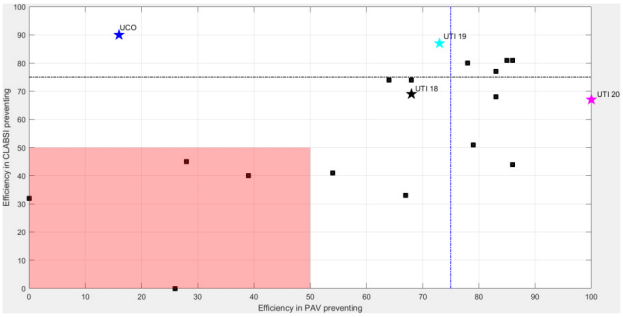
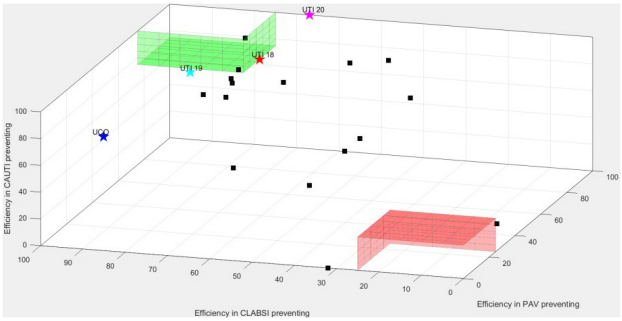
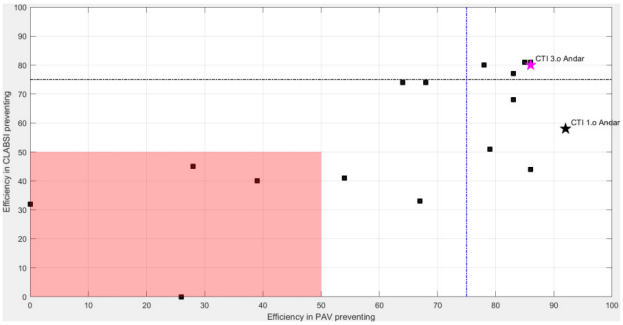
2D benchmark for the MSICUs from Lifecenter Hospital, Brazil, Jan-Dez/2019: UCO & UTI 19 =excellence in CLABSI control and opportunity to prevent VAP; UTI 20=excellence in VAP control and opportunity for CLABSI prevention; UTI 18=opportunity to prevent VAP+CLABSI.




3D benchmark for the MSICUs from Lifecenter Hospital, Brazil, Jan-Dez/2019




2D benchmark for the MSICUs from Vera Cruz Hospital, Brazil, Jan-Dez/2019: CTI 3.o Andar =excellence in the control of VAP+CLABSI; CTI 1.o Andar=excellence in VAP control and opportunity for CLABSI prevention.




***Conclusion.*** 2D and 3D benchmarks are easy to understand and summarize the efficiency in prevention the mains infections of MSICU.

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

**824. Isolation Rounding - Enforcing Existing Isolation Policies to Conserve Personal Protective Equipment**

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**PPE Conservation Team**

**Session:** P-35. HAI: Epidemiologic Methods

***Background.*** During the COVID-19 pandemic, supplies of personal protective equipment (PPE) have been limited and sold at increased cost. Prior to the pandemic, we had initiated a project to improve PPE adherence and decrease cost by removing eligible patients from transmission based precautions (TBPs). At baseline, ordering providers are responsible for TBP utilization with orders through the electronic medical record. We observed that patients were in TBP when not indicated; remained in TBP beyond the appropriate time; and a reluctance on the part of providers to discontinue the orders. We tested the effect on TBP duration and PPE utilization house-wide through frequent review of TBP by a nurse educator with communication to providers of discontinuation opportunities.

***Methods.*** From November 2019 to February 2020, all TBP orders in the pediatric intensive care unit (PICU) were reviewed intermittently. In March 2020, review was expanded to all inpatients with daily reviews in all units. Changes recommended and completed were tracked for all reviewed patients. We estimated cost of PPE in the PICU over time based on the number of patients in isolation and type of TBP utilized to determine whether our intervention resulted in reduced PPE use.

***Results.*** Regular rounding in the PICU increased the proportion of patients in appropriate TBP and reduced the need to communicate with providers directly (33% vs 3% requiring intervention, Figure 1). Over the same time period, less PPE was used and PPE-related costs lowered (average total PPE cost $306.18 vs $95.15 per day, Figure 2). Less of an effect was seen when analyzing house-wide data.

