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.

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

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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

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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.