A previous single-center study had created a prediction tool to assist clinicians in identifying patients at risk for ESBL bloodstream infections. The purpose of our research project was to assess validity of this tool while also identifying risk factors for ESBL bacteremia within our own institution, which would allow for assessment of alternative prediction tools.

Methods. We performed a retrospective chart review of adult patients admitted to an urban university hospital who were found to have bacteremia with *Escherichia coli*, *Klebsiella pneumoniae*, and/or *Klebsiella oxytoca* between October 2016 and April 2018. Demographics and comorbidities were assessed, along with other potential risk factors including exposure to antibiotics and hospitalizations within the past 6 months.

Results. A total of 214 instances of bacteremia were identified and 14% were due to ESBL organisms. Risk factors for ESBL bacteremia in our cohort included history of positive culture for ESBL (RR = 5.9) or MRSA (RR = 3.5) and antibiotic usage in the past 6 months (RR = 2.3). Patients with ESBL bacteremia were hospitalized longer (mean 16 days vs. 6 days for non-ESBL), received longer durations of antibiotic therapy (11.7 days vs. 5.3 days), and were exposed to greater numbers of different antibiotics (1.9 vs. 0.7) in the previous 6 months. Multivariate logistic regression showed that history of prior ESBL infection (OR 14.7, CI 1.7–12.2) and increasing number of different antibiotic classes administered in the prior 6 months (OR 4.3, CI 1.7–11.2) were significant risk factors for ESBL bacteremia. The previously created prediction tool did not sufficiently differentiate higher and lower risk for ESBL bacteremia in our cohort. While the previous prediction model might better assess risk across institutions. Additionally, the number of different antibiotics received was associated with risk for ESBL bacteremia and should be investigated further.

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187. The 30-Day Readmission and 30-Day Mortality of Hemodialysis Patients with Antibiotic-Resistant Gram-Negative Bacteremia
Jomi K. Oommen, PharmD; Eris Cani, BS; PharmD; BCPS; Cosmina Zeanu, MD and Tai E. Park, PharmD; BronxCare Health System, New Hyde Park, New York

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Background. Although antibiotic-resistant (AR) Gram-negative infections are more prevalent in hemodialysis (HD) patients, there are limited data on the impact of antibiotic resistance on clinical outcomes. The primary objective of this study was evaluating 30-day readmission and 30-day all-cause mortality of HD patients with AR Gram-negative bacteremia (GNB). The secondary objective was assessing the association of risk factors for AR-GNB and Infectious Diseases (ID) consult with the primary outcomes.

Methods. This was a single-center, retrospective, cohort study, which enrolled adult HD patients with AR-GNB between January 1, 2010 and December 31, 2018. The AR included extended-spectrum β-lactamase (ESBL), carbapenem resistance (CR, resistant to at least one carbapenem), and multidrug resistance (MDR, resistant to at least one agent in three antibiotic classes). The risk factors for AR-GNB included: antibiotic use and long-term care facility stay within 90 days, hospitalization >30 days, central line, urinary catheter, and invasive medical device use, and severe underlying illness. Statistical analysis involved chi-square and Fisher’s exact tests.

Results. A total of 90 patients were included. The most common pathogen and source were *Klebsiella pneumoniae* (42.2%) and urine (29.5%), respectively. The most common AR was ESBL (30.6%), followed by CR and MDR (both 29.7%). Overall, 30-day readmission and 30-day all-cause mortality were 22% and 38.5%, respectively. Long-term care facility stay within 90 days was more likely associated with 30-day readmission (odds ratio [OR] 3.46, 95% confidence interval [CI] 0.99–12.15, P = 0.048), although it was not observed with multivariate analysis (P = 0.223). Hospitalization >30 days (OR 0.25, 95% CI 0.1–0.64; P = 0.003) and ID consult (OR 0.13, 95% CI 0.05–0.36; P < 0.0001) were less likely associated with 30-day all-cause mortality according to multivariate analysis. Overall, MDR was more likely associated with 30-day all-cause mortality than ESBL (P = 0.02) and CR (P = 0.002).

Conclusion. To our knowledge, this is the first study evaluating the impact of AR-GNB in HD patients on 30-day readmission and 30-day all-cause mortality. Hospitalization >30 days and having ID consult were less likely associated with 30-day all-cause mortality.

