Figure 1: Medically Assisted Therapy Prescribed at Discharge

Conclusion. Gender, more complicated infections, and prolonged LOS may increase the likelihood of receiving a prescription for MAT at discharge. MAT prescription at discharge may decrease the risk of 30-day SAB related readmission (NNT 5.9). The results suggest that provision of MAT to patients with SAB and history of IVDU should be incorporated into standardized treatment guidelines.

Table 1: Baseline Characteristics

| Variable                | MAT at Discharge | No MAT at Discharge | P Value |
|-------------------------|------------------|---------------------|---------|
| All participants        | (n=48)           | (n=125)             |         |
| 30-day mortality (inpatient deaths excluded) | 6 (12.5%) | 6 (4.8%) | 0.26 |
| 90 day mortality (inpatient deaths excluded) | 13 (27.1%) | 15 (12.0%) | 0.04 |
| SAB associated 30-day readmission* | 9 (18.8%) | 32 (25.6%) | 0.40 |
| SAB associated 90-day readmission* | 6 (12.5%) | 15 (12.0%) | 0.82 |

*SAB-associated readmission defined as including progressive worsening of original infectious focus, disseminated bacterial seeding from original focus, issues with subsequent parenteral antimicrobial therapy, or adverse drug reaction.

Table 2: MAT & Clinical Outcomes in S. aureus Bacteremia

| MAT at Discharge | No MAT at Discharge | P Value |
|------------------|---------------------|---------|
| All patients     | (n=48)              | (n=125) |         |
| 30-day mortality (inpatient deaths excluded) | 6 (12.5%) | 6 (4.8%) | 0.26 |
| 90 day mortality (inpatient deaths excluded) | 13 (27.1%) | 15 (12.0%) | 0.04 |
| SAB associated 30-day readmission* | 9 (18.8%) | 32 (25.6%) | 0.40 |
| SAB associated 90-day readmission* | 6 (12.5%) | 15 (12.0%) | 0.82 |

*SAB-associated readmission defined as including progressive worsening of original infectious focus, disseminated bacterial seeding from original focus, issues with subsequent parenteral antimicrobial therapy, or adverse drug reaction.

Disclosures. All Authors: No reported disclosures

40. The Impact of Medically Assisted Therapy for Opiate Use Disorder in Staphylococcus Aureus Bacteremia Patients Within a Large Hospital System - A Retrospective Cohort Study

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Session: O-8. Bacteremia and Endocarditis

Background. Intravenous drug use (IVDU) is a risk factor for development of S. aureus bacteremia (SAB) and prevalent in opiate use disorder (OUD). While the standard of care involves treating the underlying OUD with medically assisted therapy (MAT), it is unknown how much this has on clinical endpoints.

Methods. We conducted a retrospective cohort study of patients with IVDU with hospitalizations for SAB during a 28-month period from 9/2016 through 12/2018 in 10 urban and rural North Carolina hospitals in a single large health system. We compared outcomes for patients receiving prescription for MAT at discharge versus non-MAT at discharge.MAT was defined as receiving methadone, buprenorphine, or naltrexone. Patients who expired inpatient were excluded from analysis. Clinical endpoints were 30- and 90-day mortality and 30-day SAB-related readmissions.

Results. Of the 174 patients, 28% received a prescription for MAT at discharge. The majority of the patients were Caucasian (88%), female (57%), with mean age of 37 years. Factors that significantly increased likelihood of MAT at discharge were female gender (34% vs 20%, p=0.04), having a complicated SAB (33% vs 28%, p=0.01), presence of a spinal/epidural abscess (57% vs 43%, p=0.002), and increased length of stay (LOS) (37 days vs 24 days, p=0.002). No difference in 30- and 90-day mortality was observed; only one patient in each group died within 90 days. Prescription for any MAT at discharge was associated with a significant decrease in the risk of SAB-related 30-day readmission (0% vs 17%, p=0.002).

