**Session:** Molecular and Genomic Epidemiology of Resistant Pathogens

**Background:** Ventriculoperitoneal (VP) shunt is one of the most common procedures in neurosurgical practice. A significant problem encountered in shunt procedures is infection, with infection rates ranging from 2% to 27%, often with poor outcome. The objectives of the study were to retrospectively evaluate the infection rate associated with central nervous system (CNS) shunts, assess the frequency of the pathogens as well as their antibiotic sensitivity patterns to aim at suitable prophylaxis.

**Methods:** Materials and Methods. Retrospective study conducted in the Microbiology Department, SGPGI, Lucknow from December 2017 to August 2018. A total of 168 CSF samples were received with a suspected shunt infection. Samples were analyzed by wet mount, India ink, gram stain and inoculated on blood agar and MacConkey agar. Identification and AST were done by MALDI-TOF system (VITEK-MS) and Vitek 2 automated sensitivity system.

**Results:** During the study period, 37/168 (22.02%) CSF were positive by culture. Most common isolates were Enterococcus species. 18/37 (48.65%) were Enterococcus faecalis and 28/37 (75.67%) were Enterococcus faecium. VCE accounted for 12% of our isolates while VCE accounted for 12% of our isolates while E. faecalis accounted for 66% and 16%, respectively. All VCE were susceptible to amoxicillin and vancomycin.

**Conclusion:** Discussion and Conclusion. The antibiotic resistance pattern suggests aminoglycosides, colistin and vancomycin to be a better choice of antibiotics either prophylactically/therapeutically, which may result in effective sterilization of the CSF infections following VP shunt procedure is secondary to catheter blockage complicating the results of surgery and are associated with high morbidity and mortality rates.

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

### 63.5 Genomic Evolution and Progression of Antimicrobial Resistance in a Series of Extensively Drug-Resistant Pseudomonas aeruginosa (XDR-Pa) Isolates from a Cystic Fibrosis Lung Transplant Recipient

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**Session:** Molecular and Genomic Epidemiology of Resistant Pathogens

**Background:** Chronic respiratory infection due to extensively drug-resistant *Pseudomonas aeruginosa* (XDR-Pa) is a significant cause of mortality in cystic fibrosis (CF) patients. The CF respiratory antibiotic use, antibiotic resistance, and PA colonization creates a milieu for high evolutionary pressure and genetic diversity. We sought to explore the progression of antibiotic resistance and genome evolution of XDR-Pa in a longitudinal series of isolates collected from an 18-year-old CF patient who underwent lung transplantation.

**Methods:** Consecutive respiratory isolates were collected from December 2016 to March 2018. Standard disk diffusion methods were used to evaluate antimicrobial susceptibility. Whole-genome sequencing (WGS) data were obtained on an Illumina NextSeq and assembled. Variants were identified using the GATK HaplotypCaller and their functional impact was determined using snpEff. Maximum likelihood phylogenetic trees were constructed using MEGA and BEAST. Panther was used to test for enrichment of Gene Ontology functional categories among mutated genes.

**Results:** Phylogenetic analysis of complete genome sequences showed that 18 isolates formed a monophyletic group. Analysis using BEAST showed that genomes shared a common ancestor followed by multiple rounds of clonal expansion. Over 300 single nucleotide variants and small insertion-deletion mutations were found, in comparison with a reconstruction of the ancestral sequence (Figure 1). Shared patterns of antibiotic susceptibility profiles were largely concordant with phylogenetic clustering and trended toward a decrease in susceptibility over time. Two different framish mutations in the DNA mismatch repair gene *mutL* were found in 15 genomes and these exhibited an increased rate of transition to transversion mutations, consistent with a hypermutator phenotype.

**Conclusion:** WGS of XDR-Pa identified variations in antibiotic resistance and virulence genes. Changes in mutL likely accelerated the accumulation of mutations. Multiple related sub-groups of strains appear to have been circulating prior to transplant and continued to diverge during the treatment period. Correlating antibiotic resistance, susceptibility profiles, and WGS in XDR-Pa from a single patient reveals the clinical impact of genomic evolution in CF.

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

### Table 2: Enterococcal bloodstream infections from 2013-2018 categorized by Enterococcus species and susceptibility to vancomycin and ampicillin

| Species             | Total % of total | Vancomycin Susceptible and Ampicillin Susceptible (Total % of species) | Vancomycin Non-susceptible and Ampicillin Susceptible (Total % of species) | Vancomycin Non-susceptible and Ampicillin Resistant (Total % of species) | Vancomycin Susceptible and Ampicillin Resistant (Total % of species) |
|---------------------|------------------|-----------------------------------------------------------------------|--------------------------------------------------------------------------|------------------------------------------------------------------------|---------------------------------------------------------------------|
| Enterococcus (all)  | 240              | 202 (84.1) 15 (6.3) 15 (6.3) 7 (3.8)                                                  |                                                                                       |                                                                                       |                                                                      |
| Enterococcus spp. (unidentified) | 7 (3)        | 6 (85.7) 1 (14.3) 0 0                                                             |                                                                                       |                                                                                       |                                                                      |
| Enterococcus clys/linos     | 33 (13.8) | 10 (30.3) 13 (39.4) 4 (12.1) 6 (18.2)                                                |                                                                                       |                                                                                       |                                                                      |
| Enterococcus divers     | 2 (0.8)       | 2 (100) 0 0 0                                                                   |                                                                                       |                                                                                       |                                                                      |
| Enterococcus faecalis     | 159 (66.9) | 133 (83.2) 15 (9.5) 1 (0.6) 0                                                     |                                                                                       |                                                                                       |                                                                      |
| Enterococcus faecium     | 10 (4)        | 2 (20) 1 (10) 0 8 (80)                                                              |                                                                                       |                                                                                       |                                                                      |
| Enterococcus gallinarum | 19 (7.8)     | 13 (68) 4 (21.1) 1 (5.3) 1 (5.3)                                                   |                                                                                       |                                                                                       |                                                                      |
| Enterococcus hirae     | 2 (0.8)       | 2 (100) 0 0 0                                                                    |                                                                                       |                                                                                       |                                                                      |

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