# Archived Editions (COVID-19 Genomics and Precision Public Health Weekly Update)

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## COVID-19 Genomics and Precision Public Health Weekly Update Content



## Pathogen and Human Genomics Studies

- Cytokine Levels in Critically Ill Patients With COVID-19 and Other Conditions. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=141)
  Kox Matthijs et al. JAMA 2020 Sep

  There were 46 patients with COVID-19 with ARDS, 51 with septic shock with ARDS, 15 with septic shock without ARDS, 30 with OHCA, and 62 with multiple traumas. Preliminary analysis suggest COVID-19 may not be characterized by cytokine storm. Whether anticytokine therapies will benefit patients with COVID-19 remains to be determined.
- Mapping genome variation of SARS-CoV-2 worldwide highlights the impact of COVID-19 super-spreaders. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=144)
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  Phylogenetic analysis indicates a TMRCA for SARS-CoV-2 genomes dating to 12 November 2019 matching epidemiological records. Sub-haplogroup A2 most likely originated in Europe from an Asian ancestor and gave rise to sub-clade A2a, which represents the major non-Asian outbreak. Multiple founder effect episodes, most likely associated with super-spreader hosts, might explain COVID-19 pandemic to a large extent.
- The association between ABO blood group and SARS-CoV-2 infection: a meta-analysis (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=148)
  D Golinelli et al, MEDRXIV, September 3, 2020

  The results of our meta-analysis indicate that SARS-CoV-2 positive individuals are more likely to have blood group A (pooled OR 1.23, 95%CI: 1.09-1.40) and less likely to have blood group O (pooled OR=0.77, 95%CI: 0.67-0.88).
- Systems biological assessment of immunity to mild versus severe COVID-19 infection in humans. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=152)
  Arunachalam Prabhu S et al. Science (New York, N.Y.) 2020 Sep (6508) 1210-1220
- Deep immune profiling of COVID-19 patients reveals distinct immunotypes with therapeutic implications. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=155)
  Mathew Divij et al. Science (New York, N.Y.) 2020 Sep (6508)

  Three immunotypes revealing different patterns of lymphocyte responses were identified in hospitalized COVID-19 patients. These three major patterns may each represent a different suboptimal response associated with hospitalization and disease
- In vivo antiviral host transcriptional response to SARS-CoV-2 by viral load, sex, and age. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=160)
  Lieberman Nicole A P et al. PLoS biology 2020 Sep (9) e3000849

  We examined host response gene expression across infection status, viral load, age, and sex among shotgun RNA sequencing profiles of nasopharyngeal (NP) swabs from 430 individuals with PCR-confirmed SARS-CoV-2 and 54 negative controls. Our data demonstrate that host responses are dependent on viral load with effects of age and sex that contribute to disease severity.

## Non-Genomics Precision Health Studies

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## News, Reviews and Commentaries

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