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188. Which patients with gram-negative bacteremia need follow-up blood cultures?
JongTak Jung, MD1; Sung Moon Mo, MD, PhD1; Eun Suk Kim, MD, PhD2; Hong Bin Kim, MD, PhD3; Ji Hwan Bang, MD, PhD4; Sang Won Park, MD, PhD5; Wan Beom Park, MD, PhD6; Nam-Joong Kim, MD, PhD7; Myoung-don Oh, MD, PhD7 and Kyong-Ho Song, MD, PhD8; 1Department of Internal Medicine, Seoul National University Bundang Hospital, Seongbuk-gu, Seoul-ypukyosi, Republic of Korea; 2Department of Internal Medicine, Seoul National University College of Medicine, Seoul, Korea, Seoul, Seoul-ypukyosi, Republic of Korea; 3Division of Infectious Diseases, Department of Internal Medicine, Seoul National University Bundang Hospital, Seongnam, Korea, Korea; 4Division of Infectious Disease, Department of Internal Medicine, Seoul National University Bundang Hospital, Seongnam, Korea, Korea; 5Division of Infectious Disease, Department of Internal Medicine, Seoul National University Bundang Hospital, Seongnam, Korea, Korea; 6Department of Internal Medicine, Seoul National University Bundang Hospital, Seoul, Seoul-ypukyosi, Republic of Korea; 7Department of Internal Medicine, Seoul National University Bundang Hospital, Seoul, Seoul-ypukyosi, Republic of Korea; 8Department of Internal Medicine, Seoul National University Bundang Hospital, Seoul, Seoul-ypukyosi, Republic of Korea

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Background. Universal follow-up blood culture (FUBC) in gram-negative bacteremia (GNB) is not recommended, but it has been routinely conducted in many acute-care hospitals. In contrast with *Staphylococcus aureus bacteremia*, risk factors for positive FUBC in GNB have not been well investigated. Therefore, we tried to identify the risk factors for and develop predictive scores of positive FUBC.

Methods. All adults (≥18 years-old) with GNB were identified in a tertiary-care hospital during the 2-year period, retrospectively. Death within 2 days of GNB and polymicrobial infection with gram-positive bacteria or fungus were excluded. GNB were classified into eradicable and non-eradicable source of infection groups, according to the possibility of source removal. We performed multivariate analyses for identifying risk factors for positive FUBC and built prediction scores using the coefficients of the multivariate logistic regression models.

Results. Of total 1,473 GNB, FUBC was drawn in 1,268 (86%) patients and 122 (9.6%) had positive results. In patients with eradicable source of infection, ESBL-producing microorganisms, catheter-related bloodstream infection, unfavorable treatment response, and quick sequential organ failure assessment (qSOFA) score (≥2) were associated. On the other hand, administration of effective antibiotics and adequate source control were negatively associated with positive FUBC. In non-eradicable source of infection, end-stage renal disease on hemodialysis, and unfavorable treatment response were related to positive FUBC and administration of effective antibiotics was negatively associated (Table 1). When we built prediction scores according to the coefficients, the areas under the curves were 0.864 (95% confidence interval [CI] 0.816–0.912) and 0.792 (CI 0.571–0.981), respectively. When we applied a cutoff of 0, specificities/negative predictive values in eradicable and non-eradicable source of infection groups were 84.7%/95.6% and 95.5%/95.0%, respectively (Table 2).

Conclusion. Our prediction scores based on adequate source control and use of effective antibiotics showed high specificities and negative predictive values. Therefore, we could expect these score systems to contribute to reducing unnecessary FUBC in GNB.

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189. A Case Series of *Elizabethkingia meningoseptica* Bacteremia in the Cancer Population
Dae Hyun Lee, MD1; Jisun Mehra, MBBS2; Sanjay Chandrasekar, MD3; Abu Saeed Mirza, MD1, Rahul Shenoy, MBBS2; Annie Topham, MD1; Sowmya Nanjappa, MBBS3 and John Greene, MD3; 1University of South Florida, Moffitt Cancer Center, Tampa, Florida; 2University of South Florida, Moffitt Cancer Center, Tampa, Florida; 3Moffitt Cancer Center, Tampa, Florida

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Background. *Elizabethkingia meningoseptica* (E. meningoseptica) is a ubiquitous microorganism previously known as *Chryseobacterium meningosepticum*. It is emerging as a pathogen responsible for bacteremia in immunocompromised patients such as cancer patients especially those with a history of prolonged hospital stay and frequent instrumentation.

Methods. A retrospective chart review of all cases over 10 years in Moffitt Cancer Center showed a total of three patients with *E. meningoseptica* infection.