Proportional comparison of the Gram-negative bacterial species identified in patients with recurrent and non-recurrent bloodstream infections.

Conclusion. Recurrent GNB-BSI is an uncommon complication of GNB-BSI. Recurrent GNB-BSI is most often driven by relapse, as opposed to reinfection, and is associated with associated with black race, implanted cardiac devices and admission to surgical service.

Disclosures. **Vance G. Fowler, Jr., MD, MHS**, **Achaogen** (Consultant)**Advanced Liquid Logics** (Grant/Research Support)**Affinergy** (Consultant, Grant/Research Support)**Affinium** (Consultant)**Akagera** (Consultant)**Allergan** (Grant/Research Support)**Amphliphi Biosciences** (Consultant)**Aridis** (Consultant)**Armata** (Consultant)**Basilea** (Consultant, Grant/Research Support)**Bayer** (Consultant)**C3J** (Consultant)**Cerexa** (Consultant, Other Financial or Material Support, Educational fees)**Contrafect** (Consultant, Grant/Research Support)**Debiopharm** (Consultant, Other Financial or Material Support, Educational fees)**Destiny** (Consultant)**Durata** (Consultant, Other Financial or Material Support, educational fees)**Genentech** (Consultant, Grant/Research Support)**Green Cross** (Other Financial or Material Support, Educational fees)**Integrated Biotherapeutics** (Consultant)**Janssen** (Consultant, Grant/Research Support)**Karius** (Grant/Research Support)**Locus** (Grant/Research Support)**Medical Biosurfaces** (Grant/Research Support)**Medicines Co.** (Consultant)**MedImmune** (Consultant, Grant/Research Support)**Merck** (Grant/Research Support)**NIH** (Grant/Research Support)**Novadigm** (Consultant)**Novartis** (Consultant, Grant/Research Support)**Pfizer** (Grant/Research Support)**Regeneron** (Consultant, Grant/Research Support)**sepsis diagnostics** (Other Financial or Material Support, Pending patent for host gene expression signature diagnostic for sepsis .)**Tetraphase** (Consultant)**Theravance** (Consultant, Grant/Research Support, Other Financial or Material Support, Educational fees)**Trius** (Consultant)**UpToDate** (Other Financial or Material Support, Royalties)**Valanbio** (Consultant, Other Financial or Material Support, Stock options)**xBiotech** (Consultant)

60. Creation and Comparison of a Machine Learning Decision Tree and Traditional Risk Score to Predict Ceftriaxone Resistance in Cancer Patients with *E. coli* Bacteremia

Courtney Moc, PharmD, MS[1]; William Shropshire, MPH, PhD[1]; Patrick McDaneld, PharmD[2]; Samuel A. Shelburne, MD, PhD[3]; Samuel L. Aitken, PharmD, MPH, BCIDP[4]; Samuel L. Aitken, PharmD, MPH, BCIDP[4]; [1]UT MD Anderson Cancer Center, Houston, Texas; [2]University of Texas MD Anderson Cancer Center, Houston, TX; [3]The University of Texas MD Anderson Cancer Center, Houston, TX; [4]Michigan Medicine, Ann Arbor, TX

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Background. There are several clinical tools that have been developed to predict the likelihood of extended-spectrum β-lactamase producing *Enterobacterales*; however, the creation of these tools included few patients with cancer or otherwise immunosuppressed. The objectives of this retrospective cohort study were to develop a decision tree and traditional risk score to predict ceftriaxone resistance in cancer patients with *Escherichia coli* (*E. coli*) bacteremia as well as to compare the predictive accuracy between the tools.

Methods. Adults age ≥ 18 years old with *E. coli* bacteremia at The University of Texas MD Anderson Cancer Center from 1/2018 to 12/2019 were included. Isolates recovered within 1 week from the same patient were excluded. The decision tree was constructed using classification and regression tree analysis, with a minimum node size of 10. The risk score was created using a multivariable logistic regression model derived by using stepwise variable selection with backward elimination at level 0.2. The decision tree and risk score statistical metrics were compared.

Results. A total of 629 *E. coli* isolates were screened, of which 580 isolates met criteria. Ceftriaxone-resistant (CRO-R) *E. coli* accounted for 36% of isolates. The machine learning-derived decision tree included 5 predictors whereas the logistic regression-derived risk score included 7 predictors. The risk score cutoff point of ≥ 5 points demonstrated the most optimized overall classification accuracy. The positive predictive value of the decision tree was higher than that of the risk score (88% vs 74%, respectively), but the area under the receiver operating characteristic curve and model accuracy of the risk score was higher than that of the decision tree (0.85 vs 0.73 and 82% vs 74%, respectively).