Table 1: Baseline Characteristics

| Variable                | MAT at Discharge | No MAT at Discharge | P Value |
|-------------------------|------------------|---------------------|---------|
| All patients            | (n=48)           | (n=125)             |         |
| Gender                  | 26 (54.1%)       | 52 (41.6%)          | 0.32    |
| Race                    | 14 (29.1%)       | 37 (29.6%)          | 0.94    |
| Age (years)             | 9 ± 6             | 8 ± 5               | 0.32    |
| History of OUD          | 31 (64.5%)       | 77 (61.6%)          | 0.54    |
| History of SAB          | 12 (25%)         | 35 (28%)            | 0.33    |
| History of IVDU         | 29 (60.4%)       | 46 (36.8%)          | 0.04    |
| History of IVDU in last year | 8 (16.7%) | 12 (9.6%) | 0.21 |
| History of Methadone    | 18 (37.5%)       | 35 (28%)            | 0.08    |
| History of Buprenorphine| 6 (12.5%)        | 29 (23%)            | 0.16    |
| History of Naltrexone   | 4 (8.3%)         | 13 (10.4%)          | 0.60    |

Disclosures. All Authors: No reported disclosures

41. Impact of Gut Microbiome Changes on Hematopoietic Stem Cell Transplantation Outcomes in Children.

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Session: O-9. Basic and Translational Science

Background. In adults undergoing allogeneic hematopoietic cell transplantation (HCT), higher gut microbiome diversity is associated with reduced bloodstream infections (BSI) and improved overall survival (OS). Rifaximin prophylaxis in adult HCT helps to maintain microbiome diversity. We examine changes in microbiome in a cohort of pediatric patients undergoing HCT.

Methods. Patients were enrolled in an institutional biorepository (n=82) with a subset enrolled in an ongoing trial using rifaximin (n=21) between 2013–2020. All patients had HCT for a hematologic malignancy, using myeloablative conditioning. Patients in the rifaximin trial received rifaximin starting 7 days before HCT (HCT), higher gut microbiome diversity is associated with reduced bloodstream infections (BSI) and improved overall survival (OS). Rifaximin prophylaxis in adult HCT helps to maintain microbiome diversity. We examine changes in microbiome in a cohort of pediatric patients undergoing HCT.

Results. Of the 82 patients, 28% received a prescription for MAT at discharge. The majority of the patients were Caucasian (88%), female (57%), with mean age of 37 years. Factors that significantly increased likelihood of MAT at discharge were female gender (34% vs 20%, p=0.04), having a complicated SAB (33% vs 28%, p=0.01), presence of a spinal/epidural abscess (57% vs 43%, p=0.002), and increased length of stay (LOS) (37 days vs 24 days, p<0.001). No difference in 30- and 90-day mortality was observed; only one patient in each group died within 90 days. Prescription for any MAT at discharge was associated with a significant decrease in the risk of SAB-related 30-day readmission (0% vs 17%, p=0.002).

Table 1: Baseline Characteristics

| Variable                | MAT at Discharge | No MAT at Discharge | P Value |
|-------------------------|------------------|---------------------|---------|
| All patients            | (n=48)           | (n=125)             |         |
| Gender                  | 26 (54.1%)       | 52 (41.6%)          | 0.32    |
| Race                    | 14 (29.1%)       | 37 (29.6%)          | 0.94    |
| Age (years)             | 9 ± 6             | 8 ± 5               | 0.32    |
| History of OUD          | 31 (64.5%)       | 77 (61.6%)          | 0.54    |
| History of SAB          | 12 (25%)         | 35 (28%)            | 0.33    |
| History of IVDU         | 29 (60.4%)       | 46 (36.8%)          | 0.04    |
| History of Methadone    | 18 (37.5%)       | 35 (28%)            | 0.08    |
| History of Buprenorphine| 6 (12.5%)        | 29 (23%)            | 0.16    |
| History of Naltrexone   | 4 (8.3%)         | 13 (10.4%)          | 0.60    |

Disclosures. All Authors: No reported disclosures

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been reported in DCM but are exceedingly rare and cannot account for the ~500–600 cases of DCM/year.

**Methods.** We performed whole exome sequencing on 66 individuals with DCM, retaining variants predicted damaging (CADD >15) with a population frequency <10%.

**Results.** Homozygous CLEC7A c.714T >G; p.Y238* causing a truncated Dectin-1 receptor was overrepresented (OR=9.8449, 95% CI 3.0841 to 31.4260, P=0.0001). Dectin-1 signaling pathway variants included 3 homozygous and 11 heterozygous CLEC7A p.Y238* individuals, one each CLEC7A p.I223S and MALTI p.R198Q, and one PLCG2 p.R268W. Since Dectin-1 is the receptor for β-glucan, a major Coccidioides cell-wall component, we hypothesized that Dectin-1 pathway variants could affect fungal recognition and cellular response. Healthy control PBMCs stimulated with purified β-glucan or heat-killed Candida albicans induced 6-fold more TNFs than patients with homozygous or heterozygous CLEC7A, PLCG2 or MALTI variants (P=0.0022, Ordinary one-way ANOVA). Additionally, one patient with a family history of DCM but lacking a defined mutation also failed to up-regulate TNFs after stimulation.

