



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

Published on 03/25/2021

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

- Genomic and healthcare dynamics of nosocomial SARS-CoV-2 transmission.
(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=947)
Ellingford Jamie M et al. eLife 2021 3

"We sequenced SARS-CoV-2 genomes for patients and healthcare workers (HCWs) across multiple geographically distinct UK hospitals, obtaining 173 high-quality SARS-CoV-2 genomes.... Patients within [patient contact clusters] carried viruses more genetically identical to HCWs in the same ward location. SARS-CoV-2 genome sequencing integrated with patient and HCW movement data increases identification of outbreak clusters. This dynamic approach can support infection control management strategies within the healthcare setting."
- Estimating the increased transmissibility of the B.1.1.7 strain over previously circulating strains in England using fractions of GISAID sequences and the distribution of serial intervals
(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=950)
C Piantham et al, MEDRXIV, March 17, 2021
- Metagenomic sequencing of municipal wastewater provides a near-complete SARS-CoV-2 genome sequence identified as the B.1.1.7 variant of concern from a Canadian municipality concurrent with an outbreak (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=951)
C Landgraff et al, MEDRXIV, March 17, 2021
- Neutralizing Antibodies Against SARS-CoV-2 Variants After Infection and Vaccination
(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=953)
VV Edara et al, JAMA, March 19, 2021

This study found neutralizing activity of infection- and vaccine-elicited antibodies against 4 SARS-CoV-2 variants, including B.1, B.1.1.7, and N501Y. Because neutralization studies measure the ability of antibodies to block virus infection, these results suggest that infection- and vaccine-

induced immunity may be retained against the B.1.1.7 variant.

- Sequence Analysis of 20,453 SARS-CoV-2 Genomes from the Houston Metropolitan Area Identifies the Emergence and Widespread Distribution of Multiple Isolates of All Major Variants of Concern. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=961)

Long S Wesley et al. The American journal of pathology 2021 3

Based on our extensive genome sequencing program involving 20,453 COVID-19 patient samples collected from March 2020 to February 2021, we report identification of all six of these SARS-CoV-2 variants among Houston Methodist Hospital patients residing in the greater metropolitan area. Although these variants are currently at relatively low frequency (aggregate of 1.1%) in the population, they are geographically widespread. Houston is the first city in the United States in which active circulation of all six current variants of concern has been documented by genome sequencing.

- Common variants at 21q22.3 locus influence MX1 and TMPRSS2 gene expression and susceptibility to severe COVID-19 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=963)

I Andolfo et al, IScience, March 2021

We performed an in-depth genetic analysis of chromosome 21 exploiting the genome-wide association study data, including 6,406 individuals hospitalized for COVID-19 and 902,088 controls with European genetic ancestry from the COVID-19 Host Genetics Initiative. We found that five single nucleotide polymorphisms within TMPRSS2 and near MX1 gene show associations with severe COVID-19. The minor alleles of the five SNPs correlated with a reduced risk of developing severe COVID-19 and high level of MX1 expression in blood.

- Emergence of the E484K Mutation in SARS-CoV-2 Lineage B.1.1.220 in Upstate New York (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=968)

E Lesho et al, MEDRXIV, March 23, 2021

Ongoing surveillance detected a SARS-CoV-2 B.1.1.220 variant carrying the E484K substitution in four patients from a hospital network in upstate New York. Patients reported no travel history and shared no obvious epidemiological linkage. A search of online databases identified 12 additional B.1.1.220 with E484K, all of which were detected in New York since December 2020. Detailed genomic analyses suggests that the mutation has emerged independently in at least two different B.1.1.220 strains in this region.

- Rapid identification and tracking of SARS-CoV-2 variants of concern (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=970)

D Chakraborty et al, The Lancet, March 22, 2021

We propose an approach for low-resolution, yet accurate, early detection of specific variants of concern through clustered interspaced short palindromic repeats (CRISPR) diagnostics. Such tests are rapid, inexpensive, and especially suited for low-income countries. Even where sequencing is being done, CRISPR diagnostics can help to isolate variants in the first instance, which can then be sequenced to validate and map coexisting mutations (appendix). We have used this approach to identify the Asn501Tyr variant of concern, starting from RNA.

- Inflammatory profiles across the spectrum of disease reveal a distinct role for GM-CSF in severe COVID-19. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=971)

Thwaites Ryan S et al. Science immunology 2021 3 (57)

Progressive elevation of levels of numerous inflammatory cytokines and chemokines (including IL-6, CXCL10, and GM-CSF) were associated with severity and accompanied by elevated markers of endothelial injury and thrombosis. Principal component and network analyses demonstrated central roles for IL-6 and GM-CSF in COVID-19 pathogenesis. Comparing these profiles to archived samples from patients with fatal influenza, IL-6 was equally elevated in both conditions whereas GM-CSF was prominent only in COVID-19.

