CRISPRclean workflow easily integrates into next generation sequencing projects

Schematic of the Jumpcode CRISPRclean protocol

CRISPRclean was applied to contrived infected tissue samples including human lung RNA spiked with serially diluted amounts of SARS-CoV-2 RNA and bacterial RNA. NEB RNA libraries were prepared and treated with CRISPRclean protocol, then sequenced on Illumina instruments. Data analysis was performed using Jumpcode proprietary software to measure alignment and depletion rates, the Silva database for rRNA read alignment, and Kraken2 and CosmosID pipelines for k-mer based metagenomic investigation. Fold enrichment of SARS-CoV-2 reads after CRISPRclean depletion of libraries prepared from contrived samples.

Conclusion. Metatranscriptomics powered by CRISPR-mediated rRNA depletion offers a robust methodology to acquire viral genomic data, microbiome composition, co-infection information, and the transcriptional status of the host immune response in a single workflow. This sequencing-based approach can be available on the first day of the next viral outbreak and should be considered as a first-line test for novel zoonotic virus detection. Bacterial species composition of patient stool samples before and after CRISPRclean depletion.

For the sample containing 0.0001% SARS-CoV-2, (60 viral copies), the number of reads mapping to the SARS-CoV-2 genome increases from ~10,000 reads to ~70,000 reads. A similar increase in reads occurs for S. aureus. The percentage of SARS-CoV-2 genome covered at 1X and 10X also increases. Similar results were achieved even after downsampling the datasets to 5M reads. There is a 4-fold increase in bacterial species detection in these stool samples after CRISPRclean treatment. Percentage of SARS-CoV-2 genome covered at 1X and 10X increases as a result of rRNA depletion.

Coverage of the SARS-CoV-2 genome at 50 million reads.

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CosmosID Shotgun Metagenomics Analysis

Number of reads aligning to the S. aureus and SARS-CoV-2 genomes increases after CRISPRclean depletion.

CRISPRclean treatment of the fully contrived samples increases the fraction of reads that map to the SARS-CoV-2 genome by an average of ~10-fold.

Results. CRISPRclean treatment of the contrived samples increases ~10-fold of reads that map to the SARS-CoV-2 genome. For the 60 viral copies of SARS-CoV-2 sample, the number of reads mapping to the SARS-CoV-2 genome increases from ~10,000 reads to ~70,000 reads. A similar increase in reads occurs for S. aureus. The percentage of SARS-CoV-2 genome covered at 1X and 10X also increases. Similar results were achieved even after downsampling the datasets to 5M reads. There is a ~4-fold increase in bacterial species detection in these stool samples after CRISPRclean treatment. Percentage of SARS-CoV-2 genome covered at 1X and 10X increases as a result of rRNA depletion.

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994. Comparison of Lactate, Procalcitonin and a Gene Signature Assay Alone or in Combination to Differentiate Sepsis from Non-infectious Systemic Inflammation in ICU Patients

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Session: P-56. Microbial Pathogenesis

Background. Procalcitonin (PCT) and serum lactate (L) are measures of bacterial infection and tissue hypoxia, respectively, but also used to discern sepsis from infection negative systemic inflammation (INSI). However, improved tools are needed to enhance this differentiation. A previously validated gene signature assay (SeptiCyte RAPID) and its correlated score (SeptiScore (SS)) has been reported to effectively differentiate sepsis from INSI.

Objective. To compare early L, PCT and SS results (alone or in combination) in differentiating sepsis from INSI in adult intensive care unit (ICU) patients (Pt).

Methods. Data from a previously reported, prospective study (8 sites). Inclusion criteria: (i) ICU admission with ≥ 2 signs of systemic inflammatory response syndrome; (ii) Therapeutic antibiotic administration; (iii) external 3-physician clinical review classifying each Pt as sepsis or INSI with ≥ 2 reviewer agreement; (iv) L, PCT & SS values within 24 hrs of ICU admission; (v) Statistical Analysis; (iv) Area under the receiving operator curve (AUROC), 95% confidence intervals (CI) via generalized linear models for: (i) Each parameter alone (L, PCT, SS); (ii) Combinations (L + PCT, L + SS, PCT + SS, All 3); (iii) AUROC discriminated Sepsis from INSI model: (a) < 0.7 Sub-Optimal; (b) 0.7-0.8 Good; (c) > 0.8 Excellent. Comparisons conducted via paired t-test.

Results. 222 pts, sepsis=113; INSI=109 Similar demographics between groups (NS). Mean age (SD) = 57.9 (17.1) yrs; 58.1% male). Overall mechanically ventilated 60.8% and hospital mortality 17.1%. AUROC (95% CI) in Table and Figure; AUROC of L, PCT or SS alone or in combination

|     | L       | PCT     | SS       | ALL     |
|-----|---------|---------|----------|---------|
| Alone| 0.56    | 0.76   | 0.85*    | 0.80-0.90 |
|      | (0.48-0.64) | (0.70-0.83) |          |         |
| L    | 0.76    | 0.85*   | 0.80-0.90 |         |
|      | (0.70-0.82) |          |         |         |
| PCT  | 0.86*   | 0.81-0.91 |         |         |
| ALL  | 0.86*   | 0.81-0.91 |         |         |

* P<0.01 SCR vs L or PCT or combination

L, PCT, SS Comparison of Sepsis vs INSI

Discussion. An--4-fold increase in bacterial species detection in these stool samples after CRISPRclean treatment. Sequencing data downsampled to 20 million reads.

