Table 1. Patient demographics and co-morbidities.

| Variable | Total (N=108) |
|----------|---------------|
| Average Age (years) | 58.6 |
| Male – No. (%) | 64 (59.2) |
| Race/Ethnicity – No. (%) |  |
| White | 62 (57.4) |
| Black | 44 (40.7) |
| Asian | 2 (1.8) |
| Immunosuppression – No. (%) |  |
| Solid malignancy | 17 (15.7) |
| Hematologic malignancy | 6 (5.6) |
| SOT | 11 (10.2) |
| HSCT | 3 (2.8) |
| Other | 17 (15.7) |
| Diabetes – No. (%) | 34 (31.5) |
| Cardiovascular disease – No. (%) | 19 (17.6) |
| Chronic lung disease – No. (%) | 21 (19.4) |
| CKD – No. (%) | 19 (17.6) |
| ESRD – No. (%) | 8 (7.4) |
| Cirrhosis – No. (%) | 13 (12.0) |
| IVDU – No. (%) | 5 (4.6) |
| Mechanical ventilation – No. (%) | 19 (17.6) |
| Trauma at time of admission – No. (%) | 10 (9.3) |
| Burn at time of admission – No. (%) | 1 (0.9) |
| Pitt Bacteremia Score (Mean) | 2.8 |

Table 2. Gram-negative bacteria frequency.

| Gram-negative Bacteria                       | Total (%) |
|----------------------------------------------|-----------|
| *Escherichia coli*                           | 30 (27.8) |
| *Klebsiella pneumoniae*                      | 24 (22.2) |
| *Pseudomonas aeruginosa*                     | 11 (10.2) |
| *Polymicrobial*                              | 11 (10.2) |
| *Enterobacter species*                       | 9 (8.3)   |
| Other                                        | 7 (6.5)   |
| Not detected                                 | 6 (5.5)   |
| *Klebsiella oxytoca*                         | 4 (3.7)   |
| *Serratia marcescens*                        | 3 (2.8)   |
| *Acinetobacter baumannii*                    | 3 (2.8)   |

**Conclusion.** The BCID-GN panel enabled earlier time to optimal treatment of highly resistant bacteria as well as multiple opportunities for narrowing gram negative spectrum and a higher degree of certainty in cessation of broad-spectrum antibiotics.

**Methods.** 107 lung transplant recipients (79% with cystic fibrosis) were enrolled at Duke University Medical Center over a 2-year period – 59% with acute respiratory symptoms, the remainder as healthy controls. Whole blood was collected by PAXGene for RNA sequencing. Prior to undergoing biomarker analysis, each case was adjudicated to the appropriate clinical phenotype: bacterial infection, viral infection, allograft rejection, and healthy. Logistic regression models were applied to gene expression data to identify classifiers capable of identifying each etiology.

**Results.** In lung transplant recipients, 117 genes were upregulated at least 2-fold in the presence of viral infection compared to healthy transplant controls. These genes clustered into expected antiviral pathways, including type I interferon signaling, interferon gamma mediated signaling, and defense response to virus, although the magnitude of gene expression was significantly less than that seen in non-transplant cohorts.

**Conclusion.** Even in the presence of systemic immunosuppression and regardless of presence/absence of cystic fibrosis, core canonical components of the host response to infection and rejection are seen. Gene expression signatures based on these conserved components offer the potential for diagnostic capability in the setting of non-specific respiratory illness in these vulnerable hosts.

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1024. Using DOOR-MAT to Theoretically Compare Three Rapid Diagnostic Tests for Gram-Negative Bloodstream Infections in Immunocompromised Patients

**Background.** Molecular rapid diagnostic tests (RDTs) for bloodstream infections (BSI) utilize a variety of technologies and differ substantially in organisms and resistance mechanisms detected. RDT platforms decrease time to optimal antibiotics; however, data on RDTs in special populations, such as immunocompromised are extremely limited. This study aimed to compare theoretical changes in antibiotics based on differences in panel identification of organisms and resistance targets among three commercially available RDT panels.

**Methods.** Retrospective cohort of immunocompromised patients treated for gram-negative BSI at University of Maryland Medical Center from January 2018 to September 2020. Immunocompromised 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 <1000 cells/μL at any time 30 days prior to BSI diagnosis. Verigene BC-GN was performed as standard of care. GenMark eXpress BCID and BioFire FilmArray BCID 2 results were assigned based on respective identifiable organism panels.

An infectious diseases clinician blinded to final antimicrobial susceptibility testing (AST) results used RDT results to assign antibiotic treatments for each platform. Decisions were referenced against a priori DOOR-MAT matrices. A partial credit scoring system (0 to 100) was applied to each decision based on final AST results. The mean and standard deviation (SD) were compared across panels using One-Way Repeated Measures ANOVA with modified Bonferroni for multiple comparisons.

**Results.** A total of 146 patients met inclusion. Baseline characteristics are summarized in Table 1. The mean (SD) DOOR-MAT scores for the three RDT panels were: 86.1 (24.4) Verigene BC-GN vs. 88.5 (22.2) GenMark BCID vs. 87.2 (24.4) BioFire BCID 2. There was no statistically significant difference between the panels for DOOR-MAT score (P=0.6).

**Conclusion.** The BCID-GN panel enabled earlier time to optimal treatment of highly resistant bacteria as well as multiple opportunities for narrowing gram negative spectrum and a higher degree of certainty in cessation of broad-spectrum antibiotics.