

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

Published on 06/24/2021

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

- Association of Sickle Cell Trait with Risk and Mortality of COVID-19: Results from the United Kingdom Biobank. ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1351](#))
Resurreccion W Kyle et al. The American journal of tropical medicine and hygiene 2021 6

Among Black individuals who were tested for COVID-19, we found similar infection rates among SCT carriers (14/72; 19.7%) and noncarriers (167/791; 21.1%), but higher COVID-19 mortality rates among SCT carriers (4/14; 28.6%) than among noncarriers (21/167; 12.6%) (odds ratio [OR], 3.04; 95% confidence interval [CI], 0.69-11.82; $P = 0.12$). Notably, SCT carriers with preexisting diabetes had significantly higher COVID-19 mortality (4/4; 100%) than those without diabetes (0/10; 0%; (OR, 90.71; 95% CI, 5.66-infinite; $P = 0.0005$).

- Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1352](#))
C Liu et al, Cell, June 16, 2021

We study the ability of monoclonal antibodies, convalescent and vaccine sera to neutralize B.1.617.1 and B.1.617.2 and complement this with structural analyses of Fab/RBD complexes and map the antigenic space of current variants. Neutralization of both viruses is reduced when compared with ancestral Wuhan related strains but there is no evidence of widespread antibody escape as seen with B.1.351. However, B.1.351 and P.1 sera showed markedly more reduction in neutralization of B.1.617.2 suggesting that individuals previously infected by these variants may be more susceptible to reinfection by B.1.617.2.

- Sperm Parameters Before and After COVID-19 mRNA Vaccination. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1354)

Gonzalez Daniel C et al. JAMA 2021 6

In this study of sperm parameters before and after 2 doses of a COVID-19 mRNA vaccine, there were no significant decreases in any sperm parameter among this small cohort of healthy men. Because the vaccines contain mRNA and not the live virus, it is unlikely that the vaccine would affect sperm parameters.

- In vivo monoclonal antibody efficacy against SARS-CoV-2 variant strains (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1357)

RE Chen et al, Nature, June 21, 2021

Using a panel of monoclonal antibodies (mAbs) corresponding to many in advanced clinical development, we report the impact on protection in animals against authentic SARS-CoV-2 variants including viruses with B.1.1.7, B.1.351, or B.1.1.28 spike genes. Although some individual mAbs showed reduced or abrogated neutralizing activity in cell culture against B.1.351, B.1.1.28, B.1.617.1, and B.1.526 viruses with E484 spike protein mutations, low prophylactic doses of mAb combinations protected against infection by many variants.

- Characterization of a new SARS-CoV-2 variant that emerged in Brazil. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1363)

Imai Masaki et al. Proceedings of the National Academy of Sciences of the United States of America 2021 6 (27)

Recently, a new variant of SARS-CoV-2 possessing multiple mutations in the S protein, designated P.1, emerged in Brazil. Here, we characterized a P.1 variant isolated in Japan by using Syrian hamsters, a well-established small animal model for the study of SARS-CoV-2 disease (COVID-19). In hamsters, the variant showed replicative abilities and pathogenicity similar to those of early and contemporary strains (i.e., SARS-CoV-2 bearing aspartic acid [D] or glycine [G] at position 614 of the S protein). Sera and/or plasma from convalescent patients and BNT162b2 messenger RNA vaccinees showed comparable neutralization titers across the P.1 variant, S-614D, and S-614G strains. In contrast, the S-614D and S-614G strains were less well recognized than the P.1 variant by serum from a P.1-infected patient.

- Immunogenicity of SARS-CoV-2 messenger RNA Vaccines in Patients with Cancer (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1368)

A Addeo et al, Cancer Cell, June 22, 2021

Using a prospective cohort, we assessed the seroconversion rates and anti-SARS-CoV-2 spike protein antibody titers following the 1st and 2nd dose of BNT162b2 and mRNA-1273 SARS-CoV-2 vaccines in patients with cancer in U.S. and Europe from January to April 2021. Among 131 patients, most (94%) achieved seroconversion after receipt of 2 vaccine doses. Seroconversion rates and antibody titers in patients with hematological malignancy were significantly lower than those with solid tumors.

- Predicting the mutational drivers of future SARS-CoV-2 variants of concern (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1370)

MC Maher et al, MEDRXIV, June 22, 2021

We sought to predict Spike amino acid changes that could contribute to future variants of concern. We tested the importance of features comprising epidemiology, evolution, immunology, and neural network-based protein sequence modeling. This resulted in identification of the primary biological drivers of SARS-CoV-2 intra-pandemic evolution. We found evidence that resistance to population-level host immunity has increasingly shaped SARS-CoV-2 evolution over time. We identified with high accuracy mutations that will spread, at up to four months in advance, across different phases of the pandemic.

