Poster #21 *Psychosocial /Community Health*

Exploratory Analysis of Social Network Messages to Characterize Community Understanding and Behavior During the Ongoing COVID-19 Pandemic



Chenghui Li, PhD, Pharmaceutical Evaluation/Policy, College of Pharmacy;
Jake Qualls, PhD and Xiuzhen Huang, PhD, Computer Science,
Arkansas State University

The overall goal of this study is to explore Twitter messages to understand public sentiment and behaviors during the COVID-19 outbreak. Variations by demographic groups (age, gender, etc.) and geographic locations will be assessed cross-sectionally and over time to identify differences across population subgroups and trend changes. In particular, we are aiming to answer the following questions: What is the impact of COVID-19 on Americans? How does it differ by age, gender, racial/ethnicity group from those with chronic conditions and families? How does sentiment about COVID-19 change over time? How does COVID-19 sentiment differ across geographic regions or locations? Artificial intelligence and data mining techniques will be applied to Twitter messages to characterize community understanding and behavior during the ongoing COVID-19 pandemic.

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UAMS

Showcase of Medical Discoveries

A Focus on COVID-19 Research

Thursday
June 18, 2020
10:00 a.m. —12:00 p.m.

A Research and Innovation Event featuring UAMS Investigators discussing their Research and Discoveries.

Online Zoom Event

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Poster # 20 *Community/Health Disparity*

Consumer Health Information on COVID-19 Not Ideally Readable or Actionable

B. Alison Caballero, MPH, CHES; Katherine J. Leath, MPH, MA;
and Jamie C. Watson, PhD

Many similarities exist between populations at risk for severe COVID-19 and populations at risk for limited health literacy. Because individual behaviors impact disease spread, materials must be easy to read and understand, especially in high-risk groups.

Our team used validated tools to assess online COVID-19 materials. We applied 3 readability formulas and the Patient Education Materials Assessment Tool to measure readability, understandability, and actionability.

Mean readability scores placed the sample at a high school reading level, and many plain language techniques that contribute to optimal material understanding and action were routinely missing.

Given the limitations in health literacy among groups at increased risk for severe COVID-19, clear communications is essential. Our study found that online COVID-19 information is not ideally readable or actionable. To improve health education efforts, especially in vulnerable populations, materials should follow plain language guidelines and be tested formally prior to use.

Poster #19 *Genetic Epidemiology*

Detection of Covid-19 from a Wastewater Treatment Plant in Conway, Arkansas

Catherine Shoults, Tom Powell, Jing Jin, Mohammed Orloff, David Hirschberg, and Dave Ussery

The SARS-CoV-2 genome can be shed in feces and has been detected in hospital wastewater, as well as communities. There are several communities in the U.S. that are being monitored for Covid-19 by presence in sludge samples from wastewater treatment plants. We have taken two sludge samples from a wastewater treatment plant in Conway, Arkansas, and assayed for the presence of the Covid-19 genome. Results will be discussed, in terms of estimates of community infection, compared to individual testing, such as rRT-PCR and antibody studies. It is anticipated that in the future we might be able to obtain full length genome sequences from wastewater samples.

The UAMS Office of Research and Innovation is pleased to sponsor the 28th Showcase of Medical Discoveries on COVID-19 research.

Check out the latest collaborative research projects by outstanding UAMS health professionals and researchers!

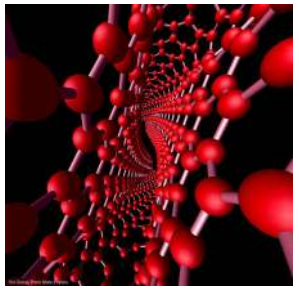
❋ ❋ ❋

Note: The COVID-19 research presentations are grouped into the following categories:

- Testing
- Transmission
- Treatment
- Epidemiology
- Psychosocial
- Community/Health Disparity

Find the associated category along with the poster # at the upper left of each page.

