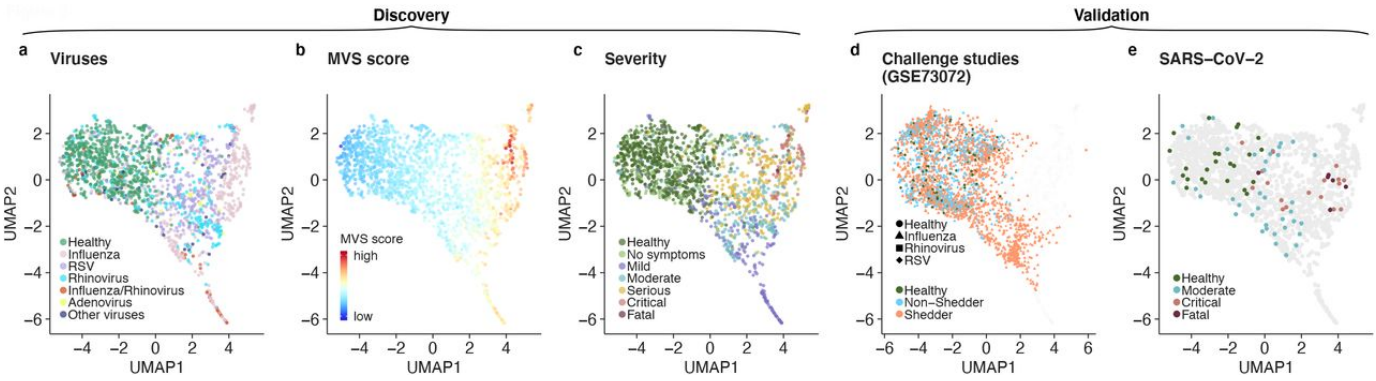
Docket #: S20-396

Biomarkers for predicting severe outcome in patients with infection

Researchers at Stanford have developed a gene expression-based method for determining a virally infected patient's risk of developing severe symptoms, irrespective of the virus. As the ongoing COVID-19 pandemic illustrates, during viral outbreaks there is an urgent need for diagnostic and prognostic tests to distinguish high-risk patients from those with mild infection who can recover at home. The researchers integrated 4,780 blood transcriptome profiles from patients infected with one of 16 viruses across 34 independent cohorts from 18 countries, and 289 scRNA-seq profiles of 702,970 immune cells across three independent cohorts. They identified four gene modules that distinguished non-severe from severe viral infection with clinically useful accuracy. Existing lab tests (e.g., white blood cell count differentials) and standardized severity of illness scores have limited clinical utility in a triage setting during viral outbreaks.



The researchers have previously described a conserved host response to respiratory viral infections, called the Meta-Virus Signature (MVS). They hypothesized that it could be used to better distinguish patients with mild versus severe infection, irrespective of the virus. Here it identifies distinct clusters of patients with non-severe and severe viral infection (image credit: the inventors)

Stage of Development

The researchers have identified a set of genes in human blood that accurately

predict severe outcome in patients with viral infection, with analysis ongoing.

Applications

- Could be integrated in point-of-care test to provide answers in as little as 30 minutes
- Useful during pandemic and non-pandemic times (e.g., influenza season)

Advantages

- Biomarkers can be measured in peripheral blood
- Early and accurate prediction
- Generalizable across a broad spectrum of viruses and patient populations across the world, irrespective of patient age
- Could help prevent healthcare systems from becoming overwhelmed
- Provides crucial insights into immune response dynamics during viral infection

Publications

- H. Zheng, A.M. Rao, D. Dermadi et al Multi-cohort analysis of host immune response identifies conserved protective and detrimental modules associated with severity across viruses *Immunity*2021.

Patents

- Published Application: WO2022066963
- Published Application: 20230323485

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