Figure 1 - P-chart of Percent Interventions Among Patients in TBP

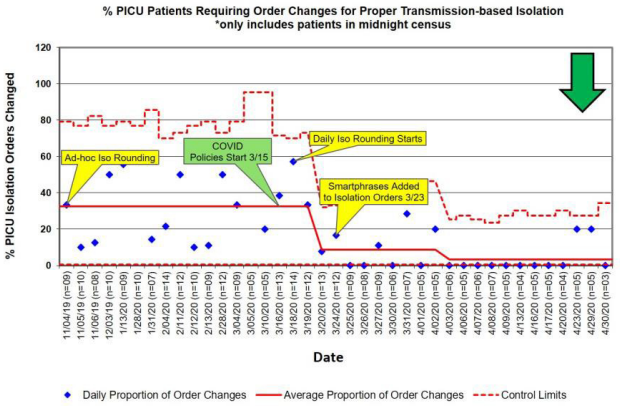
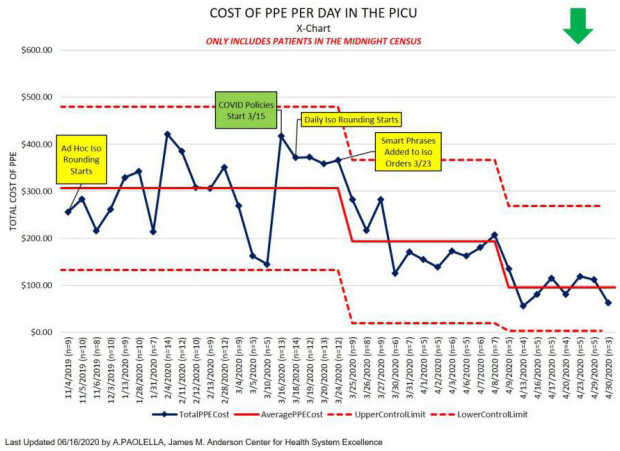



Figure 2 - X-chart of Total PPE Cost in the ICU




***Conclusion.*** Isolation rounds is an effective means to ensure proper TBP adherence and manage PPE use appropriately. Additional study is needed to confirm a return on investment, to account for variation among units, and to sustain COVID-19-influenced gains beyond the pandemic.

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

**825. An Academic-Information Technology Partnership to Create an Infectious Diseases Translational Science Database**

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**Session:** P-35. HAI: Epidemiologic Methods

***Background.*** Translational science is the process of turning observations in the laboratory, clinic, and community into interventions that improve human health. The coordinated effort to maintain integrated, validated laboratory and clinical data is often a rate-limiting step for research laboratories, especially for multi-site studies. Previous research shows a rate of error between 2.3 and 5.2% for basic data collection in clinical databases, up to 26.9% for more complex data points. The purpose of this project was to create a translational science database prototype that would be responsive to the unmet needs of the translational research community.

***Methods.*** Translational scientists, IT experts, and lab technicians mapped the workflow of a high-throughput research laboratory including clinical and laboratory data. Database goals were to develop processes that would minimize data entry time, avoid redundancies, and validate data in a secure environment (HIPAA-compliant). Unique to this platform was the ability to map creation of new samples (for example, PCR products) from parent samples (biologic samples). The platform was developed

in an iterative process utilizing interviews, workflow study, analysis of supporting artifacts, and mock-ups.

***Results.*** The current prototype allows for electronic upload or manual data entry of clinical data. In a small controlled study we found the rate of error for basic data entry to be below 1% within it. Pre-populated data entry screens map laboratory workflow with custom data entry fields produced based on laboratory results earlier in the work flow. Work-flow mapping includes microbiology, phenotypic descriptions (MIC), molecular biology (PCR), and customized experiments. Sequence data, housed separately, has data linkers stored in the database. The launch screen and data entry forms are populated based on specific criteria entered for each user.

***Conclusion.*** The Translational Science Database allows for efficient capture of high-quality data with baseline validation enabling seamless linking of translational data for single or multi-site laboratories. Future development work will expand the number of experiments and also incorporate stored biobank information into the database.