Figure 1. Clinical Decision Tree

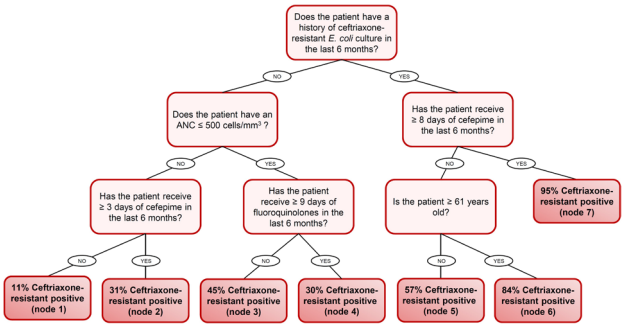

Table 1. Regression Model and Assigned Points for Clinical Risk Score

Variables	Odds Ratio (95% CI)	Assigned Points
Ceftriaxone-resistant *E. coli* colonization or infection (in the last 6 months)	10.62 (5.90-19.10)	11
Cefpodoxime/cefdinir prophylaxis at the time of blood culture	5.81 (1.75-19.26)	6
Long term acute facility (in the last 6 months)	4.95 (0.77-31.66)	5
International travel* (in the last 6 months)	2.82 (1.45-5.49)	3
ANC ≤ 500 cells/mm^3	2.33 (1.50-3.62)	2
Received ≥ 5 days of cefepime (in the last 6 months)	1.74 (1.13-2.70)	2
Presumptive infection source: genitourinary source	2.38 (0.81-6.97)	2

*Latin America, the Middle East, South Asia, Southeast Asia excluding Singapore, China

Table 2. Statistical Metrics of Clinical Decision Tree and Clinical Risk Score

	Decision Tree	Risk Score*
Number of variables	5	7
Sensitivity, %	34%	87%
Specificity, %	97%	82%
Positive predictive value, %	88%	74%
Negative predictive value, %	71%	76%
Model accuracy	74%	82%
Area under the receiver operating characteristic curve	0.73	0.85

*Using cutoff point of ≥ 5 points

Conclusion. The decision tree and risk score can be used to determine the likelihood of whether a cancer patient with *E. coli* bacteremia has a CRO-R infection. In both clinical tools, the strongest predictor was a history of CRO-R *E. coli* colonization or infection in the last 6 months. The decision tree was more user-friendly, has fewer variables, and has a better positive predictive value in comparison to the risk score. However, the risk score has a significantly better discrimination and model accuracy than that of the decision tree.

Disclosures. **Samuel L. Aitken, PharmD, MPH, BCIDP**, Melinta Therapeutoics (Individual(s) Involved: Self): Consultant, Grant/Research Support

61. Short- versus prolonged-courses of antimicrobial therapy for patients with uncomplicated *Pseudomonas aeruginosa* bloodstream infection

Moonsuk Bae, n/a[1]; Yun-Seo Jeong, n/a[2]; Seongman Bae, MD[3]; Min Jae Kim, MD[3]; Yong Pil Chong, MD[3]; Sung-Han Kim, PhD[3]; Sang-Oh Lee, MD[3]; Sang-Ho Choi, MD[3]; Yang Soo Kim, MD[3]; Jiwon Jung, MD [3]; [1]Pusan National University Yangsan Hospital, Yangsan-si, Kyongsang-namdo, Republic of Korea [2]University of Ulsan College of Medicine, Seoul, Seoul-t'ukpyolsi, Republic of Korea [3]Asan Medical Center, Songpa-gu, Seoul-t'ukpyolsi, Republic of Korea

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Background. The optimal duration of antimicrobial therapy for uncomplicated *Pseudomonas aeruginosa* bloodstream infection (BSI) is unknown. We compared the outcomes of short and prolonged courses of antimicrobial therapy in adults with uncomplicated pseudomonal BSI.

Methods. All patients with uncomplicated *P. aeruginosa* BSI admitted at a tertiary-care hospital from May 2016 to September 2020 were included. We compared the rate of recurrent *P. aeruginosa* infection and 30-day mortality among patients who underwent short (7–11 days) and prolonged (12–21 days) courses of antimicrobial therapy using propensity score analysis with the inverse probability of treatment weighting (IPTW) method.

