

Methods. miRNA from serum and RNA from PBMCs were acquired from $n = 40$ participants in a prospective cohort of Filipino septic patients: $n = 15$ developed septic shock and $n = 17$ developed renal failure. RT-qPCR was done to measure the expression of 21 sepsis-associated miRNAs. Differentially expressed miRNAs (DEMs) for each outcome was identified, followed by gene target prediction for each DEM. Gene expression microarrays covering 18,616 genes were also performed to identify differentially expressed genes (DEGs; $P < 0.05$, $\log FC > |0.3|$) for each outcome. Significant miRNA-gene pairs were selected by evaluating the overlap of the predicted gene targets of the DEMs with the DEGs for each corresponding outcome. Given the gene-silencing mechanism of miRNAs, overlap analysis was performed on only the downregulated DEGs when the specific DEM was upregulated (and vice versa).

Results. Septic participants who developed shock, compared with those who did not, had higher expression of 1 DEM, miR-223-5p, and downregulation of 20 DEGs. *NUS1* was the only predicted gene target of miR-223-5p that was also downregulated in septic shock. Participants who developed renal failure, vs. those who did not, had lower expression 6 DEMs and upregulation of 6 DEGs. *KPNA4* is a gene target of the DEMs, miR-126-5p, and miR-181a-5p, that was also upregulated in renal failure.

Conclusion. Significant miRNA-gene pairs related to worse clinical outcomes in sepsis were identified: miR-223-5p with *NUS1* for shock and either miR-126-5p or miR-181-5p with *KPNA4* for renal failure. While the biological significance of these miRNA-gene pairs still needs to be evaluated, these findings can potentially help future efforts in developing prognostic markers or therapeutic targets for shock and renal failure in sepsis.

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405. Serum Antibody Responses Against Carbapenem-Resistant *Klebsiella pneumoniae* in Infected Patients

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Background. Capsular polysaccharide (CPS) of Carbapenem-resistant *K. pneumoniae* ST258 (CR-Kp) is a potential vaccine target. CPS of these isolates generally falls within 2 homology groups named clade 1 and clade 2. We and others have made antibodies (Abs) that act against clade2 CR-Kp but failed to make therapeutic Abs against clade1 CR-Kp. Previous studies had shown that studying patient's antibody responses could help in identifying suitable candidates for developing immunotherapies. Thus, we sought to identify potential vaccine candidates by investigating the humoral response CPS in CR-Kp-infected patients.

Methods. 24 CR-Kp isolates and corresponding serums were collected from inpatients at Stony Brook Hospital. CPS was isolated and purified by size-exclusion column chromatography from CR-Kp strains 34 (clade 2), 36 (clade 1), and 38 (clade-Other). Anti-CPS Abs in patient's serum were detected by enzyme-linked immunosorbent assay (ELISA) and bulk Abs from positive serum were purified using an affinity column. These Abs were tested for activity against CR-Kp by serum bactericidal and agglutination assays.

Results. 50% of clade2 CR-Kp-infected patients had humoral responses against CPS34. 77% of clade 1-infected patients sera cross-reacted with CPS34, but none of them developed Abs against CPS36. Interestingly, 90% of clade1 and 60% of clade 2-infected patients, respectively, showed Abs binding to CPS38. Thus, we selectively purified Anti-CPS Abs from two clade-Other-infected patients and observed that they were cross-reactive with all three CPS. Further, these Anti-CPS Abs agglutinated all tested CR-Kp isolates (34, 36, and 38) when compared with control human IgG ($P < 0.005$). Additionally, these Anti-CPS Abs promoted killing of clade2 bacteria and inhibited the growth of clade1 bacteria in Ab-mediated serum bactericidal assay. These data elucidate that humoral responses developed in clade-Other CR-Kp-infected patients have therapeutic potential.

Conclusion. With the unavailability of effective antimicrobials for CR-Kp, approaches like developing novel anti-CPS vaccine could serve as an alternate therapy. Our data suggest that developing immunotherapies targeting CPS38 could potentially provide protection across both clade1 and clade2 bacteria in clinical settings.

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406. Cloning Antibodies Against Kawasaki Disease from Acute Plasmablast Responses

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Background. Kawasaki Disease (KD) is a childhood vasculitis, marked by prolonged fevers and coronary artery inflammation/aneurysms in near one-quarter of those untreated. The cause remains unknown; however, epidemiologic and demographic data support a single preceding infectious agent may lead to KD. Plasmablasts (PBs) are a stage of transitional B-cells that lead to plasma cells, the long-lived antibody-producing cells of the bone marrow. After initial infection, peripherally circulating PB populations are enriched for cells with antibodies against the preceding

infection. We have recently published data showing children with KD have similar PB responses to children with infections. We sought to define the antibody characteristics, including clonality, of these PBs during KD.

Methods. We used antibody repertoire next-generation sequencing to characterize memory and PB populations. Additionally, pairing of heavy and light chains was performed with Chromium Single Cell Gene Expression (10x Genomics, Pleasanton, CA) using the Human B cell Single Cell V(D)J Enrichment Kit.

Results. From subject 24, antibody sequences using VH4-34 and a 19 amino acid length complementarity determining region 3 showed a massive expansion between day 4 and 6 of fever. Chromium single-cell sequencing produced over 946 heavy and light chain paired sequences. Sequence comparison showed 40% of sequences demonstrated markers of clonal expansion, which represented 100 clonal groups. Seven other KD subjects are being processed and comparative analysis will be presented.

Conclusion. This clonal expansion within plasmablast populations supports that Kawasaki disease is caused by an infection. Antigen targeting of these monoclonal antibodies is currently being explored.