***Disclosures.*** Jeffrey Beairsto, BSc Eng (ME), Populus (Employee, Shareholder) Randal Neptune, BSc., MSc., Populus Global Solutions (Employee) Beth Webster, BSc, MBA, Populus Global Solutions Inc (Employee, Shareholder) John N. Rutter, BscEng, Populus Global Solutions (Board Member, Employee, Shareholder) Tristan Rutter, BA, Populus (Employee) Kevin W. Garey, PharMD, MS, FASHP, Merck & Co. (Grant/Research Support, Scientific Research Study Investigator)

### 826. Comparative Epidemiological Analysis of *Serratia marcescens* using PFGE and Whole Genome Sequence Methods

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**Session:** P-35. HAI: Epidemiologic Methods

***Background.*** Epidemiological (EPI) analyses of bacterial pathogens play an important role in infection control practices during suspected outbreaks. Pulsed field gel electrophoresis (PFGE) is the gold standard for EPI typing of most bacterial organisms, but this method has been slowly replaced by sequencing-based methods, such as multilocus sequence typing (MLST) and core genome (cg)MLST that uses whole genome sequencing (WGS) data. We evaluated the utility of WGS *ad hoc* schemas to predict relatedness among *Serratia marcescens* (SM) clinical strains.

***Methods.*** A total of 19 SM clinical isolates collected as part of the SENTRY Program and JMI worldwide collections were selected. Isolates were typed by PFGE and analyzed using GelCompar II (100% similarity scored as identical, > 85% and < 100% as genetically related and < 85% as unrelated). WGS was performed using MiSeq (Illumina) and contigs generated using SPAdes. Raw reads and assembled contigs were used to generate phylogenetic trees using kWIP and progressiveMauve (pMauve), respectively. Similarity matrices and dendrograms created by the three protocols were compared.

***Results.*** Based on PFGE analysis, 19 isolates were classified into 10 pulsotypes, A through J, and 1 subtype, A1 (Fig.1A). Among dendrograms generated based on WGS, analysis of short k-mers (Fig.1B) inaccurately showed phylogenetic separation among isolates in A/A1, C and G types, while analysis of much longer contigs (Fig.1C) accurately clustered isolates according to groups defined using PFGE. One isolate in the A/A1 group (517323) was separated from the group using kWIP; however, using the more sophisticated pMauve, this isolate was accurately clustered within the A/A1 isolates.

***Conclusion.*** Concordance was observed between PFGE- and WGS-based phylogenetic analysis of SM for genetic relatedness. Based on this analysis, WGS data can be used to predict EPI of this bacterial species on an *ad hoc* basis. This methodology can be expanded to other species.

Figure 1

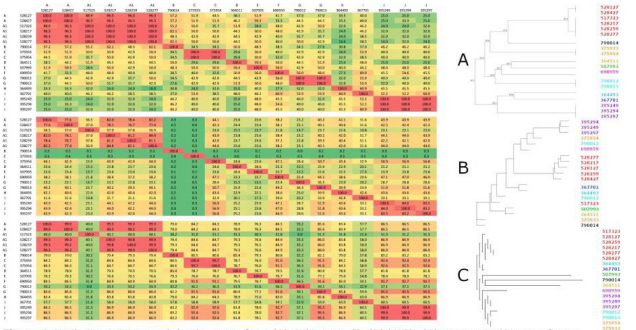


**Figure 1** Similarity matrices and dendrograms from (A) GelCompar II, (B) kWIP, (C) progressiveMauve software. Matrix columns and rows are ordered by class, alphabetically. Dendograms are labeled by isolate and colored by class.

***Disclosures.*** Rodrigo E. Mendes, PhD, A. Menarini Industrie Farmaceutiche Riunite S.R.L. (Research Grant or Support)Allergan (Research Grant or Support) Allergan (Research Grant or Support)Basilea Pharmaceutica International, Ltd (Research Grant or Support)Cipla Ltd. (Research Grant or Support)Department of Health and Human Services (Research Grant or Support)GlaxoSmithKline (Research Grant or Support)Melinta Therapeutics, Inc. (Research Grant or Support)Merck (Research Grant or Support)Pfizer (Research Grant or Support) Mariana Castanheira, PhD, 1928 Diagnostics (Research Grant or Support) A. Menarini Industrie Farmaceutiche Riunite S.R.L. (Research Grant or Support) Allergan (Research Grant or Support)Allergan (Research Grant or Support)Amplyx Pharmaceuticals (Research Grant or Support)Cidara Therapeutics (Research Grant or Support)Cidara Therapeutics (Research Grant or Support)Cipla Ltd. (Research Grant or Support)Cipla Ltd. (Research Grant or Support)Fox Chase Chemical Diversity Center (Research Grant or Support)GlaxoSmithKline (Research Grant or Support) Melinta Therapeutics, Inc. (Research Grant or Support)Melinta Therapeutics, Inc. (Research Grant or Support)Melinta Therapeutics, Inc. (Research Grant or Support) Merck (Research Grant or Support)Merck (Research Grant or Support)Merck & Co, Inc. (Research Grant or Support)Merck & Co, Inc. (Research Grant or Support)Paratek Pharma, LLC (Research Grant or Support)Pfizer (Research Grant or Support)Qpex Biopharma (Research Grant or Support)

### 827. Does Patient Location (Rural or Urban) influence risk factors and incidence rate for 30-day readmission after gram positive pneumonia?

