

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

Published on 08/26/2021

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

- A third COVID-19 vaccine shot markedly boosts neutralizing antibody potency and breadth (https://www.medrxiv.org/content/10.1101/2021.08.11.21261670v1)
 S Iketani et al, MEDRXIV, August 18, 2021
- Post-vaccination COVID-19: A case-control study and genomic analysis of 119 breakthrough infections in partially vaccinated individuals. (https://pubmed.ncbi.nlm.nih.gov/34410361)
 Baltas Ioannis et al. Clinical infectious diseases: an official publication of the Infectious Diseases Society of America 2021 8

We matched 119 cases of post-vaccination SARS-CoV-2 infection with BNT162b2 mRNA, or ChAdOx1 nCOV-19, to 476 unvaccinated patients with COVID-19 (Sept 2020-March 2021), according to age and sex. Differences in 60-day all-cause mortality, hospital admission, and hospital length of stay were evaluated. Phylogenetic, single nucleotide polymorphism (SNP) and minority variant allele (MVA) full genome sequencing analysis was performed.

 The Rapid Assessment of Aggregated Wastewater Samples for Genomic Surveillance of SARS-CoV-2 on a City-Wide Scale (https://www.medrxiv.org/content/10.1101/2021.08.17.21262170v1)
 EC Rouchka et al, MEDRXIV, August 20, 2021

We present the results of a collaborative effort between public health and metropolitan wastewater management authorities and the University of Louisville to monitor the SARS-CoV-2 pandemic through the monitoring of aggregate wastewater samples over a period of 28 weeks. Our data indicates that wastewater monitoring of water quality treatment centers and smaller neighborhood-

scale catchment areas is a viable means by which the prevalence and genetic variation of SARS-CoV-2 within a metropolitan community of approximately one million individuals may be monitored.

- Diminishing immune responses against variants of concern in dialysis patients four months after SARS-CoV-2 mRNA vaccination (https://www.medrxiv.org/content/10.1101/2021.08.16.21262115v1)
 A Dulovic et al, MEDRXIV, August 20, 2021
- X-linked recessive TLR7 deficiency in ~1% of men under 60 years old with life-threatening COVID-19. (https://pubmed.ncbi.nlm.nih.gov/34413140)

Asano Takaki et al. Science immunology 2021 8 (62)

Autosomal inborn errors of type I IFN immunity and autoantibodies against these cytokines underlie at least 10% of critical COVID-19 pneumonia cases. We report very rare, biochemically deleterious X-linked TLR7 variants in 16 unrelated male individuals aged 7 to 71 years (mean: 36.7 years) from a cohort of 1,202 male patients.

 Large-scale study of antibody titer decay following BNT162b2 mRNA vaccine or SARS-CoV-2 infection (https://www.medrxiv.org/content/10.1101/2021.08.19.21262111v1)
 A Israel et al, MEDRXIV, August 22, 2021

Six months after BNT162b2 vaccination 16.1% subjects had antibody levels below the seropositivity threshold of <50 AU/mL, while only 10.8% of convalescent patients were below <50 AU/mL threshold after 9 months from SARS-CoV-2 infection. This study demonstrates individuals who received the Pfizer-BioNTech mRNA vaccine have different kinetics of antibody levels compared to patients who had been infected with the SARS-CoV-2 virus, with higher initial levels but a much faster exponential decrease in the first group.

 Delta variant and mRNA Covid-19 vaccines effectiveness: higher odds of vaccine infection breakthroughs (https://www.medrxiv.org/content/10.1101/2021.08.14.21262020v1)
 I Kislaya et al, MEDRXIV August 22, 2021

We found significantly higher odds of vaccine infection breakthrough in Delta cases when compared to Alpha cases, suggesting lower effectiveness of the mRNA vaccines in preventing infection with the Delta variant. Additionally, the vaccine breakthrough cases are estimated to be of higher mean Ct values, suggesting higher infectiousness with the Delta variant infection.

Effectiveness of BNT162b2 and mRNA-1273 covid-19 vaccines against symptomatic SARS-CoV-2 infection and severe covid-19 outcomes in Ontario, Canada: test negative design study.
 (https://pubmed.ncbi.nlm.nih.gov/34417165)

Chung Hannah et al. BMJ (Clinical research ed.) 2021 8 n1943

324 033 community dwelling people aged =16 years who had symptoms of covid-19 and were tested for SARS-CoV-2. Two doses of mRNA covid-19 vaccines were observed to be highly effective against symptomatic infection and severe outcomes. Vaccine effectiveness of one dose was observed to be lower, particularly for older adults shortly after the first dose.