Non-Genomics Precision Health Studies

- Genomic and healthcare dynamics of nosocomial SARS-CoV-2 transmission.

(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=947)

Ellingford Jamie M et al. eLife 2021 3

"We sequenced SARS-CoV-2 genomes for patients and healthcare workers (HCWs) across multiple geographically distinct UK hospitals, obtaining 173 high-quality SARS-CoV-2 genomes.... Patients within [patient contact clusters] carried viruses more genetically identical to HCWs in the same ward location. SARS-CoV-2 genome sequencing integrated with patient and HCW movement data increases identification of outbreak clusters. This dynamic approach can support infection control management strategies within the healthcare setting."

- Estimating the increased transmissibility of the B.1.1.7 strain over previously circulating strains in England using fractions of GISAID sequences and the distribution of serial intervals

(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=950)

C Piantham et al, MEDRXIV, March 17, 2021

- Metagenomic sequencing of municipal wastewater provides a near-complete SARS-CoV-2 genome sequence identified as the B.1.1.7 variant of concern from a Canadian municipality concurrent with an outbreak (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=951)

C Landgraaf et al, MEDRXIV, March 17, 2021

- Neutralizing Antibodies Against SARS-CoV-2 Variants After Infection and Vaccination

(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=953)

VV Edara et al, JAMA, March 19, 2021

This study found neutralizing activity of infection- and vaccine-elicited antibodies against 4 SARS-CoV-2 variants, including B.1, B.1.1.7, and N501Y. Because neutralization studies measure the ability of antibodies to block virus infection, these results suggest that infection- and vaccine-induced immunity may be retained against the B.1.1.7 variant.

- Sequence Analysis of 20,453 SARS-CoV-2 Genomes from the Houston Metropolitan Area Identifies the Emergence and Widespread Distribution of Multiple Isolates of All Major Variants of Concern.

(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=961)

Long S Wesley et al. The American journal of pathology 2021 3

Based on our extensive genome sequencing program involving 20,453 COVID-19 patient samples

collected from March 2020 to February 2021, we report identification of all six of these SARS-CoV-2 variants among Houston Methodist Hospital patients residing in the greater metropolitan area. Although these variants are currently at relatively low frequency (aggregate of 1.1%) in the population, they are geographically widespread. Houston is the first city in the United States in which active circulation of all six current variants of concern has been documented by genome sequencing.

- Common variants at 21q22.3 locus influence MX1 and TMPRSS2 gene expression and susceptibility to severe COVID-19 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=963)
I Andolfo et al, IScience, March 2021

We performed an in-depth genetic analysis of chromosome 21 exploiting the genome-wide association study data, including 6,406 individuals hospitalized for COVID-19 and 902,088 controls with European genetic ancestry from the COVID-19 Host Genetics Initiative. We found that five single nucleotide polymorphisms within TMPRSS2 and near MX1 gene show associations with severe COVID-19. The minor alleles of the five SNPs correlated with a reduced risk of developing severe COVID-19 and high level of MX1 expression in blood.

- Emergence of the E484K Mutation in SARS-CoV-2 Lineage B.1.1.220 in Upstate New York (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=968)
E Lesho et al, MEDRXIV, March 23, 2021

Ongoing surveillance detected a SARS-CoV-2 B.1.1.220 variant carrying the E484K substitution in four patients from a hospital network in upstate New York. Patients reported no travel history and shared no obvious epidemiological linkage. A search of online databases identified 12 additional B.1.1.220 with E484K, all of which were detected in New York since December 2020. Detailed genomic analyses suggests that the mutation has emerged independently in at least two different B.1.1.220 strains in this region.

- Rapid identification and tracking of SARS-CoV-2 variants of concern (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=970)
D Chakraborty et al, The Lancet, March 22, 2021

We propose an approach for low-resolution, yet accurate, early detection of specific variants of concern through clustered interspaced short palindromic repeats (CRISPR) diagnostics. Such tests are rapid, inexpensive, and especially suited for low-income countries. Even where sequencing is being done, CRISPR diagnostics can help to isolate variants in the first instance, which can then be sequenced to validate and map coexisting mutations (appendix). We have used this approach to identify the Asn501Tyr variant of concern, starting from RNA.

- Inflammatory profiles across the spectrum of disease reveal a distinct role for GM-CSF in severe COVID-19. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=971)
Thwaites Ryan S et al. Science immunology 2021 3 (57)

Progressive elevation of levels of numerous inflammatory cytokines and chemokines (including IL-6, CXCL10, and GM-CSF) were associated with severity and accompanied by elevated markers of endothelial injury and thrombosis. Principal component and network analyses demonstrated central roles for IL-6 and GM-CSF in COVID-19 pathogenesis. Comparing these profiles to archived samples from patients with fatal influenza, IL-6 was equally elevated in both conditions

whereas GM-CSF was prominent only in COVID-19.

