

CAMO (COMPARING ANIMAL MODELS TO ORGANOIDS) - TESTING MEDICAL COUNTERMEASURES WITH MICROPHYSIOLOGICAL SYSTEMS AND COMPARING TO TRADITIONAL ANIMAL MODELS AND CLINICAL TRAILS

Impact Of Co-infection On Disease Progression

Sara Ruiz USAMRIID Christopher Klimko USAMRIID Christopher Cote USAMRIID J. Matthew Meinig USAMRIID
 Annette Gray USAMRIID Stephanie Halasohoris USAMRIID Ashley Babyak USAMRIID Mary Hourihan USAMRIID
 Bobby Curry USAMRIID Marjorie Torres USAMRIID Nancy Twenhafel USAMRIID Franco Rossi USAMRIID

Co-infections are likely an underreported but common occurrence that directly impacts clinical outcome. Numerous complex infections have been reported in human clinical cases to include HIV, Hepatitis B, Hepatitis C, malaria, tuberculosis, and Ebola. Co-infection with influenza and a secondary bacterial pathogen, commonly *Staphylococcus aureus* and *Streptococcus pneumoniae*, contributes to higher rates of pneumonia-associated deaths in both seasonal and pandemic viral strains. This underscores the need to not only understand the interplay between the host and pathogens, but also the downstream effects of direct microbial competition within a singular host. It is unknown the impact these types of infections may have on therapeutic strategies and interventions. Therefore, it is necessary to establish models to allow for efficacy testing when presented with a polymicrobial infection. There is a high potential for co-infections in the current COVID-19 outbreak. The long-term hospitalization and respiratory interventions being utilized increases the likelihood of a secondary nosocomial infection. In addition, the time frame in which SARS-CoV-2 emerged aligns with the US influenza season, thus creating a potential for an individual to be simultaneously infected with both pathogens. Case studies have been published documenting co-infections with SARS-CoV-2, demonstrating that this phenomenon is occurring in the current pandemic. It is likely the true burden of co-infections is underreported and overlooked due to the limited resources and rapid response necessary in the hospitals. Given that co-infections typically result in unfavorable clinical outcomes, it is imperative to better understand this phenomenon in order to assess contributing comorbidities to negative outcomes of disease and develop better predictors and intervention strategies to protect military personnel in addition to the general public. One such pathogen of concern to the military is *Coxiella burnetii*, the causative agent of Q Fever. A pilot study performed at USAMRIID demonstrated that co-infection between SARS-CoV-2 and *C. burnetii* resulted in a worse outcome whereby no mortality was noted in mice challenged with *C. burnetii* alone and 56% in the SARS-CoV-2 only group; however it was noted that the two coinfecting groups had 100% (SARS-CoV-2 followed by *C. burnetii*) and 89% (*C. burnetii* followed by SARS-CoV-2) lethality depending upon the challenge order. Developing models for complex infections is necessary to evaluate current and future medical countermeasures in these real-world scenarios.

The opinions, interpretations, conclusions, and recommendations presented are those of the authors and are not necessarily endorsed by the US Army.

This worked was funded by the Defense Threat Agency (CB10201 and CB11399).