Results. We evaluated 1,477 patients with uncomplicated *P. aeruginosa* BSI; of them, 290 met the eligibility criteria, including 97 (33%) who underwent short-course therapy (9 [interquartile range (IQR), 8–11] days) and 193 (67%) who underwent prolonged-course therapy (15 [IQR, 14–18] days). We found no significant difference in the risk of recurrence or 30-day mortality between the prolonged-course and short-course groups (n=10, 11% vs. n=32, 16%; IPTW-adjusted hazard ratio (HR) 0.61; 95% confidence interval (CI) 0.30–1.24; *p*=0.17). The recurrence of *P. aeruginosa* infection at any site within 180 days of completing therapy occurred significantly more in the prolonged-course group (n=10, 10% vs. n=38, 20%; IPTW-adjusted HR 0.48; 95% CI 0.24–0.96, *p*=0.04). The resistance acquisition in subsequent *P. aeruginosa* isolates was more frequent in the prolonged-course group, although the difference was not statistically significant (n=2, 20% vs. n=12, 32%; *p*=0.70).

Table 1. Clinical characteristics of 290 patients with *Pseudomonas aeruginosa* bloodstream infections by duration of antimicrobial therapy before and after inverse probability of treatment weighting

Characteristic	Entire Cohort				Weighted Cohort[a]		
	Short course (n=97; 33%)	Prolonged course (n=193; 67%)	*p*-value	Standardized differences	Short course (n=98; 34%)	Prolonged course (n=192; 66%)	Standardized differences
Age, median (IQR), y	64 (53–73)	64 (55–72)	0.77	0.031	62 (53–73)	64 (55–72)	0.002
Male sex, n (%)	64 (66.0)	123 (63.7)	0.71	0.047	64 (64.8)	122 (63.6)	0.026
Body weight, mean ± SD, kg	58.2±11.7	57.8±9.6	0.76	0.037	57.0±11.8	57.8±9.5	−0.076
Source of bloodstream infection							
Biliary, n (%)	48 (49.5)	77 (39.9)	0.12	0.194	46 (47.1)	81 (42.2)	0.099
Primary, n (%)	16 (16.5)	37 (19.2)	0.58	−0.070	17 (17.6)	35 (18.1)	−0.013
Pulmonary, n (%)	8 (8.2)	30 (15.5)	0.08	−0.227	12 (11.8)	26 (13.3)	−0.047
Urinary tract, n (%)	12 (12.4)	18 (9.3)	0.42	0.098	10 (10.1)	21 (11.0)	−0.028
Central venous catheter, n (%)	5 (5.2)	15 (7.8)	0.41	−0.107	5 (5.4)	13 (6.9)	−0.063
Others, n (%)	8 (8.2)	16 (8.3)	0.99	−0.002	8 (7.9)	16 (8.4)	−0.017
Source control achieved, n (%)	93 (95.9)	184 (95.3)	0.83	0.026	86 (87.8)	183 (95.3)	−0.272
Intensive care unit, day 1, n (%)	6 (6.2)	23 (11.9)	0.13	−0.201	10 (10.1)	20 (10.2)	−0.002
Pitt bacteremia score, median (IQR), day 1	2 (0–3)	2 (0–3)	0.56	−0.084	2 (0–3)	2 (0–3)	−0.030
Diabetes mellitus, n (%)	15 (15.5)	45 (23.3)	0.12	−0.200	27 (27.6)	39 (20.4)	0.168
Liver cirrhosis, n (%)	14 (14.4)	17 (8.8)	0.14	0.176	9.3 (9.5)	19 (10.0)	−0.019
HSCT, past 12 months, n (%)	3 (3.1)	8 (4.1)	0.66	−0.056	4 (4.1)	8 (4.0)	0.005
Chemotherapy, past 6 months, n (%)	35 (36.1)	87 (45.1)	0.14	−0.184	49 (50.2)	83 (43.0)	0.146
Immunosuppressive therapy[b], n (%)	7 (7.2)	33 (17.1)	0.02	−0.306	12 (12.3)	27 (14.2)	−0.056
Neutropenia[c], day 1, n (%)	18 (18.6)	44 (22.8)	0.41	−0.105	21 (21.8)	41 (21.5)	0.008
CRPA isolation	15 (15.5)	42 (21.8)	0.20	−0.162	14 (14.5)	37 (19.2)	−0.126
Combination antimicrobial therapy, n (%)	3 (3.1)	18 (9.3)	0.05	−0.411	4 (4.5)	14 (7.1)	0.140
Transitioned to oral therapy, n (%)	3 (3.1)	28 (14.5)	0.003	−0.261	15 (15.5)	21 (10.7)	−0.110

