Short Communication

Cellular Signaling Correlates for SARS-CoV-2 Infection

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ABSTRACT

Middle East Respiratory Syndrome Coronavirus (MERS-CoV) outbreaks in 2002 and 2012, respectively, the Coronavirus Disease 2019 (COVID-19) pandemic caused by SARS-CoV-2 is the third deadly human outbreak in less than 20 years. SARS-CoV-2 and other coronaviruses. Generating knowledge databases to inform medical countermeasure (MCM) development against SARS-CoV-2 and other coronaviruses is critical to the COVID-19 response, and to preparedness for future outbreaks.

Keywords: SARS-CoV-2; Genomics; Respiratory Syndrome

INTRODUCTION

To conduct multiplexed single-cell analysis of blood samples using CyTOF mass cytometry a technology that combines flow cytometry and mass spectrometry to simultaneously measure dozens of features located on and in cells to identify circulating immune cell responses related to stage of disease and severity of outcome following coronavirus infection [1]. Parallel assessments of cases in humans and nonhuman primates (NHPs) will shed light on similarities and differences across species.

To perform multiplexed antibody-based imaging of respiratory and immune tissues collected from COVID-19 patients or during NHP coronavirus challenge studies being conducted and funded outside of this project, using CO-Detection by indexing (CODEX). The team will use computational tools to extract single-cell data from CODEX images to precisely identify cell types responding to coronavirus infection, and the spatial relationships of these cells contributing to effective or ineffective immune responses. To apply a new technique merging multiplexed antibody-based protein measurements with viral RNA detection to analyze coronavirus infection [2]. This method, called viral Multiplexed Ion Beam Imaging will also be applied to tissues from previous clinical and nonclinical studies to gain a deeper understanding of the relationships between presence of viral RNA and viral and host proteins during coronavirus infections. COVID-19 pathology tissue imaging, leveraging novel tools to define the characteristics of tissue viral reservoirs (cell types or areas of the body where the virus persists), and learning more about how SARS-CoV-2 affects different systems in the body [3].

Collaborators include: During this project, the Stanford University School of Medicine will perform tissue imaging and analysis of samples from existing clinical and nonclinical SARS-CoV-2 studies [4].

CONCLUSION

The project will identify immune correlates of protection, which could potentially help identify and inform development of new coronavirus MCMs, such as drug and vaccine candidates. The project will also help enhance understanding and use of immune correlates for the regulatory review of MCMs.

REFERENCES

1. Jiang S, Chan CN, Rovira-Clave X, Chen H, Bai Y, Zhu B et al. Virus-Dependent Immune Conditioning of Tissue Microenvironments. Cell. 2021;185(2): 25-27.

2. Gallaher WR. A palindromic RNA sequence as a common breakpoint contributor to copy-choice recombination in SARS-COV-2. Arch Virol. 2020;165(2):2341-2492.

3. Siegel R, Naishadham D, Jemal A. Cancer statistics. J Clin. 2013;63(2): 11-30.

4. Feyaerts D, Hedou J, Gillard J, Chen H, Tsai ES, Peterson LS et al. Integrated plasma proteomic and single-cell immune signaling network signatures demarcate mild, moderate, and severe COVID-19. Cell. 2021;64(2):1-11.