 Nanopore Metagenomic Sequencing for Detection and Characterization of SARS-CoV-2 in Clinical Samples (https://www.medrxiv.org/content/10.1101/2021.08.13.21261922v1)
 NPG Gauthier et al, MEDRXIV, August 23, 2021

Metagenomic Next-Generation Sequencing approaches provide the opportunity to examine the entire genomic material of a sample; allowing for detection of emerging and clinically relevant pathogens that may be missed in targeted assays. Here we present a pilot study on the performance of Sequence-Independent Single Primer Amplification (SISPA) to amplify RNA randomly for the detection of SARS-CoV-2. We designed a classifier that corrects for barcode crosstalk between specimens. Our assay yielded 100% specificity and 95.2% sensitivity for specimens with a RT-qPCR cycle threshold value less than 30.

 Association of COVID-19 vaccines ChAdOx1 and BNT162b2 with major venous, arterial, and thrombocytopenic events: whole population cohort study in 46 million adults in England (https://www.medrxiv.org/content/10.1101/2021.08.18.21262222v1)
 W Whiteley et al, MEDRXIV, August 23, 2021

This study aimed to quantify associations of vaccination with ChAdOx1-S and BNT162b2 with major arterial, venous and thrombocytopenic events. Design: Cohort study based on linked electronic health records among adults registered with an NHS general practice in England. Increases in ICVT and thrombocytopenia after ChAdOx1-S vaccination in adults aged <70 years are small compared with its effect in reducing COVID-19 morbidity and mortality, although more precise estimates for adults <40 years are needed. For people aged =70 years, rates of arterial or venous thrombotic, events were generally lower after either vaccine.

- Model-based assessment of SARS-CoV-2 Delta variant transmission dynamics within partially vaccinated K-12 school populations (https://www.medrxiv.org/content/10.1101/2021.08.20.21262389v1)
 JR Head et al, MEDRXIV, August 23, 2021
- Superspreaders drive the largest outbreaks of hospital onset COVID-19 infections (https://elifesciences.org/articles/67308)
 Illingworth JR, et al. eLife, Aug 24, 2021.

To build their algorithm, Illingworth, Hamilton et al. collected SARS-CoV-2 genetic data from patients and staff in a hospital, and combined it with information about how SARS-CoV-2 spreads and how these people moved in the hospital. The algorithm showed that, for the most part, patients were infected by other patients (20 out of 22 cases), while staff were infected equally by patients and staff. By further probing these data, Illingworth, Hamilton et al. revealed that 80% of hospital-acquired infections were caused by a group of just 21% of individuals in the study, identifying a ?superspreader? pattern.

 Emergence and expansion of SARS-CoV-2 B.1.526 after identification in New York. (https://pubmed.ncbi.nlm.nih.gov/34428777)
 Annavajhala Medini K et al. Nature 2021 8 We report the emergence of variant lineage B.1.526 that contains E484K and its alarming rise to dominance in New York City in early 2021. This variant is partially or completely resistant to two therapeutic monoclonal antibodies in clinical use and less susceptible to neutralization by convalescent plasma or vaccinee sera, posing a modest antigenic challenge. The B.1.526 lineage has now been reported from all 50 states in the United States and numerous other countries.

• Clinical and virological features of SARS-CoV-2 variants of concern: a retrospective cohort study comparing B.1.1.7 (Alpha), B.1.315 (Beta), and B.1.617.2 (Delta).

(https://pubmed.ncbi.nlm.nih.gov/34423834)

Ong Sean Wei Xiang et al. Clinical infectious diseases : an official publication of the Infectious Diseases Society of America 2021 8

In this retrospective study, we compared outcomes of patients infected with B.1.1.7, B.1.351, and B.1.617.2 with those with wild-type strains from early 2020.... After adjusting for age and sex, B.1.617.2 was associated with higher odds of oxygen requirement, ICU admission, or death (adjusted odds ratio (aOR) 4.90, [95% CI 1.43-30.78]). 157 of these patients were admitted to our center. After adjusting for age, sex, comorbidities, and vaccination, aOR for pneumonia with B.1.617.2 was 1.88 [95% CI 0.95-3.76]) compared with wild-type. These differences were not seen with B.1.1.7 and B.1.351.