Have more questions? Join us immediately following the Showcase for a ***COVID-19 Networking*** *time.*



Poster #1 *Testing / Treatment / Epidemiology*

CAVHS and VA Research Related to COVID-19

Richard Owen, MD, Prof. Psychiatry/Epidemiology, Assoc. Chief of Staff for Research, CAVHS and Richard Dennis, PhD, Assoc. Prof. Geriatrics, Deputy Assoc. Chief of Staff for Research, CAVHS

The national research leadership of the Veterans Healthcare System acted quickly when the COVID-19 pandemic became evident in the US. The Office of Research and Development (ORD) took actions to accelerate research related to this illness, expediting legal and regulatory processes, coordinating with pharmaceutical companies and other organizations, and soliciting new research proposals and supplemental funding requests. ORD also immediately established plans to implement a national VA specimen biorepository associated with COVID-19 and future infectious disease outbreaks.

This presentation will summarize national and local research activities including grant submissions.

Poster #18 *Epidemiology*

Development of a High-density Protein Array for COVID-19 Antibody Binding Assays

Visanu Wanchai, Søren Brunak, David Hirschberg, and David Ussery

Viruses have limited genome sizes, but can encode many proteins, taking advantage of multiple reading frames, mRNA editing, and alternative splicing. We have designed a high-density protein array, containing 4 million probes (16mer peptides), from a set of several thousand genomes from the coronavirus family. The peptides are based on all known and annotated proteins (about half, or 1.9 million probes) as well as alternative proteins based on post-transcriptional modification and frame shifts (2.1 million peptides). These high-density arrays will be probed by antibodies from sera from a set of ~1,000 Covid-19 positive patients (in Washington state) and from frozen blood sera from two years ago, for the control set. From this, we anticipate finding a small set of strong epitopes that can be useful in designing antibodies that are specific for Covid-19, and will have little cross reactivities with other coronaviruses. Peptide binding data is important in building better epitope prediction models.

Poster #17 *Epidemiology*

Recovering High Quality SARS-COV2 Genome Sequence and Microbiome from Clinical Samples for Genomic Epidemiology

Intawat Nookaew[1], Thidathip Wongsurawat[1], Mariah Taylor[2], Piroon Jenjaroenpun[1], Wannee Kantakamalakul[3], Ruengpung Sutthent[3], Navin Horthongkham[3], Colleen B Jonsson[2]

[1]Biomedical Informatics, UAMS; [2]Microbiology, Immunology and Biochemistry, Univ. of Tennessee Health Science Center, Memphis, TN; [3]Microbiology, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, Thailand

Pathogen genome sequencing provides the concrete foundation to understanding how disease spreads, its pathogenicity, potential clinical treatment and the development of new vaccines. We implemented and assessed two different strategies, which are: 1) direct deep RNA sequencing on an Illumina sequencer, and 2) amplicon sequencing on Oxford Nanopore Technology pocket-sized sequencer using a primer set of ARCTIC network to recover SARS-COV2 genome sequences from nasal swab samples. The two methods gave an excellent sequencing depth and resulted in a high quality complete genome sequence. We obtained additional nasal microbiome and host transcriptome information from the direct deep RNA-seq associated with the viral infection. The method was also used to recover the SARS-COV2 genome sequence derived from cell culture. Interestingly, additional mutations were identified when compared with the original genome recovered from the same clinical sample.

Poster #2 *Testing*

Detection of Viruses in Body Fluids in Real-Time using SpecID

Dan Buzatu, Pierre Alusta, Marli Azevedo (all FDA/NCTR) and Tony Wang (FDA/CBER)

FDA NCTR previously developed a rapid, field portable, mass spectrometry method, SpecID for detection of bacteria and compound adulteration. It was recently shown that SpecID can be used for detection of a virus spiked into saliva; cucumber leaf spot virus (28nm) was used as a surrogate for coronaviruses as proof of concept. Saliva was spiked with virus at the typical load found in an infected patient. Results show that we can tell the difference between control and virus-spiked saliva samples in seconds. We performed a limit of detection study by reducing the viral load in saliva and this was determined to be <300 viral particles/microliter of saliva. Based on the Covid19 global pandemic and the need for fast methods to screen people for infection, this new FDA developed technology can provide a real time detection solution for viruses in many scenarios including: field, hospital/clinic, health labs, airports, etc.