Abbreviation: CRPA, carbapenem-resistant *Pseudomonas aeruginosa*; HSCT, hematologic stem cell transplantation; IQR, interquartile range; SD, standard deviation
[a]As weighting decreases or increases the representation of each patient to create a pseudopopulation of patients receiving short-course therapy who look similar to those in the prolonged-course group, the counts and proportions for the new weighted cohort were determined.
[b]Immunosuppressive therapy included corticosteroids (prednisolone-equivalent ≥10 mg per day for longer than 2 weeks), biologic agents, or immune modulator therapy (including those used for solid organ transplant recipients)
[c]absolute neutrophil count <500 cells/mL

Table 2. Clinical outcomes of short-course antimicrobial therapy versus prolonged-course antimicrobial therapy over 30 days

Outcome	Univariate analysis		Multivariate analysis		IPTW-adjusted HR	
	unadjusted HR (95% CI)	p value	adjusted HR (95% CI)	p value	IPTW-adjusted HR (95% CI)	p value
Recurrence/death	0.60 (0.29–1.21)	0.15	0.69 (0.32–1.47)	0.34	0.61 (0.30–1.24)	0.17
Recurrence	0.57 (0.21–1.54)	0.27	0.75 (0.25–2.21)	0.60	0.51 (0.17–1.52)	0.23
All-cause mortality	0.53 (0.20–1.43)	0.21	0.46 (0.16–1.32)	0.15	0.62 (0.25–1.53)	0.30

Abbreviation: CI, confidence interval; HR, hazard ratio; IPTW, inverse probability treatment weighted.

Conclusion. Short-course antimicrobial therapy could be as effective as prolonged-course therapy for uncomplicated *P. aeruginosa* bloodstream infection.

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

62. Follow-Up Blood Culture Practices for Gram-Negative Bloodstream Infections in Immunocompromised Hosts at a Large Academic Medical Center

Lauren Groft, PharmD[1]; James Mease, PharmD[2]; Jacqueline Bork, MD[3]; Ciera L. Bernhardi, PharmD[4]; J. Kristie Johnson, PhD, D(ABMM)[5]; Kimberly C. Claeys, PharmD[2]; [1]The Johns Hopkins Hospital, Baltimore, MD; [2]University of Maryland School of Pharmacy, Baltimore, Maryland; [3]University of Maryland School of Medicine, Baltimore, Maryland; [4]University of Maryland Medical Center, Arnold, Maryland; [5]University of Maryland, Baltimore, MD

Session: O-13. GNB bacteremia

Background. Routine follow-up blood cultures (FUBC) are strongly recommended for *Staphylococcus aureus* and *Candida* spp. bloodstream infections (BSI), but the role of FUBC in Gram-negative (GN) BSI remains controversial. Factors that may result in persistent GN BSI include critical illness, endovascular infection, lack of source control, multidrug resistant organisms (MDRO), end-stage renal disease, or immunocompromised status. As such, FUBC in patients with any of these factors may be warranted to improve clinical outcomes, but the true balance of benefit versus harm remains unknown. Our objective was to evaluate the role of FUBC in immunocompromised patients with GN BSI.

Methods. This was a retrospective observational cohort of adult, immunocompromised patients treated for confirmed GN BSI between January 2019 and December 2020 at University of Maryland Medical Center. Immunocompromise was defined as active hematologic or solid tumor malignancy at time of BSI diagnosis, history of hematopoietic stem cell transplantation (HSCT) or solid organ transplantation (SOT), or absolute neutrophil count (ANC) < 1000 cells/mm^3 at any time 30 days prior to BSI diagnosis. FUBC were defined as blood cultures drawn between 24 hours and 7 days from index blood culture, within the same hospital encounter. Positive FUBC was defined as a FUBC with same pathogenic GN organism identified. Comparison of patient and microbiologic characteristics was made between patients with and without FUBC.

Results. A total of 146 patients with GN BSI were included. Baseline characteristics are reported in Table 1. FUBC were collected in 129 (88.4%) patients. Neutropenia (49.6% vs. 19.4%, *P*=0.122), presence of central line (69.8% vs. 30.2%, *P*=0.061), and hospital-acquired origin of BSI (63.6% vs. 36.4%, *P*=0.395) resulted in increased frequency of FUBC. Patients with FUBC had a significantly longer post-BSI mean (SD) length of stay (17.3 [35.4] vs. 6.5 [6.0] days; *P*=0.005). Positive FUBC occurred in only 2 cases (1.4%) and both patients had persistent fevers at time of FUBC.

