

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

Published on 04/15/2021

### 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

- Estimation of secondary household attack rates for emergent spike L452R SARS-CoV-2 variants detected by genomic surveillance at a community-based testing site in San Francisco. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1045)

Peng James et al. Clinical infectious diseases : an official publication of the Infectious Diseases Society of America 2021 4

" 928 high quality genomes were generated. Certain viral lineages bearing spike mutations, defined in part by L452R, S13I, and W152C, comprised 54.4% of the total sequences from January, compared to 15.7% in November. Household contacts exposed to the "California" or "West Coast" variants (B.1.427 and B.1.429) were at higher risk of infection compared to household contacts exposed to lineages lacking these variants (0.36 vs 0.29, RR=1.28; 95% CI:1.00-1.64)."

- Association of Sociodemographic Factors and Blood Group Type With Risk of COVID-19 in a US Population. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1049)

Anderson Jeffrey L et al. JAMA network open 2021 4 (4) e217429

With contrasting reports from China,1 Europe, Boston, New York, and elsewhere, we embarked on a large, prospective case-control study that included more than 11?000 individuals who were newly infected with SARS-CoV-2, and we found no ABO associations with either disease susceptibility or severity

- S-Gene Target Failure as a Marker of Variant B.1.1.7 Among SARS-CoV-2 Isolates in the Greater Toronto Area, December 2020 to March 2021. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1052)

Brown Kevin A et al. JAMA 2021 4

A rapid increase in the proportion of SARS-CoV-2 samples with SGTF was identified in regions of England affected by B.1.1.7, and, after validation with whole genome sequencing, SGTF was determined to be a reliable marker of B.1.1.7 across the country. This study found that SGTF was a reliable marker of B.1.1.7, and that prevalence of B.1.1.7 has consistently grown more rapidly than preexisting variants, suggesting increased transmissibility.

- Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1056)

L Gaziano et al Nature Medicine, April 9, 2021

To identify therapeutic targets relevant to COVID-19, we conducted Mendelian randomization analyses, deriving genetic instruments based on transcriptomic and proteomic data for 1,263 actionable proteins that are targeted by approved drugs or in clinical phase of drug development. Using summary statistics from the Host Genetics Initiative and the Million Veteran Program, we studied 7,554 patients hospitalized with COVID-19 and >1 million controls. We found significant Mendelian randomization results for three proteins (ACE2, IFNAR2, and IL-10RB).

- Neutralization of SARS-CoV-2 variants by convalescent and vaccinated serum (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1057)

TA Bates et al, MEDRXIV, April 9, 2021

We tested human sera from large, demographically balanced cohorts of BNT162b2 vaccine recipients (n=51) and COVID-19 patients (n=44) for neutralizing antibodies against SARS-CoV-2 variants B.1.1.7 and B.1.351. Although the effect is more pronounced in the vaccine cohort, both B.1.1.7 and B.1.351 show significantly reduced levels of neutralization by vaccinated and convalescent sera. Age is negatively correlated with neutralization in vaccine.

- Evidence for increased breakthrough rates of SARS-CoV-2 variants of concern in BNT162b2 mRNA vaccinated individuals (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1058)

T Kustin et al, MEDRXIV, April 9, 2021

We performed a case-control study that examined whether BNT162b2 vaccinees with documented SARS-CoV-2 infection were more likely to become infected with B.1.1.7 or B.1.351 compared with unvaccinated individuals. Vaccinees infected at least a week after the second dose were disproportionately infected with B.1.351 (odds ratio of 8:1). Those infected between two weeks after the first dose and one week after the second dose, were disproportionately infected by B.1.1.7 (odds ratio of 26:10), suggesting reduced vaccine effectiveness against both VOCs under different dosage/timing conditions.

- Early evidence of COVID-19 vaccine effectiveness within the general population of California (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1060)

K Andrekjo et al, MEDRXIV, April 10, 2021

Among 325 cases, 23 (7%) and 13 (4%) received BNT162b2 and mRNA-1273, respectively; 8 (2%) were fully vaccinated with either product. Among 260 controls, 49 (19%) and 49 (19%) received BNT162b2 and mRNA-1273, respectively; 42 (16%) were fully vaccinated with either product. Among fully vaccinated individuals, vaccine effectiveness was 86%. Vaccine effectiveness was 66% and 78% one week following a first and second dose, respectively.