Poster #3 *Testing*

Development of a Serologic Test for SARS-CoV2

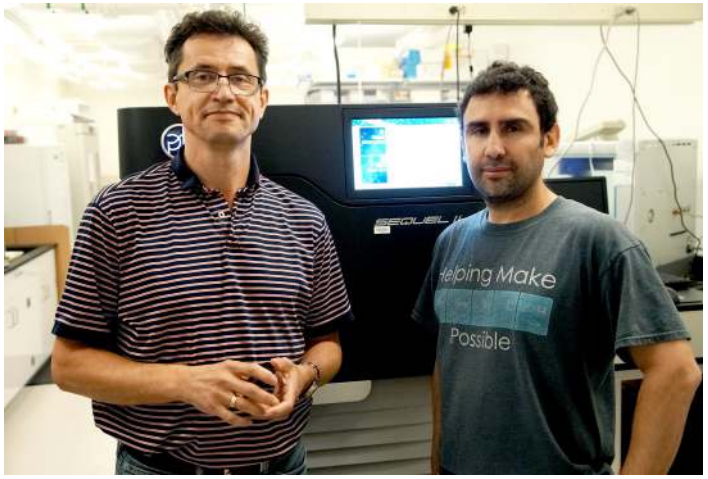


Karl W. Boehme, PhD, Joshua L. Kennedy, MD,
and J. Craig Forest , PhD

The 2019 coronavirus disease (COVID-19) is a pandemic caused by SARS-CoV2, a coronavirus not previously seen in the human population. To effectively combat COVID-19 and limit the impact of disease in the human population, there is a need to understand immune responses to SARS-CoV2. We developed an ELISA to screen blood samples for antibodies that recognize the receptor binding domain (RBD) from the SARS-CoV2 Spike protein and validated the assay using samples obtained from the UAMS Pathology Laboratory. The 7 pre-COVID-19 samples tested were negative and 9/9 samples from SARS-CoV2 patients (6-23 days post-PCR confirmation) were positive for RBD-specific antibodies. We have begun screening pediatric samples from Arkansas Children's Hospital and adult samples from UAMS. Defining antibody-mediated immunity to SARS-CoV2 will help determine the overall infection rate, inform back-to-work and back-to-school decisions, and assess whether convalescent serum can be used as a treatment option.

Poster #16 *Treatment*

Evaluating Genotoxic Potential of Antiviral Ribonucleoside Analog β-D -N4-hydroxycytidine in Rat Pig-a and MN Assays



Vasily N. Dobrovolsky, Robert H. Heflich, Javier R. Revollo,
Mason Pearce, and Timothy Robison

Developed at Emory Institute for Drug Discovery (EIDD), ribonucleoside analog β-D-N_4-hydroxycytidine (NHC, EIDD-1931) and a related pro-drug compound, β-D-N_4-hydroxycytidine-5'-isopropyl ester (NHCE, EIDD-2801), are touted as effective antivirals against a broad spectrum of coronaviruses, including SARS-CoV2. If so, it is envisioned that NHC/NHCE may be used as drugs for prophylactics and treatment of COVID-19, perhaps in large doses, even for patients that may not necessarily develop severe cases of the disease. Being nucleoside analogs, the novel anti-retrovirals may interfere with endogenous eukaryotic DNA and RNA metabolism resulting in DNA damage and mutation. Therefore, they may be potential carcinogens. Objective: To test clastogenicity and mutagenicity of NHC/NHCE in a rat model using peripheral blood RBC micronucleus test and recently developed NCTR *Pig-a* test, and possibly T-cell *Pig-a* and *Hprt* mutation assays. The results of the non-clinical study will inform regulators on risk vs benefit of using these antivirals for treating human patients.