**Conclusion.** Normalized TNF production from healthy control and DCM patient’s peripheral blood mononuclear cells were consonant with increased dissemination in Clec7a−/− mice as well as in patients receiving anti-TNF biologics. These gene variants accounted for 31% of our DCM cohort (21/66 patients). This is the first demonstration of variants outside the IL12-IFNγ pathway impairing fungal recognition and cellular response in coccidioidomycosis. Common heterozygous variants may be sufficient for disease susceptibility to highly pathogenic organisms.

**Disclosures.** Michail Lionakis, MD, ScD, Matinas BioPharma (Research Grant or Support)

**43. The Capsule and Beyond: Genetic Determinants of Pediatric streptococcus Pneumoniae empyema**

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**Session:** O-9, Basic and Translational Science

**Background.** *Streptococcus pneumoniae* is the most common cause of pneumonia in children, including empyema, a severe complication with increasing incidence in the post-pneumococcal vaccine era. Only a subset of > 90 serotypes cause empyema. Virulence determinants of empyema remain largely unknown.

**Methods.** We performed Illumina sequencing of invasive Pneumococcal isolates from pediatric patients at Primary Children’s Hospital (Salt Lake City, UT) isolated between 1996–2018, de novo genome assembly (SPADES), annotation (PROKKA), serotyping (Quelling and SeroBA), and pan-genome assembly (ROARY). SCOARY and pan-genome were used for microbiome diversity. Approaches to preserve microbiome diversity and prevent BSI will inform future treatment and prevention.

**Results.** 366 pneumococcal isolates were analyzed from 39 serotypes and multiple phenotypes including pneumonia (n=76), empyema (n=63), CNS infection (n=24), and isolated bacteremia (n=79). Serotypes and empyema phenotype clustered roughly by phylogeny. Most analyzed empyema isolates after 2010 were serotype 3 (19/25); prior to PCV-13 introduction serotypes 1 (8/38), 7F (7/38), and 19A (11/38) were more highly represented. Genes implicated in capsule synthesis, transposases, and metabolism were statistically correlated with the empyema phenotype.

**Conclusion.** Specific capsular or metabolic genes may confer optimal fitness for pleural disease. Further characterization of these genetic associations is needed and will inform future treatment and prevention.

**Disclosures.** Carrie L. Byington, MD, BioFire (Other Financial or Material Support, Royalties for Intellectual Property)IDbyDNA (Advisor or Review Panel member) Krow Ampofo, MCBCh, Merck (Grant/Research Support)

**44. In-host Infection Dynamics Of Pseudomonas Aeruginosa Pneumonia**

Byington, Kelly E. R., Bachta, Allen P., Nielsen, John N., et al.

**Session:** OFID 2020:7 (Suppl 1)

**Background.** *Pseudomonas aeruginosa* infection is a major contributor to mortality in cystic fibrosis (CF) and other disorders. Infections are often polymicrobial and can be chronic and life-threatening. The current study evaluates the in-host infection dynamics of *P. aeruginosa* in the setting of acute or chronic respiratory infection in CF and cystic fibrosis transmembrane conductance regulator (CFTR) null patients.

**Methods.** A total of 364 *P. aeruginosa* isolates from 312 pediatric and adult patients with acute or chronic respiratory infection were investigated. Isolates were collected from clinical samples and stored at −80°C. Clinical and epidemiological data were collected. Total bacterial 16S rRNA gene was sequenced, and 16S rRNA gene copies were quantified by qPCR.

**Results.** The mean total bacterial 16S rRNA gene and *P. aeruginosa* 16S rRNA gene copies were log transformed and the relative abundance of bacterial 16S rRNA gene copies and *P. aeruginosa* 16S rRNA gene copies was calculated. The relative abundance of *P. aeruginosa* 16S rRNA gene copies was compared with the total bacterial 16S rRNA gene by a linear regression model. The association between clinical data and relative abundance of bacterial 16S rRNA gene and *P. aeruginosa* 16S rRNA gene copies was evaluated by a logistic regression model.

**Conclusion.** The in-host infection dynamics of *P. aeruginosa* in the setting of acute or chronic respiratory infection in CF and CFTR null patients were characterized. The relative abundance of *P. aeruginosa* 16S rRNA gene copies was associated with clinical data. These findings may inform future infection prevention and treatment strategies.

**Disclosures.** Byington K. E. R, Bachta A., Allen P. J., Nielsen J. N., others (Research Grant or Support, Royalties for Intellectual Property, Other Financial or Material Support, Patent Royalties, Other)