- Genomic characteristics and clinical effect of the emergent SARS-CoV-2 B.1.1.7 lineage in London, UK: a whole-genome sequencing and hospital-based cohort study (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1065)

D Frampton et al, The Lancet, April 12, 2021

Of 496 patients with samples positive for SARS-CoV-2 on PCR and who met inclusion criteria, 341 had samples that could be sequenced. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. We found no evidence of an association between severe disease and death and lineage (B.1.1.7 vs non-B.1.1.7) in unadjusted analyses, or in analyses adjusted for hospital, sex, age, comorbidities, and ethnicity.

- Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1066)

MS Graham et al, The Lancet, April 12, 2021

The SARS-CoV-2 variant B.1.1.7 was first identified in December, 2020, in England. We aimed to investigate whether increases in the proportion of infections with this variant are associated with differences in symptoms or disease course, reinfection rates, or transmissibility.

- Genetic evidence for the association between COVID-19 epidemic severity and timing of non-pharmaceutical interventions (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1069)

MR Cronin et al, Nature Comms, April 12, 2021

We carried out a phylogenetic analysis of more than 29,000 publicly available whole genome SARS-CoV-2 sequences from 57 locations to estimate the time that the epidemic originated in different places. These estimates were examined in relation to the dates of the most stringent interventions in each location as well as to the number of cumulative COVID-19 deaths and phylodynamic estimates of epidemic size.

- SARS-CoV-2 Detection from the Built Environment and Wastewater and Its Use for Hospital Surveillance (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1070)

A Hinz et al, MEDRXIV, April 13, 2021

We performed a prospective multi-center study of environmental sampling of SARS-CoV-2 from hospital surfaces and wastewater and evaluated their relationships with regional and hospital COVID-19 burden. We developed and validated a qPCR-based approach to surface sampling, and swab samples were collected weekly from different locations and surfaces across two tertiary care hospital campuses for a 10-week period during the pandemic, along with wastewater samples.

- Serum sample neutralisation of BBIBP-CorV and ZF2001 vaccines to SARS-CoV-2 501Y.V2 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1073)

B Huang et al, The Lancet Microbe, April 13, 2021

Our findings suggest that the 501Y.V2 variant does not escape the immunity induced by vaccines targeting the whole virus (BBIBP-CorV) or S protein dimeric RBD (ZF2001). The potential 1.5 to 1.6 times reduction in neutralising GMTs should be taken into account for their effect on the clinical efficacy of these vaccines.

## Non-Genomics Precision Health Studies

- Estimation of secondary household attack rates for emergent spike L452R SARS-CoV-2 variants detected by genomic surveillance at a community-based testing site in San Francisco. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1045)

Peng James et al. Clinical infectious diseases : an official publication of the Infectious Diseases Society of America 2021 4

" 928 high quality genomes were generated. Certain viral lineages bearing spike mutations, defined in part by L452R, S13I, and W152C, comprised 54.4% of the total sequences from January, compared to 15.7% in November. Household contacts exposed to the "California" or "West Coast" variants (B.1.427 and B.1.429) were at higher risk of infection compared to household contacts exposed to lineages lacking these variants (0.36 vs 0.29, RR=1.28; 95% CI:1.00-1.64)."

- Association of Sociodemographic Factors and Blood Group Type With Risk of COVID-19 in a US Population. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1049)

Anderson Jeffrey L et al. JAMA network open 2021 4 (4) e217429

With contrasting reports from China,1 Europe, Boston, New York, and elsewhere, we embarked on a large, prospective case-control study that included more than 11?000 individuals who were newly infected with SARS-CoV-2, and we found no ABO associations with either disease susceptibility or severity

- S-Gene Target Failure as a Marker of Variant B.1.1.7 Among SARS-CoV-2 Isolates in the Greater Toronto Area, December 2020 to March 2021. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1052)

Brown Kevin A et al. JAMA 2021 4

A rapid increase in the proportion of SARS-CoV-2 samples with SGTF was identified in regions of England affected by B.1.1.7, and, after validation with whole genome sequencing, SGTF was determined to be a reliable marker of B.1.1.7 across the country. This study found that SGTF was a reliable marker of B.1.1.7, and that prevalence of B.1.1.7 has consistently grown more rapidly than preexisting variants, suggesting increased transmissibility.

- Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1056)

L Gaziano et al Nature Medicine, April 9, 2021

To identify therapeutic targets relevant to COVID-19, we conducted Mendelian randomization analyses, deriving genetic instruments based on transcriptomic and proteomic data for 1,263 actionable proteins that are targeted by approved drugs or in clinical phase of drug development. Using summary statistics from the Host Genetics Initiative and the Million Veteran Program, we studied 7,554 patients hospitalized with COVID-19 and >1 million controls. We found significant Mendelian randomization results for three proteins (ACE2, IFNAR2, and IL-10RB).

- Neutralization of SARS-CoV-2 variants by convalescent and vaccinated serum (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1057)

TA Bates et al, MEDRXIV, April 9, 2021

We tested human sera from large, demographically balanced cohorts of BNT162b2 vaccine recipients (n=51) and COVID-19 patients (n=44) for neutralizing antibodies against SARS-CoV-2 variants B.1.1.7 and B.1.351. Although the effect is more pronounced in the vaccine cohort, both B.1.1.7 and B.1.351 show significantly reduced levels of neutralization by vaccinated and convalescent sera. Age is negatively correlated with neutralization in vaccine.

- Evidence for increased breakthrough rates of SARS-CoV-2 variants of concern in BNT162b2 mRNA vaccinated individuals (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1058)

T Kustin et al, MEDRXIV, April 9, 2021

We performed a case-control study that examined whether BNT162b2 vaccinees with documented SARS-CoV-2 infection

were more likely to become infected with B.1.1.7 or B.1.351 compared with unvaccinated individuals. Vaccinees infected at least a week after the second dose were disproportionately infected with B.1.351 (odds ratio of 8:1). Those infected between two weeks after the first dose and one week after the second dose, were disproportionately infected by B.1.1.7 (odds ratio of 26:10), suggesting reduced vaccine effectiveness against both VOCs under different dosage/timing conditions.

- Early evidence of COVID-19 vaccine effectiveness within the general population of California (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1060)

K Andrekjo et al, MEDRXIV, April 10, 2021

Among 325 cases, 23 (7%) and 13 (4%) received BNT162b2 and mRNA-1273, respectively; 8 (2%) were fully vaccinated with either product. Among 260 controls, 49 (19%) and 49 (19%) received BNT162b2 and mRNA-1273, respectively; 42 (16%) were fully vaccinated with either product. Among fully vaccinated individuals, vaccine effectiveness was 86%. Vaccine effectiveness was 66% and 78% one week following a first and second dose, respectively.

- Genomic characteristics and clinical effect of the emergent SARS-CoV-2 B.1.1.7 lineage in London, UK: a whole-genome sequencing and hospital-based cohort study (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1065)

D Frampton et al, The Lancet, April 12, 2021

Of 496 patients with samples positive for SARS-CoV-2 on PCR and who met inclusion criteria, 341 had samples that could be sequenced. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. We found no evidence of an association between severe disease and death and lineage (B.1.1.7 vs non-B.1.1.7) in unadjusted analyses, or in analyses adjusted for hospital, sex, age, comorbidities, and ethnicity.

- Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1066)

MS Graham et al, The Lancet, April 12, 2021

The SARS-CoV-2 variant B.1.1.7 was first identified in December, 2020, in England. We aimed to investigate whether increases in the proportion of infections with this variant are associated with differences in symptoms or disease course, reinfection rates, or transmissibility.

- Genetic evidence for the association between COVID-19 epidemic severity and timing of non-pharmaceutical interventions (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1069)

MR Cronin et al, Nature Comms, April 12, 2021

We carried out a phylogenetic analysis of more than 29,000 publicly available whole genome SARS-CoV-2 sequences from 57 locations to estimate the time that the epidemic originated in different places. These estimates were examined in relation to the dates of the most stringent interventions in each location as well as to the number of cumulative COVID-19 deaths and phylodynamic estimates of epidemic size.

- SARS-CoV-2 Detection from the Built Environment and Wastewater and Its Use for Hospital Surveillance (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1070)

A Hinz et al, MEDRXIV, April 13, 2021

We performed a prospective multi-center study of environmental sampling of SARS-CoV-2 from hospital surfaces and wastewater and evaluated their relationships with regional and hospital COVID-19 burden. We developed and validated a qPCR-based approach to surface sampling, and swab samples were collected weekly from different locations and surfaces across two tertiary care hospital campuses for a 10-week period during the pandemic, along with wastewater samples.