Poster #15 *Treatment*

Artificial Intelligence (AI)-powered Drug Repositioning for Treating COVID-19

Zhichao Liu[1], Dong Wang[1], Madhu Lal-Nag[2], Shraddha Thakkar[2], Wendy Carter[2], Takashi Komatsu[2], Kirk Chan-Tack[2], Leonard Sacks[2], Sean Belouin[2], Sonia Pahwa[2], Nicholas Petrick[3], Kenny Cha[3], Asiyah Yu Lin[3], Hatim Qais[2], Kevin Snyder[2], and Weida Tong[1]

[1] Division of Bioinformatics/Biostatistics, NCTR FDA [2] ; CDER FDA [3] CDRH FDA

Emerging infectious diseases have been an ever-present threat to public health and COVID-19 is a recent example. There is an urgent need to develop a robust framework to comeback the disease with safe and effective therapeutic options. Great efforts are being achieved as data continues to be generated for a better understanding of the underlying mechanisms of COVID-19. It provides a unique opportunity to implement computational drug repositioning approaches to not only accelerate the discovery of COVID-19 treatments, but also prepare us for future infectious diseases. In the showcase, we will elaborate on how AI facilitates development of COVID-19 treatment with several examples.

Poster #4 *Testing*

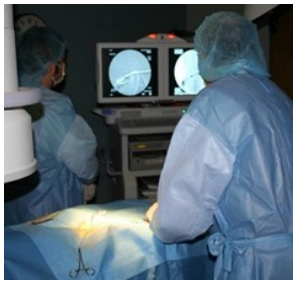
Flow Cytometry Analysis of Anti-SARS-CoV-2 Antibodies in Human Plasma

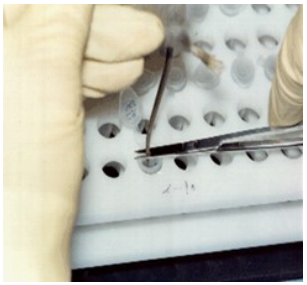
Jia-Long Fang, Leeza Shrestha, Frederick A. Beland

CoVID-19 is an infectious disease caused by a new strain of severe acute respiratory syndrome coronavirus (SARS-CoV-2). Knowledge of the presence and levels of anti-SARS-CoV-2 antibodies in humans can provide critical information for the prevention and treatment of CoVID-19 and have a direct public health benefit. In this study, we propose to develop a flow cytometric assay, with high sensitivity and specificity, to assess simultaneously anti-SARS-CoV-2 IgM, IgG, and IgA in humans, and to determine whether there is a difference in antibody recognition to the viral proteins.

Poster #5 *Testing*

DLAM Technical Services Core



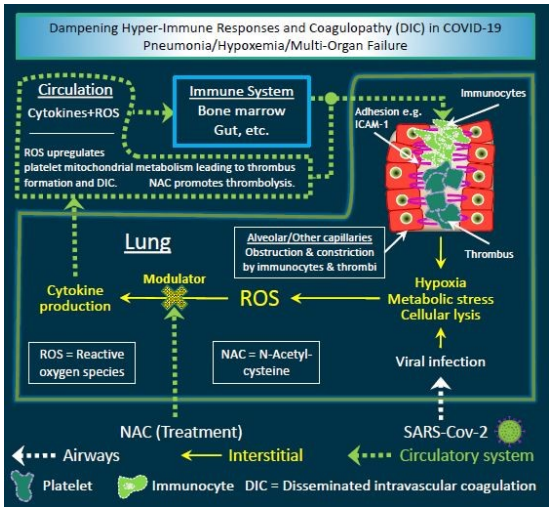



Engi, BN; Schutte, BR; Mulkey, RL; Lowery, JD, Randolph, MR;
and Simecka, CM

DLAM's mission is to provide humane animal care, veterinary and technical services in support of biomedical research at the University of Arkansas for Medical Sciences. DLAM's new Technical Services Core (DTS) supports and assists faculty, staff and students involved in initiating and sustaining research projects. Our goal is to provide a one-stop information and technical resource, which will facilitate research efforts. The Technical Services Core will provide campus researchers with specialized scientific services to support every component of their studies. We have highly qualified and trained personnel that can assist and/or perform all aspects of any research project from writing an Animal Use Protocol to performing procedures such as maintaining breeding colonies, injections, blood collection, surgeries and tissue harvest.