 Safety of the BNT162b2 mRNA Covid-19 Vaccine in a Nationwide Setting. (https://pubmed.ncbi.nlm.nih.gov/34432976)
 Barda Noam et al. The New England journal of medicine 2021 8

In this study in a nationwide mass vaccination setting in Israel, the BNT162b2 vaccine was not associated with an elevated risk of most of the adverse events examined. The vaccine was associated with an excess risk of myocarditis (1 to 5 events per 100,000 persons). The risk of this potentially serious adverse event and of many other serious adverse events was substantially increased after SARS-CoV-2 infection.

 Viral dynamics of SARS-CoV-2 variants in vaccinated and unvaccinated individuals (https://www.medrxiv.org/content/10.1101/2021.02.16.21251535v3)
 SM Kissler et al, MEDRXIV, AUgust 25, 2021

We measured the duration of viral proliferation and clearance and the peak viral concentration separately for individuals infected with alpha, delta, and non-variants of interest/variants of concern (non-VOI/VOC), and for vaccinated and unvaccinated individuals. We found that Alpha, delta, and non-VOI/VOC infections feature similar viral trajectories. Acute infections in vaccinated and unvaccinated people feature similar proliferation and peak Ct, but vaccinated individuals cleared the infection more quickly.

 Predominance of antibody-resistant SARS-CoV-2 variants in vaccine breakthrough cases from the San Francisco Bay Area, California (https://www.medrxiv.org/content/10.1101/2021.08.19.21262139v1) Fully vaccinated were more likely than unvaccinated persons to be infected by variants carrying mutations associated with decreased antibody neutralization (L452R, L452Q, E484K, and/or F490S) (78% versus 48%, p = 1.96e-08), but not by those associated with increased infectivity (L452R and/or N501Y) (85% versus 77%, p = 0.092). Differences in viral loads were non-significant between unvaccinated and fully vaccinated persons overall (p = 0.99) and according to lineage (p = 0.09 - 0.78).

Non-Genomics Precision Health Studies

- A third COVID-19 vaccine shot markedly boosts neutralizing antibody potency and breadth (https://www.medrxiv.org/content/10.1101/2021.08.11.21261670v1)
 S Iketani et al, MEDRXIV, August 18, 2021
- Post-vaccination COVID-19: A case-control study and genomic analysis of 119 breakthrough infections in partially vaccinated individuals. (https://pubmed.ncbi.nlm.nih.gov/34410361)
 Baltas Ioannis et al. Clinical infectious diseases: an official publication of the Infectious Diseases Society of America 2021 8

We matched 119 cases of post-vaccination SARS-CoV-2 infection with BNT162b2 mRNA, or ChAdOx1 nCOV-19, to 476 unvaccinated patients with COVID-19 (Sept 2020-March 2021), according to age and sex. Differences in 60-day all-cause mortality, hospital admission, and hospital length of stay were evaluated. Phylogenetic, single nucleotide polymorphism (SNP) and minority variant allele (MVA) full genome sequencing analysis was performed.

 The Rapid Assessment of Aggregated Wastewater Samples for Genomic Surveillance of SARS-CoV-2 on a City-Wide Scale (https://www.medrxiv.org/content/10.1101/2021.08.17.21262170v1)
 EC Rouchka et al, MEDRXIV, August 20, 2021

We present the results of a collaborative effort between public health and metropolitan wastewater management authorities and the University of Louisville to monitor the SARS-CoV-2 pandemic through the monitoring of aggregate wastewater samples over a period of 28 weeks. Our data indicates that wastewater monitoring of water quality treatment centers and smaller neighborhood-scale catchment areas is a viable means by which the prevalence and genetic variation of SARS-CoV-2 within a metropolitan community of approximately one million individuals may be monitored.

- Diminishing immune responses against variants of concern in dialysis patients four months after SARS-CoV-2 mRNA vaccination (https://www.medrxiv.org/content/10.1101/2021.08.16.21262115v1)
 A Dulovic et al, MEDRXIV, August 20, 2021
- X-linked recessive TLR7 deficiency in ~1% of men under 60 years old with life-threatening COVID-19. (https://pubmed.ncbi.nlm.nih.gov/34413140)

Autosomal inborn errors of type I IFN immunity and autoantibodies against these cytokines underlie at least 10% of critical COVID-19 pneumonia cases. We report very rare, biochemically deleterious X-linked TLR7 variants in 16 unrelated male individuals aged 7 to 71 years (mean: 36.7 years) from a cohort of 1,202 male patients.