- Serum sample neutralisation of BBIBP-CorV and ZF2001 vaccines to SARS-CoV-2 501Y.V2 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1073)

B Huang et al, The Lancet Microbe, April 13, 2021

Our findings suggest that the 501Y.V2 variant does not escape the immunity induced by vaccines targeting the whole virus (BBIBP-CorV) or S protein dimeric RBD (ZF2001). The potential 1.5 to 1.6 times reduction in neutralising GMTs should be taken into account for their effect on the clinical efficacy of these vaccines.

## News, Reviews and Commentaries

- Estimation of secondary household attack rates for emergent spike L452R SARS-CoV-2 variants detected by genomic surveillance at a community-based testing site in San Francisco. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1045)

Peng James et al. Clinical infectious diseases : an official publication of the Infectious Diseases Society of America 2021 4

" 928 high quality genomes were generated. Certain viral lineages bearing spike mutations, defined in part by L452R, S13I, and W152C, comprised 54.4% of the total sequences from January, compared to 15.7% in November. Household contacts exposed to the "California" or "West Coast" variants (B.1.427 and B.1.429) were at higher risk of infection compared to household contacts exposed to lineages lacking these variants (0.36 vs 0.29, RR=1.28; 95% CI:1.00-1.64)."

- Association of Sociodemographic Factors and Blood Group Type With Risk of COVID-19 in a US Population. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1049)

Anderson Jeffrey L et al. JAMA network open 2021 4 (4) e217429

With contrasting reports from China,1 Europe, Boston, New York, and elsewhere, we embarked on a large, prospective case-control study that included more than 11?000 individuals who were newly infected with SARS-CoV-2, and we found no ABO associations with either disease susceptibility or severity

- S-Gene Target Failure as a Marker of Variant B.1.1.7 Among SARS-CoV-2 Isolates in the Greater Toronto Area, December 2020 to March 2021. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1052)

Brown Kevin A et al. JAMA 2021 4

A rapid increase in the proportion of SARS-CoV-2 samples with SGTF was identified in regions of England affected by B.1.1.7, and, after validation with whole genome sequencing, SGTF was determined to be a reliable marker of B.1.1.7 across the country. This study found that SGTF was a reliable marker of B.1.1.7, and that prevalence of B.1.1.7 has consistently grown more rapidly than preexisting variants, suggesting increased transmissibility.

- Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1056)

L Gaziano et al Nature Medicine, April 9, 2021

To identify therapeutic targets relevant to COVID-19, we conducted Mendelian randomization analyses, deriving genetic instruments based on transcriptomic and proteomic data for 1,263 actionable proteins that are targeted by approved drugs or in clinical phase of drug development. Using summary statistics from the Host Genetics Initiative and the Million Veteran Program, we studied 7,554 patients hospitalized with COVID-19 and >1 million controls. We found significant Mendelian randomization results for three proteins (ACE2, IFNAR2, and IL-10RB).

- Neutralization of SARS-CoV-2 variants by convalescent and vaccinated serum (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1057)

TA Bates et al, MEDRXIV, April 9, 2021

We tested human sera from large, demographically balanced cohorts of BNT162b2 vaccine recipients (n=51) and COVID-19 patients (n=44) for neutralizing antibodies against SARS-CoV-2 variants B.1.1.7 and B.1.351. Although the effect is more pronounced in the vaccine cohort, both B.1.1.7 and B.1.351 show significantly reduced levels of neutralization by vaccinated and convalescent sera. Age is negatively correlated with neutralization in vaccine.

- Evidence for increased breakthrough rates of SARS-CoV-2 variants of concern in BNT162b2 mRNA vaccinated individuals (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1058)

T Kustin et al, MEDRXIV, April 9, 2021

We performed a case-control study that examined whether BNT162b2 vaccinees with documented SARS-CoV-2 infection were more likely to become infected with B.1.1.7 or B.1.351 compared with unvaccinated individuals. Vaccinees infected at least a week after the second dose were disproportionately infected with B.1.351 (odds ratio of 8:1). Those infected between two weeks after the first dose and one week after the second dose, were disproportionately infected by B.1.1.7 (odds ratio of 26:10), suggesting reduced vaccine effectiveness against both VOCs under different dosage/timing conditions.