Poster #14 *Treatment*

A Radiation Mitigator as a Potential Treatment for COVID-19



Robert J. Griffin, Nukhet Aykin-Burns, Michael Borrelli,
and Peter M Corry

Previous work in the Corry and Griffin research groups used the FDA approved antioxidant N-acetylcysteine (NAC) as a mitigant for lethal radiation effects and to block adhesion molecule-induced vascular shutdown. Briefly, 62% of mice were rescued from a lethal 20 Gy dose of ionizing radiation, localized to the abdomen, by the administration of NAC up to four hours post irradiation. In addition, we found that NAC was able to blunt or eliminate the adhesion molecule induction associated with vascular shutdown/hypoxemia. At the time we posited that this protective effect came about by tamping down the deleterious effects of high concentrations of reactive oxygen species (ROS) both locally and in the bone marrow. Here, we hypothesize that ROS driven cytokine storms leading to excessive marrow-alveolar abscopal interactions are involved in COVID-19 critical patients and propose that NAC treatment should be investigated to reduce mortality and the need for mechanical ventilation.

Poster #13 *Treatment*

SARS-CoV-2 Cross-protection Study using Surrogate Coronavirus and Recombinant Proteins

Marli P. Azevedo, PhD; Lisa Mullis; Bruce Erickson, PhD; Kuppan Gokulan, PhD; Sangeeta Khare, PhD and R. Doug Wagner, PhD.

Antibody-Dependent Enhancement (ADE) has been reported to occur during SARS-CoV infection, and because of their similarities it is likely that SARS-CoV-2 may cause ADE as well. Therefore, predicting the success of future vaccines depends on investigating the role of the S protein in ADE and examining alternative solutions such as use of selected epitopes for the vaccine target. We have generated recombinant SARS-CoV-2 and NL63 Spike proteins in a baculovirus system. We will next generate polyclonal antibodies against the rS. We have identified epitope peptides from the spike protein. The protein/epitope peptide reagents will be used to immunize hACE2 mice followed by heterologous challenge with HCoV NL63. Monoclonal antibodies against the selected epitopes will be used as therapy/prophylaxis in hACE2 mice. We aim to select antigenic epitopes capable of inducing neutralizing antibodies to prevent viral entry and infection, screening for their usefulness to avoid ADE

Poster #6 *Transmission*

Novel Intubating Frame to Reduce Contamination in COVID-19 Patients

Faiza A. Khan, M.D, Zachary B. Lewis, MD. , Sina B. Ekici, M.D., and Nadir Sharawi, M.B.B.S.

Aerosol generating procedures, including intubation and extubation, pose significant risk to health care providers. Several guidelines are in place for such procedures including use of personal protective equipment (PPE) and doffing/donning checklists to minimize contamination. Several devices or barrier enclosures including aerosol box and face tent have been created or modified to minimize this risk. However, they are not without their limitations; the PVC aerosol box restricts hand movements and was noted to be difficult to use during simulated difficult intubation scenarios.

The emergency medicine team at our institute devised a novel reusable PVC frame that is easy to assemble and has an attached filter and suction port. A HEPA filter and suction are attached to the frame to facilitate removal of virus particles.

Poster #7 *Transmission*

Sprayable Anti-viral Cellulose Materials for Surface Coatings

Soma Shekar Dachavaram[1], John P. More II[2], Jamie A. Hestekin[2], and Peter A. Crooks[1]
[1]Pharmaceutical Sciences, College of Pharmacy, UAMS
[2]Chemical Engineering, UAF

With the current COVID-19 pandemic, movement of individuals throughout the US has changed as fears of being infected rise. However, when the current lockdowns end, there will be a need for the public to feel safe about going out and about again.

We are developing a cellulose-based nanomaterial that is sprayed onto surfaces to deactivate viruses over a relatively long period of time (about 50 days in initial tests). This surface coating is engineered as a sprayable material that will adhere to door-knobs, countertops, walls, etc. to form an effective decontaminating barrier protecting the public, by enabling them to touch any commonly encountered surface without risk of being infected. Our patented TEMPO cellulose form-I is the key intermediate for chemical incorporation of a variety of commercially available antiviral agents, either as ion-paired deposits, or as more permanent covalently linked conjugates with carboxylate groups on the TEMPO cellulose polymer surface.