Disclosures. Keith Brown, n/a. Jumpcode Genomics (Board Member, Employee, Shareholder)

995. A Nurture Model of Klebsiella pneumoniae Gastrointestinal Colonization with Parenteral Vancomycin Administration

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Session: P-56. Microbial Pathogenesis

Background. Klebsiella pneumoniae poses a significant threat due to its propensity to acquire resistance to many classes of antibiotics, including carbapenems. Gastrointestinal (GI) colonization by K. pneumoniae is a risk factor for subsequent infection as well as transmission to other patients. To study this crucial step in pathogenesis, we developed a mouse model of K. pneumoniae GI colonization using a clinically relevant parenteral anti-biotic regimen.

Methods. To improve the clinical relevance of our model, we elected to use intra-peritoneal injections of vancomycin, one of the most highly utilized antibiotics in the United States.

Results. To optimize dosage in C57bl/6 mice, we injected 20mg/kg, 350mg/kg, or vehicle (PBS) for three days prior to gastric gavage with 10^6 colony forming units (CFU) of a low-resistance strain of K. pneumoniae. The mice who received 350mg/kg (a mouse equivalent of a human dose of 1g/day calculated through the FDA guidelines for estimating safe dosing) shed about 10^6 CFU/g of feces at Day 7 while those receiving the lower dose or vehicle shed 10^2 CFU/g. Next, we compared 3- or 5-day pre-treatment with vancomycin prior to inoculation with an ST258 (epidemic carbapenem-resistant) strain. At Day 7 post-inoculation, mice who received 5 days shed 10^{11} CFU/g feces while those who received vancomycin for 3 days or vehicle for 5 days (PBS) shed 10^6 or 10^5 CFU/g feces respectively. Thus, we chose 5 days of 350mg/kg vancomycin injection as our regimen for inducing robust GI colonization in mice. Finally, we tested the durability of colonization by following fecal shedding in mice up to Day 60 post-inoculation with a second ST258 strain. Shedding during the first 7 days occurs at about 10^{10}-10^{11} CFU/g feces, and from day 14 to day 60 fecal loads are stable around 10^6 CFU/g feces. Results are comparable between male and female mice.

Conclusion. In conclusion, we have developed a mouse model of robust, prolonged GI colonization with multiple strains of K. pneumoniae using controlled dosing of a clinically relevant antibiotic. This model may be used to study a key step in K. pneumoniae pathogenesis and infection prevention in the future.

Disclosures. All Authors: No reported disclosures

996. CD4+ T-Cell Lymphopenia Associated with Frequent Plateletpheresis in Healthy Donors

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Session: P-56. Microbial Pathogenesis

Background. Frequent plateletpheresis using the Time Accel leukoreduction system chamber may result in lymphopenia in healthy donors, with increased donation in the previous year associated with CD4+ T-cell count of less than 200 cells/µL. However, this finding has not been replicated and the clinical significance of plateletpheresis-associated lymphopenia remains unclear.

Methods. A prospective observational study of healthy plateletpheresis donors aged 18 or older who donated at least once in the previous year was conducted at the Kraft Blood Center at Brigham and Women’s Hospital/Dana Farber Cancer Institute, where the Time Accel system is used exclusively. Blood was drawn immediately before plateletpheresis or at least 2 weeks after the last donation to assess for total lymphocyte and CD4+ T-cell counts.

Results. A total of 86 participants were enrolled: 23 had 1-5 donations, 36 had 6-19 donations, and 27 had 20-49 donations within the previous 365 days (Figure 1). For the low-, medium-, and high-frequency donation groups, the median age was 53 years (IQR: 43-64), 61 years (IQR: 53-68), and 61 years (IQR: 55-65), respectively. The median total lymphocyte count was 1.5x10^{12} µL (IQR: 1.3-1.9), 1.2 (IQR: 0.9-1.5), 0.8 (IQR: 0.6-0.9) x10^{12} cells/µL, and the median CD4+ T-cell count was 648 (IQR: 531-843), 525 (IQR: 348-698), and 220 (IQR: 184-347) cells/µL. CD4+ T-cell counts were < 200 cells/µL in 0/23 (0%), 3/36 (8%), and 9/27 (33%) participants across the three groups. Total lymphocyte and CD4+ T-cell counts were inversely correlated with the number of platelet donations in the prior 365 days, R^2 = 0.384 (Fig 2) and 0.402 (Fig 3) respectively.

Disclosures. Erkan Hassan, Pharm.D., FCCM (Consultant) Roy Davis, M.D., Immunexpress (Consultant) Immunexpress (Consultant, Shareholder) Dayle Sampson, Ph.D., Immunexpress (Employee, Shareholder)