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**Session:** P-35. HAI: Epidemiologic Methods

***Background.*** In the US, pneumonia is the most common cause of a hospital admission. Prior analysis has shown that nearly one in six patients will have an all-cause 30-day readmission. Given the disparities in access to healthcare between rural and urban settings, we sought to see if patient location influenced the incidence rate for 30-day readmission after treatment for Gram Positive Pneumonia.

***Methods.*** We utilized Agency of Healthcare Research and Quality's (AHRQ) 2014 Nationwide Readmission Database to identify index admissions with a principal diagnosis of Gram Positive Pneumonia (ICD-9 codes 482.3, 482.31, 482.32, and 482.39 for streptococcus and 482.40, 482.41, 482.42, and 482.49 for staphylococcus). The 2013 NCHS Urban-Rural Classification System was used to classify if originating from an urban or rural location. Applicable admissions were all adults (age >= 18) from January 1 to November 30, 2014. Patients who died during index admission and those with missing covariates were excluded. All-cause readmissions within 30-days of an index admission were analyzed. Predictors for readmission were determined using a multivariable logistic regression model.

***Results.*** A total of 8,130 patients met criteria for inclusion of which 1,631 (20.06%) were readmitted (all-cause) within 30-days. There was no statistically significant difference in readmission between patients from a rural (18.7%) or urban (20.4%) location. The statistically significant predictors for readmission for patients from a rural location were those admitted on a weekend (OR: 1.41, CI: 1.04-1.90), discharged to short term hospital (OR: 2.70, CI: 1.18-6.19) or AMA (OR: 6.53, CI: 1.46-29.10), and those with a LOS between 7 and 14 days (OR: 1.48, CI: 1.10-2.00). For patients from an urban location, statistically significant predictors were those admitted on a weekend (OR: 1.17, CI 1.02-1.34), discharged AMA (OR: 2.89, CI: 1.74-4.78), LOS between 7 and 14 days (OR: 1.19, CI: 1.03-1.37) and those with CKD (OR: 1.20, CI: 1.03-1.39).

***Conclusion.*** The risk factors for readmission after Gram Positive Pneumonia for patients from a rural and urban location are similar. More research is needed to develop interventions for those who are at risk for readmission after Pneumonia to reduce future morbidity and mortality.

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

### 828. Evaluation of Home Time as a Patient-Centered Metric for Pneumonia Hospitalizations: A Retrospective Cohort Study of Medicare Fee-For-Service Beneficiaries

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**Session:** P-35. HAI: Epidemiologic Methods

***Background.*** The Centers for Medicare & Medicaid Services (CMS) uses hospital readmission to incentivize hospital care delivery for acute conditions including pneumonia. However, current CMS performance metrics do not account for the competing risk of mortality in the post-discharge period or during the hospital stay. Our objective was to assess home time within 30 days after discharge among pneumonia hospitalizations, as a patient-centered metric.

***Methods.*** A retrospective observational study was conducted in a cohort of Medicare fee-for-service beneficiaries admitted between 01/01/2015 and 11/30/2017. Home time was the number of days spent alive, out of an acute care setting, skilled nursing facility, or a rehabilitation facility within 30 days of discharge. If a patient spends any part of a day in a care facility or died after discharge, then that day was not included in the calculation for home time. Hospital-level rates of risk-adjusted home time were calculated using multilevel regression models. We compared hospital performance on 30-day risk-standardized home time with its performance on 30-day risk standardized readmission rate (RSRR) and mortality rate (RSMR). Characteristics of hospitals with high and low risk-adjusted home-time were compared.

***Results.*** Among 1.7 million pneumonia admissions admitted to 3,116 hospitals, the median 30-day risk-standardized home time was 20.5 days (interquartile range: 18.9-21.9 days). Hospital-level characteristics such as case volume, bed size, for-profit ownership, rural location of hospital, teaching status, and participation in the bundle payment program were significantly associated with home-time. RSRR (rho: -0.233, p< 0.0001) and RSMR (rho: -0.223, p< 0.0001) had weak, inverse correlations with