.1 (± 11.4)
30-Day Mortality	384 (8%)	16 (1%)	127 (13%)	31 (4%)	116 (17%)	17 (3%)	24 (6%)	38 (28%)	5 (5%)	10 (13%)
Diabetes Mellitus	3161 (66%)	931 (86%)	537 (55%)	574 (67%)	377 (57%)	314 (63%)	227 (58%)	73 (53%)	86 (83%)	42 (54%)
Chronic Heart, Coronary Artery Disease	1515 (32%)	296 (27%)	310 (32%)	283 (33%)	271 (41%)	132 (26%)	142 (36%)	37 (27%)	31 (30%)	13 (17%)
Chronic Renal Disease	1332 (28%)	302 (28%)	286 (29%)	230 (27%)	210 (32%)	103 (21%)	125 (32%)	35 (25%)	25 (24%)	16 (21%)
Chronic Pulmonary Disease	1325 (28%)	236 (22%)	285 (29%)	225 (26%)	267 (40%)	124 (25%)	114 (29%)	39 (28%)	14 (14%)	21 (27%)
Peripheral Vascular Disease	1146 (24%)	344 (32%)	204 (21%)	188 (22%)	171 (26%)	86 (17%)	94 (24%)	24 (17%)	24 (23%)	11 (14%)
Cancer	1037 (22%)	136 (13%)	282 (29%)	165 (19%)	197 (30%)	92 (18%)	94 (24%)	38 (28%)	12 (12%)	21 (27%)
Cerebrovascular Disease	768 (16%)	142 (13%)	181 (19%)	116 (14%)	153 (23%)	55 (11%)	87 (22%)	11 (8%)	8 (8%)	15 (19%)
Chronic Liver Disease	702 (15%)	105 (10%)	159 (16%)	109 (13%)	101 (15%)	67 (13%)	73 (19%)	64 (46%)	6 (6%)	18 (23%)
Paralysis	310 (6%)	118 (11%)	74 (8%)	31 (4%)	40 (6%)	20 (4%)	14 (4%)	4 (3%)	2 (2%)	7 (9%)
Dementia	207 (4%)	24 (2%)	75 (8%)	21 (2%)	49 (7%)	12 (2%)	20 (5%)	4 (3%)	0 (0%)	2 (3%)
Peptic Ulcer Disease	187 (4%)	26 (2%)	41 (4%)	30 (4%)	36 (5%)	15 (3%)	20 (5%)	13 (9%)	1 (1%)	5 (6%)
Rheumatic Disease	117 (2%)	21 (2%)	17 (2%)	28 (3%)	15 (2%)	22 (4%)	10 (3%)	3 (2%)	0 (0%)	1 (1%)
HIV/AIDS	61 (1%)	8 (1%)	14 (1%)	12 (1%)	10 (2%)	6 (1%)	5 (1%)	3 (2%)	0 (0%)	3 (4%)

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

221. Newly-Named Klebsiella aerogenes Is Associated with Poor Clinical Outcomes Relative to Enterobacter cloacae Complex in Patients with Bloodstream Infection

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Session: 37. Bacteremia, CLABSI, and Endovascular Infections
Thursday, October 3, 2019: 12:15 PM

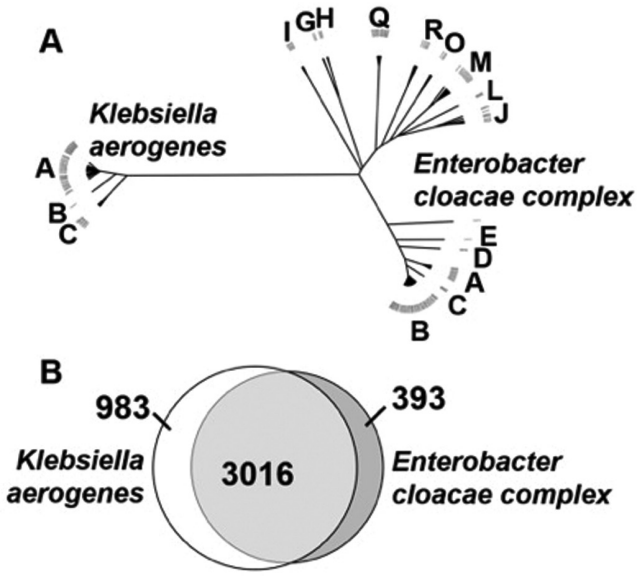
Background. Whole-genome-based comparative bacterial phylogenetics led to *Enterobacter aerogenes* being renamed *Klebsiella aerogenes*. It is unclear how infections with *K. aerogenes* differ from *Enterobacter cloacae* complex (Ecc) regarding clinical characteristics, antibiotic resistance, patient outcomes, and bacterial virulence genes.

