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 • Non-Genomics Precision Health Studies • News, Reviews and Commentaries

Pathogen and Human Genomics Studies

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  MJ van Gils et al, MEDRXIV, September 28, 2021

e performed a head-to-head comparison of the ability of sera from individuals vaccinated with either one of four vaccines (BNT162b2, mRNA-1273, AZD1222 or Ad26.COV2.S) to recognize and neutralize the four SARS-CoV-2 variants of concern (VOCs; Alpha, Beta, Gamma and Delta). Four weeks after completing the vaccination series, SARS-CoV-2 wild-type neutralizing antibody titers were highest in recipients of BNT162b2 and mRNA-1273 (median titers of 1891 and 3061, respectively), and substantially lower in those vaccinated with the adenovirus vector-based vaccines AZD1222 and Ad26.COV2.S (median titers of 241 and 119, respectively). VOCs neutralization was reduced in all vaccine groups, with the largest (5.8-fold) reduction in neutralization being observed against the Beta variant. Overall, the mRNA vaccines appear superior to adenovirus vector-based vaccines in inducing neutralizing antibodies against VOCs four weeks after the final vaccination.

- Resurgence of SARS-CoV-2 Infection in a Highly Vaccinated Health System Workforce (https://www.nejm.org/doi/full/10.1056/NEJMc2112981?query=featured_home)

J Keehner et al, NEJM, September 30, 2021

> The dramatic change in vaccine effectiveness from June to July is likely to be due to both the emergence of the delta variant and waning immunity over time, compounded by the end of masking requirements in California and the resulting greater risk of exposure in the community.

- The Evolving Faces of the SARS-CoV-2 Genome. (https://pubmed.ncbi.nlm.nih.gov/34578345)
  Schmidt Maria et al. Viruses 2021 9 (9)

> We applied molecular portrayal using self-organizing maps machine learning (SOM portrayal) to characterize the diversity of the virus genomes, their mutual relatedness and development since the beginning of the pandemic. The genetic landscape obtained visualizes the relevant mutations in a lineage-specific fashion and provides developmental paths in genetic state space from early lineages towards the variants of concern alpha, beta, gamma and delta

- Smoking and COVID-19 outcomes: an observational and Mendelian randomisation study using the UK Biobank cohort. (https://pubmed.ncbi.nlm.nih.gov/34580193)
  Clift Ashley K et al. Thorax 2021 9

> Conflicting evidence has emerged regarding the relevance of smoking on risk of COVID-19 and its severity. We undertook large-scale observational and Mendelian randomisation (MR) analyses using UK Biobank. Genetically predicted higher number of cigarettes smoked per day was associated with higher risks of all outcomes (infection OR 2.51, 95% CI 1.20 to 5.24; hospitalization OR 5.08, 95% CI 2.04 to 12.66; and death OR 10.02, 95% CI 2.53 to 39.72). Congruent results from two analytical approaches support a causal effect of smoking on risk of severe COVID-19.

- Impact of sickle cell trait on morbidity and mortality from SARS-CoV-2 infection.
  (https://pubmed.ncbi.nlm.nih.gov/34581772)
  Merz Lauren E et al. Blood advances 2021 9 (18) 3690-3693

> Patients admitted for SARS-CoV-2 infection who identified as black or African American were included in the study (n = 166). Blood remnants were tested for SCT, and clinical data were abstracted from the chart. There was no difference in mortality between those with SCT and those without. There was no difference in respiratory complications between groups, but those without SCT had a much higher burden of chronic lung disease (P = .004). Those with SCT had higher creatinine on admission (P = .004), but no difference in in-hospital renal complications (P = .532).

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(https://www.cdc.gov/od/science/index.htm)