News, Reviews and Commentaries

- Genomic and healthcare dynamics of nosocomial SARS-CoV-2 transmission.

(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=947)

Ellingford Jamie M et al. eLife 2021 3

"We sequenced SARS-CoV-2 genomes for patients and healthcare workers (HCWs) across multiple geographically distinct UK hospitals, obtaining 173 high-quality SARS-CoV-2 genomes.... Patients within [patient contact clusters] carried viruses more genetically identical to HCWs in the same ward location. SARS-CoV-2 genome sequencing integrated with patient and HCW movement data increases identification of outbreak clusters. This dynamic approach can support infection control management strategies within the healthcare setting."

- Estimating the increased transmissibility of the B.1.1.7 strain over previously circulating strains in England using fractions of GISAID sequences and the distribution of serial intervals

(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=950)

C Piantham et al, MEDRXIV, March 17, 2021

- Metagenomic sequencing of municipal wastewater provides a near-complete SARS-CoV-2 genome sequence identified as the B.1.1.7 variant of concern from a Canadian municipality concurrent with an outbreak (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=951)

C Landgraff et al, MEDRXIV, March 17, 2021

- Neutralizing Antibodies Against SARS-CoV-2 Variants After Infection and Vaccination

(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=953)

VV Edara et al, JAMA, March 19, 2021

This study found neutralizing activity of infection- and vaccine-elicited antibodies against 4 SARS-CoV-2 variants, including B.1, B.1.1.7, and N501Y. Because neutralization studies measure the ability of antibodies to block virus infection, these results suggest that infection- and vaccine-induced immunity may be retained against the B.1.1.7 variant.

- Sequence Analysis of 20,453 SARS-CoV-2 Genomes from the Houston Metropolitan Area Identifies the Emergence and Widespread Distribution of Multiple Isolates of All Major Variants of Concern.

(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=961)

Long S Wesley et al. The American journal of pathology 2021 3

Based on our extensive genome sequencing program involving 20,453 COVID-19 patient samples collected from March 2020 to February 2021, we report identification of all six of these SARS-CoV-2 variants among Houston Methodist Hospital patients residing in the greater metropolitan area. Although these variants are currently at relatively low frequency (aggregate of 1.1%) in the population, they are geographically widespread. Houston is the first city in the United States in which active circulation of all six current variants of concern has been documented by genome sequencing.

- Common variants at 21q22.3 locus influence MX1 and TMPRSS2 gene expression and susceptibility to severe COVID-19 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=963)
I Andolfo et al, IScience, March 2021

We performed an in-depth genetic analysis of chromosome 21 exploiting the genome-wide association study data, including 6,406 individuals hospitalized for COVID-19 and 902,088 controls with European genetic ancestry from the COVID-19 Host Genetics Initiative. We found that five single nucleotide polymorphisms within TMPRSS2 and near MX1 gene show associations with severe COVID-19. The minor alleles of the five SNPs correlated with a reduced risk of developing severe COVID-19 and high level of MX1 expression in blood.

- Emergence of the E484K Mutation in SARS-CoV-2 Lineage B.1.1.220 in Upstate New York (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=968)
E Lesho et al, MEDRXIV, March 23, 2021

Ongoing surveillance detected a SARS-CoV-2 B.1.1.220 variant carrying the E484K substitution in four patients from a hospital network in upstate New York. Patients reported no travel history and shared no obvious epidemiological linkage. A search of online databases identified 12 additional B.1.1.220 with E484K, all of which were detected in New York since December 2020. Detailed genomic analyses suggests that the mutation has emerged independently in at least two different B.1.1.220 strains in this region.

- Rapid identification and tracking of SARS-CoV-2 variants of concern (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=970)
D Chakraborty et al, The Lancet, March 22, 2021

We propose an approach for low-resolution, yet accurate, early detection of specific variants of concern through clustered interspaced short palindromic repeats (CRISPR) diagnostics. Such tests are rapid, inexpensive, and especially suited for low-income countries. Even where sequencing is being done, CRISPR diagnostics can help to isolate variants in the first instance, which can then be sequenced to validate and map coexisting mutations (appendix). We have used this approach to identify the Asn501Tyr variant of concern, starting from RNA.

- Inflammatory profiles across the spectrum of disease reveal a distinct role for GM-CSF in severe COVID-19. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=971)
Thwaites Ryan S et al. Science immunology 2021 3 (57)

Progressive elevation of levels of numerous inflammatory cytokines and chemokines (including IL-6, CXCL10, and GM-CSF) were associated with severity and accompanied by elevated markers of endothelial injury and thrombosis. Principal component and network analyses demonstrated central roles for IL-6 and GM-CSF in COVID-19 pathogenesis. Comparing these profiles to archived samples from patients with fatal influenza, IL-6 was equally elevated in both conditions whereas GM-CSF was prominent only in COVID-19.

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 02, 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>)