Table 1. Baseline Characteristics

Age; mean (SD), years	57 (15)
Male; n (%)	92(63)
Type of immunosuppression; n (%)*	
Hematologic malignancy only	45 (30.8)
SOT only	45 (30.8)
Any history of HSCT	44 (30.1)
Hematologic malignancy and history of HSCT	43 (29.5)
Solid tumor malignancy only	12 (8.2)
Solid tumor malignancy and history of HSCT	1 (0.7)
Neutropenic; n (%)	70 (47.9)
Presence of central line; n (%)	48 (67.1)
Definitive or probable source of BSI; n (%)	
Gastrointestinal/intraabdominal	75 (51.4)
Urinary	26 (17.8)
Central line-associated	15 (10.3)
Pulmonary	9 (6.2)
Absence of source control; n (%)	22 (15.1)
Most common organisms isolated; n (%)	
Escherichia coli	48 (32.9)
Pseudomonas aeruginosa	34 (23.3)
Klebsiella pneumoniae	32 (21.9)

*Patients classified into multiple categories of immunosuppression if applicable

Conclusion. Positive FUBC were uncommon in this immunocompromised cohort with GN BSI, which challenges the need for routine collection of FUBC in this patient population.

Disclosures. **Ciera L. Bernhardi, PharmD**, **Servier Pharmaceuticals** (Advisor or Review Panel member) **J. Kristie Johnson, PhD, D(ABMM)**, **GenMark** (Speaker's Bureau) **Kimberly C. Claeys, PharmD**, **GenMark** (Speaker's Bureau)

63. PK-RNN-V: A Deep Learning Model for Vancomycin Therapeutic Drug Monitoring using Electronic Health Record Data

Nigo Masayuki, MD[1]; Hong Thoai Nga Tran, MS[2]; Ziqian Xie, n/a[2]; Han Feng, n/a[3]; Laila Bekhet, n/a[2]; Miao Hongyu, MS, PhD[4]; Degui Zhi, Ph. D[2]; [1]University of Texas in Houston, Houston, TX; [2]School of Biomedical Informatics, University of Texas Health Science Center at Houston, Houston, Texas; [3]School of Public Health, University of Texas Health Science Center at Houston, Houston, Texas; [4]University of Texas Health Science Center, Houston, Texas

Session: O-14. Have We Peaked? Updates in PK/PD

Background. Therapeutic drug monitoring (TDM) for vancomycin (VAN) with Bayesian models is recommended by national guidelines. However, limited data incorporating the models may hurt the performance. Our aim is to develop a novel deep learning-based pharmacokinetic model for vancomycin (PK-RNN-V) using electronic medical records (EHRs) data to achieve more accurate and personalized predictions for VAN levels.

Methods. EHR data were retrospectively retrieved from Memorial Hermann Hospital System, comprising 14 hospitals in the greater Houston area. All patients who received VAN and had any VAN levels were eligible. Patients receiving hemodialysis and extracorporeal membrane oxygenation were excluded. Demographic data, vital signs, diagnostic codes, concomitant medications, VAN administration, and laboratory data were preprocessed as longitudinal data. VAN infusion, VAN level measurement, or each hospital day were the time steps for the models. The dataset was splited 70:15:15 for training, validation, and test sets. Our PK-RNN-V model predicted individual patient volume distribution (v) and VAN elimination (k) at each time step using an irregular timesteps GRU model. To compare, Bayesian models were developed from publicly available models, and tuned to feedback the first VAN level to update the v and k. (VTDM)

Results. A total of 12,258 patients with 195,140 encounters were identified from Aug, 2019 and March, 2020. After exclusion of 6,775 patients, 5,483 patients with 8,689 encounters were included. Table 1 summarized the characteristics of patients included in our study. 55,336 doses of VAN were administered with a median dosage of 1.0 gm. VAN levels were measured 18,588 times at various timings. The median VAN level was 14.7 mcg/mL Table 2 described the performance of our models and VTDM models. Our model exhibited better performance compared to VTDM model (RMSE: 5.64 vs. 6.57, respectively). Figure 1 shows example prediction curves of VAN levels from each model.