Methods. Adult inpatients with *K. aerogenes* or Ecc bloodstream infection (BSI) were prospectively enrolled at Duke from 2002–2015. Whole-genome bacteria sequencing was performed. Chi-squared, Fisher's exact, Mann–Whitney U, t-tests, and multivariable logistic regression models identified risk factors for infection and clinical outcomes. PanOCT algorithm identified flexible genomic islands (fgi). *Multidrug resistance* (MDR) was defined as resistance to ≥3 drug classes and *poor clinical outcome* as death before discharge and/or BSI complication (septic shock, acute kidney injury, acute lung injury/acute respiratory distress syndrome, disseminated intravascular coagulation).

Results. We identified 104 (69%) patients with Ecc BSI and 46 (31%) with *K. aerogenes* BSI (N = 150). Patients with Ecc BSI more often required hemodialysis (23% vs. 9%, P = 0.04). MDR was similar between Ecc and *K. aerogenes* (30% vs. 33%; P = 0.85). Total (21% vs. 28%; P = 0.3) and attributable in-hospital mortality (12% vs. 20%; P = 0.3) did not differ between the two genera. Poor clinical outcome was more common with *K. aerogenes* BSI (70% vs. 40%, P = 0.001) and remained significant after adjusting for age, source of BSI, site of acquisition (e.g., hospital), days to appropriate antibiotic, and chronic APACHE-II score (odds ratio 2.8, 95% CI 1.2–6.4, P = 0.001). Ecc and *K. aerogenes* isolates formed 14 and 3 phylogenetic clades, respectively (Fig 1A). *K. aerogenes* contained 983 core genes, grouped within 324 fgi, that were not present in Ecc (Fig 1B). These included homologs to virulence genes involved in iron acquisition, flagella synthesis, and fimbriae production.

Conclusion. Patients with BSI due to *K. aerogenes* had poor clinical outcomes relative to Ecc. Multiple unique *K. aerogenes* genes homologous to virulence factors may contribute to this difference.

Figure 1. (A) Phylogenetic tree containing *Klebsiella aerogenes* and *Enterobacter cloacae* complex (Ecc) isolates along with clade designations. (B) Venn diagram of core genes that are shared and unique in *K. aerogenes* and Ecc.



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

222. Bloodstream Infections by Gram(−) Bacteria in Kidney Transplant Patients: Risk Factors, Incidence and Outcome; Bloodstream Infections by Gram(−) Bacteria in Kidney Transplant Patients: Risk Factors, Incidence and Outcome

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Session: 38. Transplant ID: Bloodsteam Infections
Thursday, October 3, 2019: 12:15 PM

Background. Kidney transplant recipients are at increased risk for infections. The aims of this study were: i) to estimate the incidence of bloodstream infections (BSI) caused by Gram(−) bacteria in kidney transplant recipients, ii) to identify risk factors for BSI by multidrug-resistant Gram(−) bacteria, and iii) to identify predictors for outcome (death/loss of transplanted kidney).

Methods. We conducted a retrospective cohort study at the renal transplant unit (RTU) of a tertiary care hospital located in Athens, Greece, between September 2008 and September 2018. Kidney transplant recipients with Gram(−) BSIs were identified from the microbiology laboratory electronic records. Patient-, infection-, and treatment-related factors were extracted from the medical records. Species identification and susceptibility testing were performed by MicroScan automated system. The statistical analysis was performed using IBM SPSS Statistics v20.

Results. During the study period, 1962 kidney transplant patients were followed at our RTU. A total of 195 BSI episodes were recorded in 182 patients (male/female=97/85), with median (25th, 75th) age 57.2 (44, 64.9) years. The incidence of BSI was 1.393/100 patient-years. Median (25^{th}, 75^{th}) time interval between transplantation date and onset of BSI was 67.67 (8.3, 148) months. *Escherichia coli* was the most common cause (64.3%, 117/182), while the most common source of infection was urinary tract (70.9%, 129/182). 19.2% (53/182) of BSIs were caused by multidrug-resistant organisms (MDR). 6% (11/182) of patients died and 2.2% (4/182) were subjected to nephrectomy. Multivariate logistic regression showed that diabetes mellitus (odds ratio [OR] 7.714; 95% confidence interval [CI] 1.311–45.385), *Pseudomonas aeruginosa* BSI (OR 35.788; CI 3.3–388.182) and septic shock (OR 74.468; CI 3.513–1578.513) were predictors of an unfavorable outcome. Previous antibiotic use (OR 11.964; CI 2.686–53.293) and previous stay in Intensive Care Unit (OR 18.055; CI 1.046–311.536) were associated with MDR BSIs.

Conclusion. BSIs in kidney transplant recipients is a critical factor of morbidity and mortality. Recognizing the risk factors for unfavorable outcome and emergence of MDR bacteria could offer a significant advantage in early diagnosis and appropriate treatment.

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