Poster #12 *Treatment*

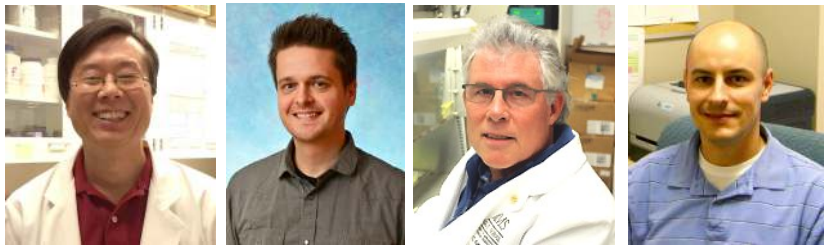
Application of Human in vitro Airway Tissue Models for Coronavirus Antiviral drug Screening and Drug Repositioning

Rui Xiong, Ph.D. (DGMT/NCTR)
Xuefei Cao, Ph.D. (DGMT/NCTR), Yue Wu, Ph.D. (DBB/NCTR), Robert Heflich, Ph.D. (DGMT/NCTR), Marli Azevedo, Ph.D. (DM/NCTR), Carol Weiss, Ph.D. (OVRR/CBER), Wei Sun, Ph.D. (OND/CDER), Xiaochun Chen, Ph.D. (OND/CDER), Anup Srivastava, Ph.D. (OND/CDER), Timothy Robison, Ph.D. (OND/CDER) and Ilona Bebenek, Ph.D. (OND/CDER)

Human coronaviruses are commonly associated with respiratory illnesses. The current COVID-19 pandemic is a reminder of the threat coronaviruses pose to human populations and emphasizes the need to develop effective antiviral therapies. Human *in vitro* airway tissue models derived from primary airway epithelial cells mimic the natural infection site of many human respiratory coronaviruses, such as SARS-CoV, HCoV-NL63, and SARS-CoV-2, and are appropriate *in vitro* culture systems for studying the pathogenesis of coronaviruses as well as evaluating the efficacy of clinically approved drugs. In this proposal, both large airway and alveolar human air-liquid-interface (ALI) models will be established for assessing coronavirus cell entry and cytopathic effects using SARS-CoV-2 pseudovirus and HCoV-NL63 coronavirus. A panel of clinically approved drugs will be evaluated for potential antiviral activities in ALI models. The expected outcome of this study will be to develop an *in vitro* system that can identify coronavirus antiviral candidate drugs.

Poster #11 *Treatment*

An ex vivo Human Lung Platform for Studying COVID-19 Pathogenesis and Antiviral Drug Discovery



Xuming Zhang, Roger Pechous, Richard Kurten, and Daniel Voth

The pandemic COVID-19 poses a devastating threat to public health and the worldwide economy. Since its outbreak in December 2019, more than 6 million confirmed cases with over 370,000 deaths have been reported globally, and new cases continue to rise rapidly. Unfortunately, there is no vaccine or antiviral drug currently available. A better understanding of viral pathogenesis in the lungs is critical for efficient management of the disease outcome. Here we establish the human Precision-Cut Lung Slice (hPCLS) as an *ex vivo* human lung platform for studying COVID-19 pathogenesis and for assessing the efficacy of antiviral therapeutics against SARS-CoV-2, the causative agent of COVID-19. Specifically, we will characterize SARS-CoV-2 infection and pathogenicity in human lungs by determining the susceptibility of hPCLS to SARS-CoV-2 infection and viral replication kinetics. We will also identify lung cell types that are susceptible to SARS-CoV-2 and evaluate the histopathological changes and alteration of global gene expression following virus infection. We will further characterize the local innate immune responses to SARS-CoV-2 infection in human lungs by determining the expression of cytokines and chemokines during the course of SARS-CoV-2 infection. In addition, we previously performed a large-scale screen of the NIH clinical collection small molecule library of over 700 FDA-approved drugs for anti-coronavirus activity in cell culture and identified 84 drugs that exhibited robust antiviral activities against a broad spectrum of animal and human coronaviruses. To further extend these findings and facilitate rapid discovery of anti-SARS-CoV-2 drugs for clinical use, we will assess the antiviral efficacy of top candidates against SARS-CoV-2 by using this hPCLS platform. Findings from these studies will not only provide insights into mechanisms underlying COVID-19 pathogenesis, but also validate anti-SARS-CoV-2 drugs that can immediately advance to clinical trials.