- Early evidence of COVID-19 vaccine effectiveness within the general population of California (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1060)

K Andrekjo et al, MEDRXIV, April 10, 2021

Among 325 cases, 23 (7%) and 13 (4%) received BNT162b2 and mRNA-1273, respectively; 8 (2%) were fully vaccinated with

either product. Among 260 controls, 49 (19%) and 49 (19%) received BNT162b2 and mRNA-1273, respectively; 42 (16%) were fully vaccinated with either product. Among fully vaccinated individuals, vaccine effectiveness was 86%. Vaccine effectiveness was 66% and 78% one week following a first and second dose, respectively.

- Genomic characteristics and clinical effect of the emergent SARS-CoV-2 B.1.1.7 lineage in London, UK: a whole-genome sequencing and hospital-based cohort study (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1065)  
D Frampton et al, The Lancet, April 12, 2021

Of 496 patients with samples positive for SARS-CoV-2 on PCR and who met inclusion criteria, 341 had samples that could be sequenced. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. We found no evidence of an association between severe disease and death and lineage (B.1.1.7 vs non-B.1.1.7) in unadjusted analyses, or in analyses adjusted for hospital, sex, age, comorbidities, and ethnicity.

- Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1066)  
MS Graham et al, The Lancet, April 12, 2021

The SARS-CoV-2 variant B.1.1.7 was first identified in December, 2020, in England. We aimed to investigate whether increases in the proportion of infections with this variant are associated with differences in symptoms or disease course, reinfection rates, or transmissibility.

- Genetic evidence for the association between COVID-19 epidemic severity and timing of non-pharmaceutical interventions (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1069)  
MR Cronin et al, Nature Comms, April 12, 2021

We carried out a phylogenetic analysis of more than 29,000 publicly available whole genome SARS-CoV-2 sequences from 57 locations to estimate the time that the epidemic originated in different places. These estimates were examined in relation to the dates of the most stringent interventions in each location as well as to the number of cumulative COVID-19 deaths and phylodynamic estimates of epidemic size.

- SARS-CoV-2 Detection from the Built Environment and Wastewater and Its Use for Hospital Surveillance (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1070)  
A Hinz et al, MEDRXIV April 13, 2021

We performed a prospective multi-center study of environmental sampling of SARS-CoV-2 from hospital surfaces and wastewater and evaluated their relationships with regional and hospital COVID-19 burden. We developed and validated a qPCR-based approach to surface sampling, and swab samples were collected weekly from different locations and surfaces across two tertiary care hospital campuses for a 10-week period during the pandemic, along with wastewater samples.

- Serum sample neutralisation of BBIBP-CorV and ZF2001 vaccines to SARS-CoV-2 501Y.V2 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1073)  
B Huang et al, The Lancet Microbe, April 13, 2021

Our findings suggest that the 501Y.V2 variant does not escape the immunity induced by vaccines targeting the whole virus (BBIBP-CorV) or S protein dimeric RBD (ZF2001). The potential 1.5 to 1.6 times reduction in neutralising GMTs should be taken into account for their effect on the clinical efficacy of these vaccines.

**Disclaimer:** Articles listed in COVID-19 Genomics and Precision Public Health Weekly Update are selected by the CDC Office of Public Health Genomics to provide current awareness of the scientific literature and news. Inclusion in the update does not necessarily represent the views of the Centers for Disease Control and Prevention nor does it imply endorsement of the article's methods or findings. CDC and DHHS assume no responsibility for the factual accuracy of the items presented. The selection, omission, or content of items does not imply any endorsement or other position taken by CDC or DHHS. Opinion, findings and conclusions expressed by the original authors of items included in the Clips, or persons quoted therein, are strictly their own and are in no way meant to represent the opinion or views of CDC or DHHS. References to publications, news sources, and non-CDC Websites are provided solely for informational purposes and do not imply endorsement by CDC or DHHS.

Page last reviewed: Oct 1, 2020

Page last updated: Apr 21, 2021

Content source: Office of Genomics and Precision Public Health (<http://www.cdc.gov/genomics/>), CDC Office of Science (<https://www.cdc.gov/od/science/index.htm>)