- 50-gene risk profiles in peripheral blood predict COVID-19 outcomes: A retrospective, multicenter cohort study. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1375)

Juan Guardela Brenda M et al. EBioMedicine 2021 6 103439

0-gene risk profiles discriminated severe from mild COVID-19 in the Discovery cohort ($P = 0.015$) and predicted ICU admission, need for mechanical ventilation, and in-hospital mortality (AUC: 0.77, 0.75, and 0.74, respectively, $P < 0.001$) in the COVID-19 Validation cohort. In COVID-19, 50-gene expressing cells with a high-risk profile included monocytes, dendritic cells, and neutrophils.

- Three Doses of an mRNA Covid-19 Vaccine in Solid-Organ Transplant Recipients.

(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1376)

Kamar Nassim et al. The New England journal of medicine 2021 6

Here, we report the humoral response in a group of 101 consecutive solid-organ transplant recipients (mean [\pm SD] age, 58 ± 2 years; 69% were men) who were given three doses of the messenger RNA vaccine BNT162b2 (Pfizer–BioNTech). The group included 78 kidney-transplant recipients, 12 liver-transplant recipients, 8 lung-transplant or heart-transplant recipients, and 3 pancreas-transplant recipients. The first two doses were given 1 month apart, and the third dose was administered 61 ± 1 days after the second dose.

Non-Genomics Precision Health Studies

- Association of Sickle Cell Trait with Risk and Mortality of COVID-19: Results from the United Kingdom Biobank. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1351)

Resurreccion W Kyle et al. The American journal of tropical medicine and hygiene 2021 6

Among Black individuals who were tested for COVID-19, we found similar infection rates among SCT carriers (14/72; 19.7%) and noncarriers (167/791; 21.1%), but higher COVID-19 mortality rates among SCT carriers (4/14; 28.6%) than among noncarriers (21/167; 12.6%) (odds ratio [OR], 3.04; 95% confidence interval [CI], 0.69-11.82; $P = 0.12$). Notably, SCT carriers with preexisting diabetes had

significantly higher COVID-19 mortality (4/4; 100%) than those without diabetes (0/10; 0%; (OR, 90.71; 95% CI, 5.66-infinite; P = 0.0005).

- Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum

(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1352)

C Liu et al, Cell, June 16, 2021

We study the ability of monoclonal antibodies, convalescent and vaccine sera to neutralize B.1.617.1 and B.1.617.2 and complement this with structural analyses of Fab/RBD complexes and map the antigenic space of current variants. Neutralization of both viruses is reduced when compared with ancestral Wuhan related strains but there is no evidence of widespread antibody escape as seen with B.1.351. However, B.1.351 and P.1 sera showed markedly more reduction in neutralization of B.1.617.2 suggesting that individuals previously infected by these variants may be more susceptible to reinfection by B.1.617.2.

- Sperm Parameters Before and After COVID-19 mRNA Vaccination. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1354)

Gonzalez Daniel C et al. JAMA 2021 6

In this study of sperm parameters before and after 2 doses of a COVID-19 mRNA vaccine, there were no significant decreases in any sperm parameter among this small cohort of healthy men. Because the vaccines contain mRNA and not the live virus, it is unlikely that the vaccine would affect sperm parameters.

- In vivo monoclonal antibody efficacy against SARS-CoV-2 variant strains (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1357)

RE Chen et al, Nature, June 21, 2021

Using a panel of monoclonal antibodies (mAbs) corresponding to many in advanced clinical development, we report the impact on protection in animals against authentic SARS-CoV-2 variants including viruses with B.1.1.7, B.1.351, or B.1.1.28 spike genes. Although some individual mAbs showed reduced or abrogated neutralizing activity in cell culture against B.1.351, B.1.1.28, B.1.617.1, and B.1.526 viruses with E484 spike protein mutations, low prophylactic doses of mAb combinations protected against infection by many variants.

- Characterization of a new SARS-CoV-2 variant that emerged in Brazil. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1363)

Imai Masaki et al. Proceedings of the National Academy of Sciences of the United States of America 2021 6 (27)

Recently, a new variant of SARS-CoV-2 possessing multiple mutations in the S protein, designated P.1, emerged in Brazil. Here, we characterized a P.1 variant isolated in Japan by using Syrian hamsters, a well-established small animal model for the study of SARS-CoV-2 disease (COVID-19). In hamsters, the variant showed replicative abilities and pathogenicity similar to those of early and contemporary

strains (i.e., SARS-CoV-2 bearing aspartic acid [D] or glycine [G] at position 614 of the S protein). Sera and/or plasma from convalescent patients and BNT162b2 messenger RNA vaccinees showed comparable neutralization titers across the P.1 variant, S-614D, and S-614G strains. In contrast, the S-614D and S-614G strains were less well recognized than the P.1 variant by serum from a P.1-infected patient.