Poster #8 *Transmission*

Evaluating COVID-19 Related Central Nervous System Damage

John Talpos PhD, Div. of Neurotoxicology, NCTR

Anosmia, a loss of the sense of smell, has emerged as a core symptom of COVID-19 infection. In some studies, more than 80% of COVID-19 positive patients report anosmia. Moreover, anosmia frequently precedes other symptoms, suggesting it is not the result of local inflammation or mucus production. SARS-CoV-2, the virus responsible for COVID-19, infects cells through the ACE2 receptor which is expressed throughout the body on endothelial cells, immature olfactory neurons, and in much of the brain. Previous work shows that the SARS-CoV-1 and SARS-CoV-2 virus can infect the olfactory nerve and olfactory bulb. Once the virus reaches the olfactory bulb it can travel throughout the brain, reaching even the brain stem. We hypothesis that COVID-19 related anosmia is the result of a brain infection and describe experiments with human and animal tissue designed to evaluate the extent of central nervous system damage on markers of neuronal death and inflammation.

Poster #9 *Treatment*

Can Oxygen Carrier Molecules Offer Neuroprotection in Oxygen-deficient Conditions such as During Severe COVID-19-induced Pneumonia?

Abdallah Hayar, PhD

Prolonged hypoxia due to lung infection by SARS-CoV-2 can disrupt synaptic transmission and induce neuronal cell death via apoptosis. This can result in brain failure to adequately coordinate breathing and heart rate, and subsequent multiple organ failure leading to death. Mechanical ventilation is an essential tool in intensive care for COVID-19 patients, but it can overstretch the lungs and induce lung injury and inflammation. Several perfluorocarbons have been designed to carry oxygen and may be useful to treat hypoxic COVID-19 patients. In particular, DDFPe was found to be safe to treat acute ischemic stroke patients. We will test the hypothesis that DDFPe can enhance gas exchange in a mouse model of acute lung injury, and whether it has neuroprotective effects on brainstem cardiorespiratory neurons in hypoxic brain slices. These experiments would help us determine whether DDFPe can be repurposed to improve oxygenation in COVID-19 patients.

Poster #10 *Treatment*

SARS-CoV-2 Helicase, a Target for Development of Anti-COVID Therapeutics

John Marecki, Peter Crooks, Craig E. Cameron,
and Kevin D. Raney

COVID19 is a rapidly expanding pandemic caused by infection of the SARS-CoV-2 virus. NSP13 is a helicase that is required for viral replication. Helicases are molecular motor proteins that harness energy from ATP hydrolysis, move along nucleic acids, unwinding duplex structures or displacing proteins in their path. NSP13 is proposed to be part of the replication and transcription machinery of SARS-CoV-2, making it a target for inhibition. A key to finding selective inhibitors for helicases is development of high throughput assays to rapidly evaluate many potential inhibitors. Towards these goals, NSP13 was cloned into an expression vector that allowed for isolation of authentic protein containing no peptide fusions or tags. This enzyme behaved well after purification and proved to be highly active as an RNA or DNA stimulated ATPase. The turnover number under conditions of saturating ATP and RNA was 650 s^{-1}. To our knowledge, this is one of the fastest ATPase turnover rates of any RNA helicase. For comparison, the HCV helicase has a turnover number of around 50 s^{-1}. Subsequent experiments indicated rapid unwinding of duplex nucleic acid. With our knowledge that NSP13 is a robust helicase and we will screen a library of small molecules for enzyme inhibitors to serve as lead compounds for drug development. In addition, we hypothesize that NSP13 plays a role in viral RNA replication, but is likely to be allosterically regulated, possibly through interaction with other viral proteins. Two candidates will be examined for helicase regulation, NS7p and NS8p. These proteins may play a role in the replication complex where they interact with the viral RNA dependent RNA polymerase. Identification of protein-protein interactions within this complex can reveal new approaches to disrupt viral replication.