 Large-scale study of antibody titer decay following BNT162b2 mRNA vaccine or SARS-CoV-2 infection (https://www.medrxiv.org/content/10.1101/2021.08.19.21262111v1)
 A Israel et al, MEDRXIV, August 22, 2021

Six months after BNT162b2 vaccination 16.1% subjects had antibody levels below the seropositivity threshold of <50 AU/mL, while only 10.8% of convalescent patients were below <50 AU/mL threshold after 9 months from SARS-CoV-2 infection. This study demonstrates individuals who received the Pfizer-BioNTech mRNA vaccine have different kinetics of antibody levels compared to patients who had been infected with the SARS-CoV-2 virus, with higher initial levels but a much faster exponential decrease in the first group.

 Delta variant and mRNA Covid-19 vaccines effectiveness: higher odds of vaccine infection breakthroughs (https://www.medrxiv.org/content/10.1101/2021.08.14.21262020v1)
 I Kislaya et al, MEDRXIV August 22, 2021

We found significantly higher odds of vaccine infection breakthrough in Delta cases when compared to Alpha cases, suggesting lower effectiveness of the mRNA vaccines in preventing infection with the Delta variant. Additionally, the vaccine breakthrough cases are estimated to be of higher mean Ct values, suggesting higher infectiousness with the Delta variant infection.

Effectiveness of BNT162b2 and mRNA-1273 covid-19 vaccines against symptomatic SARS-CoV-2 infection and severe covid-19 outcomes in Ontario, Canada: test negative design study.
 (https://pubmed.ncbi.nlm.nih.gov/34417165)

Chung Hannah et al. BMJ (Clinical research ed.) 2021 8 n1943

324 033 community dwelling people aged =16 years who had symptoms of covid-19 and were tested for SARS-CoV-2. Two doses of mRNA covid-19 vaccines were observed to be highly effective against symptomatic infection and severe outcomes. Vaccine effectiveness of one dose was observed to be lower, particularly for older adults shortly after the first dose.

 Nanopore Metagenomic Sequencing for Detection and Characterization of SARS-CoV-2 in Clinical Samples (https://www.medrxiv.org/content/10.1101/2021.08.13.21261922v1)
 NPG Gauthier et al, MEDRXIV, August 23, 2021

Metagenomic Next-Generation Sequencing approaches provide the opportunity to examine the entire genomic material of a sample; allowing for detection of emerging and clinically relevant pathogens that may be missed in targeted assays. Here we present a pilot study on the performance of Sequence-Independent Single Primer Amplification (SISPA) to amplify RNA randomly for the detection of SARS-

CoV-2. We designed a classifier that corrects for barcode crosstalk between specimens. Our assay yielded 100% specificity and 95.2% sensitivity for specimens with a RT-qPCR cycle threshold value less than 30.

 Association of COVID-19 vaccines ChAdOx1 and BNT162b2 with major venous, arterial, and thrombocytopenic events: whole population cohort study in 46 million adults in England (https://www.medrxiv.org/content/10.1101/2021.08.18.21262222v1)
 W Whiteley et al, MEDRXIV, August 23, 2021

This study aimed to quantify associations of vaccination with ChAdOx1-S and BNT162b2 with major arterial, venous and thrombocytopenic events. Design: Cohort study based on linked electronic health records among adults registered with an NHS general practice in England. Increases in ICVT and thrombocytopenia after ChAdOx1-S vaccination in adults aged <70 years are small compared with its effect in reducing COVID-19 morbidity and mortality, although more precise estimates for adults <40 years are needed. For people aged =70 years, rates of arterial or venous thrombotic, events were generally lower after either vaccine.

- Model-based assessment of SARS-CoV-2 Delta variant transmission dynamics within partially vaccinated K-12 school populations (https://www.medrxiv.org/content/10.1101/2021.08.20.21262389v1)
 JR Head et al, MEDRXIV, August 23, 2021
- Superspreaders drive the largest outbreaks of hospital onset COVID-19 infections (https://elifesciences.org/articles/67308)
 Illingworth JR, et al. eLife, Aug 24, 2021.

To build their algorithm, Illingworth, Hamilton et al. collected SARS-CoV-2 genetic data from patients and staff in a hospital, and combined it with information about how SARS-CoV-2 spreads and how these people moved in the hospital. The algorithm showed that, for the most part, patients were infected by other patients (20 out of 22 cases), while staff were infected equally by patients and staff. By further probing these data, Illingworth, Hamilton et al. revealed that 80% of hospital-acquired infections were caused by a group of just 21% of individuals in the study, identifying a ?superspreader? pattern.