- Immunogenicity of SARS-CoV-2 messenger RNA Vaccines in Patients with Cancer ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1368](#))

A Addeo et al, *Cancer Cell*, June 22, 2021

Using a prospective cohort, we assessed the seroconversion rates and anti-SARS-CoV-2 spike protein antibody titers following the 1st and 2nd dose of BNT162b2 and mRNA-1273 SARS-CoV-2 vaccines in patients with cancer in U.S. and Europe from January to April 2021. Among 131 patients, most (94%) achieved seroconversion after receipt of 2 vaccine doses. Seroconversion rates and antibody titers in patients with hematological malignancy were significantly lower than those with solid tumors.

- Predicting the mutational drivers of future SARS-CoV-2 variants of concern ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1370](#))

MC Maher et al, *MEDRXIV*, June 22, 2021

We sought to predict Spike amino acid changes that could contribute to future variants of concern. We tested the importance of features comprising epidemiology, evolution, immunology, and neural network-based protein sequence modeling. This resulted in identification of the primary biological drivers of SARS-CoV-2 intra-pandemic evolution. We found evidence that resistance to population-level host immunity has increasingly shaped SARS-CoV-2 evolution over time. We identified with high accuracy mutations that will spread, at up to four months in advance, across different phases of the pandemic.

- 50-gene risk profiles in peripheral blood predict COVID-19 outcomes: A retrospective, multicenter cohort study. ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1375](#))

Juan Guardela Brenda M et al. *EBioMedicine* 2021 6 103439

0-gene risk profiles discriminated severe from mild COVID-19 in the Discovery cohort ($P = 0.015$) and predicted ICU admission, need for mechanical ventilation, and in-hospital mortality (AUC: 0.77, 0.75, and 0.74, respectively, $P < 0.001$) in the COVID-19 Validation cohort. In COVID-19, 50-gene expressing cells with a high-risk profile included monocytes, dendritic cells, and neutrophils.

- Three Doses of an mRNA Covid-19 Vaccine in Solid-Organ Transplant Recipients. ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1376](#))

Kamar Nassim et al. *The New England journal of medicine* 2021 6

Here, we report the humoral response in a group of 101 consecutive solid-organ transplant recipients (mean [\pm SD] age, 58 ± 2 years; 69% were men) who were given three doses of the messenger RNA vaccine BNT162b2 (Pfizer–BioNTech). The group included 78 kidney-transplant recipients, 12 liver-

transplant recipients, 8 lung-transplant or heart-transplant recipients, and 3 pancreas-transplant recipients. The first two doses were given 1 month apart, and the third dose was administered 61±1 days after the second dose.

News, Reviews and Commentaries

- Association of Sickle Cell Trait with Risk and Mortality of COVID-19: Results from the United Kingdom Biobank. ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1351](#))
Resurreccion W Kyle et al. The American journal of tropical medicine and hygiene 2021 6

Among Black individuals who were tested for COVID-19, we found similar infection rates among SCT carriers (14/72; 19.7%) and noncarriers (167/791; 21.1%), but higher COVID-19 mortality rates among SCT carriers (4/14; 28.6%) than among noncarriers (21/167; 12.6%) (odds ratio [OR], 3.04; 95% confidence interval [CI], 0.69-11.82; $P = 0.12$). Notably, SCT carriers with preexisting diabetes had significantly higher COVID-19 mortality (4/4; 100%) than those without diabetes (0/10; 0%; (OR, 90.71; 95% CI, 5.66-infinite; $P = 0.0005$).

- Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1352](#))
C Liu et al, Cell, June 16, 2021

We study the ability of monoclonal antibodies, convalescent and vaccine sera to neutralize B.1.617.1 and B.1.617.2 and complement this with structural analyses of Fab/RBD complexes and map the antigenic space of current variants. Neutralization of both viruses is reduced when compared with ancestral Wuhan related strains but there is no evidence of widespread antibody escape as seen with B.1.351. However, B.1.351 and P.1 sera showed markedly more reduction in neutralization of B.1.617.2 suggesting that individuals previously infected by these variants may be more susceptible to reinfection by B.1.617.2.