 Emergence and expansion of SARS-CoV-2 B.1.526 after identification in New York. (https://pubmed.ncbi.nlm.nih.gov/34428777)
 Annavajhala Medini K et al. Nature 2021 8

We report the emergence of variant lineage B.1.526 that contains E484K and its alarming rise to dominance in New York City in early 2021. This variant is partially or completely resistant to two therapeutic monoclonal antibodies in clinical use and less susceptible to neutralization by convalescent plasma or vaccinee sera, posing a modest antigenic challenge. The B.1.526 lineage has now been reported from all 50 states in the United States and numerous other countries.

 Clinical and virological features of SARS-CoV-2 variants of concern: a retrospective cohort study comparing B.1.1.7 (Alpha), B.1.315 (Beta), and B.1.617.2 (Delta). (https://pubmed.ncbi.nlm.nih.gov/34423834)

Ong Sean Wei Xiang et al. Clinical infectious diseases : an official publication of the Infectious Diseases Society of America 2021 8

In this retrospective study, we compared outcomes of patients infected with B.1.1.7, B.1.351, and B.1.617.2 with those with wild-type strains from early 2020.... After adjusting for age and sex, B.1.617.2 was associated with higher odds of oxygen requirement, ICU admission, or death (adjusted odds ratio (aOR) 4.90, [95% CI 1.43-30.78]). 157 of these patients were admitted to our center. After adjusting for age, sex, comorbidities, and vaccination, aOR for pneumonia with B.1.617.2 was 1.88 [95% CI 0.95-3.76]) compared with wild-type. These differences were not seen with B.1.1.7 and B.1.351.

 Safety of the BNT162b2 mRNA Covid-19 Vaccine in a Nationwide Setting. (https://pubmed.ncbi.nlm.nih.gov/34432976)
 Barda Noam et al. The New England journal of medicine 2021 8

In this study in a nationwide mass vaccination setting in Israel, the BNT162b2 vaccine was not associated with an elevated risk of most of the adverse events examined. The vaccine was associated with an excess risk of myocarditis (1 to 5 events per 100,000 persons). The risk of this potentially serious adverse event and of many other serious adverse events was substantially increased after SARS-CoV-2 infection.

 Viral dynamics of SARS-CoV-2 variants in vaccinated and unvaccinated individuals (https://www.medrxiv.org/content/10.1101/2021.02.16.21251535v3)
 SM Kissler et al, MEDRXIV, AUgust 25, 2021

We measured the duration of viral proliferation and clearance and the peak viral concentration separately for individuals infected with alpha, delta, and non-variants of interest/variants of concern (non-VOI/VOC), and for vaccinated and unvaccinated individuals. We found that Alpha, delta, and non-VOI/VOC infections feature similar viral trajectories. Acute infections in vaccinated and unvaccinated people feature similar proliferation and peak Ct, but vaccinated individuals cleared the infection more quickly.

 Predominance of antibody-resistant SARS-CoV-2 variants in vaccine breakthrough cases from the San Francisco Bay Area, California (https://www.medrxiv.org/content/10.1101/2021.08.19.21262139v1)
 V Servellita et al MEDRXIV, August 25, 2021

Fully vaccinated were more likely than unvaccinated persons to be infected by variants carrying mutations associated with decreased antibody neutralization (L452R, L452Q, E484K, and/or F490S) (78% versus 48%, p = 1.96e-08), but not by those associated with increased infectivity (L452R and/or N501Y) (85% versus 77%, p = 0.092). Differences in viral loads were non-significant between unvaccinated and fully vaccinated persons overall (p = 0.99) and according to lineage (p = 0.09-0.78).

News, Reviews and Commentaries

•	A third COVID-19 vaccine shot markedly boosts neutralizing antibody potency and breadth
	(https://www.medrxiv.org/content/10.1101/2021.08.11.21261670v1)
	S Iketani et al, MEDRXIV, August 18, 2021

 Post-vaccination COVID-19: A case-control study and genomic analysis of 119 breakthrough infections in partially vaccinated individuals. (https://pubmed.ncbi.nlm.nih.gov/34410361)
 Baltas Ioannis et al. Clinical infectious diseases: an official publication of the Infectious Diseases Society of America 2021 8

We matched 119 cases of post-vaccination SARS-CoV-2 infection with BNT162b2 mRNA, or ChAdOx1 nCOV-19, to 476 unvaccinated patients with COVID-19 (Sept 2020-March 2021), according to age and sex. Differences in 60-day all-cause mortality, hospital admission, and hospital length of stay were evaluated. Phylogenetic, single nucleotide polymorphism (SNP) and minority variant allele (MVA) full genome sequencing analysis was performed.