- Sperm Parameters Before and After COVID-19 mRNA Vaccination. ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1354](#))
Gonzalez Daniel C et al. JAMA 2021 6

In this study of sperm parameters before and after 2 doses of a COVID-19 mRNA vaccine, there were no significant decreases in any sperm parameter among this small cohort of healthy men. Because the vaccines contain mRNA and not the live virus, it is unlikely that the vaccine would affect sperm parameters.

- In vivo monoclonal antibody efficacy against SARS-CoV-2 variant strains ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1357](#))
RE Chen et al, Nature, June 21, 2021

Using a panel of monoclonal antibodies (mAbs) corresponding to many in advanced clinical development, we report the impact on protection in animals against authentic SARS-CoV-2 variants including viruses with B.1.1.7, B.1.351, or B.1.1.28 spike genes. Although some individual mAbs showed reduced or abrogated neutralizing activity in cell culture against B.1.351, B.1.1.28, B.1.617.1, and B.1.526 viruses with E484 spike protein mutations, low prophylactic doses of mAb combinations protected against infection by many variants.

- Characterization of a new SARS-CoV-2 variant that emerged in Brazil. ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1363](#))
Imai Masaki et al. *Proceedings of the National Academy of Sciences of the United States of America* 2021 6 (27)

Recently, a new variant of SARS-CoV-2 possessing multiple mutations in the S protein, designated P.1, emerged in Brazil. Here, we characterized a P.1 variant isolated in Japan by using Syrian hamsters, a well-established small animal model for the study of SARS-CoV-2 disease (COVID-19). In hamsters, the variant showed replicative abilities and pathogenicity similar to those of early and contemporary strains (i.e., SARS-CoV-2 bearing aspartic acid [D] or glycine [G] at position 614 of the S protein). Sera and/or plasma from convalescent patients and BNT162b2 messenger RNA vaccinees showed comparable neutralization titers across the P.1 variant, S-614D, and S-614G strains. In contrast, the S-614D and S-614G strains were less well recognized than the P.1 variant by serum from a P.1-infected patient.

- immunogenicity of SARS-CoV-2 messenger RNA Vaccines in Patients with Cancer ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1368](#))
A Addeo et al, *Cancer Cell*, June 22, 2021

Using a prospective cohort, we assessed the seroconversion rates and anti-SARS-CoV-2 spike protein antibody titers following the 1st and 2nd dose of BNT162b2 and mRNA-1273 SARS-CoV-2 vaccines in patients with cancer in U.S. and Europe from January to April 2021. Among 131 patients, most (94%) achieved seroconversion after receipt of 2 vaccine doses. Seroconversion rates and antibody titers in patients with hematological malignancy were significantly lower than those with solid tumors.

- Predicting the mutational drivers of future SARS-CoV-2 variants of concern ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1370](#))
MC Maher et al, *MEDRXIV*, June 22, 2021

We sought to predict Spike amino acid changes that could contribute to future variants of concern. We tested the importance of features comprising epidemiology, evolution, immunology, and neural network-based protein sequence modeling. This resulted in identification of the primary biological drivers of SARS-CoV-2 intra-pandemic evolution. We found evidence that resistance to population-level host immunity has increasingly shaped SARS-CoV-2 evolution over time. We identified with high accuracy mutations that will spread, at up to four months in advance, across different phases of the pandemic.

- 50-gene risk profiles in peripheral blood predict COVID-19 outcomes: A retrospective, multicenter cohort study. ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1375](#))

Juan Guardela Brenda M et al. *EBioMedicine* 2021 6 103439

0-gene risk profiles discriminated severe from mild COVID-19 in the Discovery cohort ($P = 0.015$) and predicted ICU admission, need for mechanical ventilation, and in-hospital mortality (AUC: 0.77, 0.75, and 0.74, respectively, $P < 0.001$) in the COVID-19 Validation cohort. In COVID-19, 50-gene expressing cells with a high-risk profile included monocytes, dendritic cells, and neutrophils.

- Three Doses of an mRNA Covid-19 Vaccine in Solid-Organ Transplant Recipients.

([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1376](#))

Kamar Nassim et al. *The New England journal of medicine* 2021 6

Here, we report the humoral response in a group of 101 consecutive solid-organ transplant recipients (mean [\pm SD] age, 58 ± 2 years; 69% were men) who were given three doses of the messenger RNA vaccine BNT162b2 (Pfizer–BioNTech). The group included 78 kidney-transplant recipients, 12 liver-transplant recipients, 8 lung-transplant or heart-transplant recipients, and 3 pancreas-transplant recipients. The first two doses were given 1 month apart, and the third dose was administered 61 ± 1 days after the second dose.

***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: Jun 26, 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>)