 The Rapid Assessment of Aggregated Wastewater Samples for Genomic Surveillance of SARS-CoV-2 on a City-Wide Scale (https://www.medrxiv.org/content/10.1101/2021.08.17.21262170v1)
 EC Rouchka et al, MEDRXIV, August 20, 2021

We present the results of a collaborative effort between public health and metropolitan wastewater management authorities and the University of Louisville to monitor the SARS-CoV-2 pandemic through the monitoring of aggregate wastewater samples over a period of 28 weeks. Our data indicates that wastewater monitoring of water quality treatment centers and smaller neighborhood-scale catchment areas is a viable means by which the prevalence and genetic variation of SARS-CoV-2 within a metropolitan community of approximately one million individuals may be monitored.

- Diminishing immune responses against variants of concern in dialysis patients four months after SARS-CoV-2 mRNA vaccination (https://www.medrxiv.org/content/10.1101/2021.08.16.21262115v1)
 A Dulovic et al, MEDRXIV, August 20, 2021
- X-linked recessive TLR7 deficiency in ~1% of men under 60 years old with life-threatening COVID-19.
 (https://pubmed.ncbi.nlm.nih.gov/34413140)

Asano Takaki et al. Science immunology 2021 8 (62)

Autosomal inborn errors of type I IFN immunity and autoantibodies against these cytokines underlie at least 10% of critical COVID-19 pneumonia cases. We report very rare, biochemically deleterious X-linked TLR7 variants in 16 unrelated male individuals aged 7 to 71 years (mean: 36.7 years) from a cohort of 1,202 male patients.

 Large-scale study of antibody titer decay following BNT162b2 mRNA vaccine or SARS-CoV-2 infection (https://www.medrxiv.org/content/10.1101/2021.08.19.21262111v1)
 A Israel et al, MEDRXIV, August 22, 2021

Six months after BNT162b2 vaccination 16.1% subjects had antibody levels below the seropositivity threshold of <50 AU/mL, while only 10.8% of convalescent patients were below <50 AU/mL threshold after 9 months from SARS-CoV-2 infection. This study demonstrates individuals who received the Pfizer-BioNTech mRNA vaccine have different kinetics of antibody levels compared to patients who had been infected with the SARS-CoV-2 virus, with higher initial levels but a much faster exponential decrease in the first group.

 Delta variant and mRNA Covid-19 vaccines effectiveness: higher odds of vaccine infection breakthroughs (https://www.medrxiv.org/content/10.1101/2021.08.14.21262020v1)
 I Kislaya et al, MEDRXIV August 22, 2021

We found significantly higher odds of vaccine infection breakthrough in Delta cases when compared to Alpha cases, suggesting lower effectiveness of the mRNA vaccines in preventing infection with the Delta variant. Additionally, the vaccine breakthrough cases are estimated to be of higher mean Ct values, suggesting higher infectiousness with the Delta variant infection.

Effectiveness of BNT162b2 and mRNA-1273 covid-19 vaccines against symptomatic SARS-CoV-2 infection and severe covid-19 outcomes in Ontario, Canada: test negative design study.
 (https://pubmed.ncbi.nlm.nih.gov/34417165)
 Chung Hannah et al. BMJ (Clinical research ed.) 2021 8 n1943

324 033 community dwelling people aged =16 years who had symptoms of covid-19 and were tested for SARS-CoV-2. Two doses of mRNA covid-19 vaccines were observed to be highly effective against symptomatic infection and severe outcomes. Vaccine effectiveness of one dose was observed to be lower, particularly for older adults shortly after the first dose.

 Nanopore Metagenomic Sequencing for Detection and Characterization of SARS-CoV-2 in Clinical Samples (https://www.medrxiv.org/content/10.1101/2021.08.13.21261922v1)
 NPG Gauthier et al, MEDRXIV, August 23, 2021

Metagenomic Next-Generation Sequencing approaches provide the opportunity to examine the entire genomic material of a sample; allowing for detection of emerging and clinically relevant pathogens that may be missed in targeted assays. Here we present a pilot study on the performance of Sequence-Independent Single Primer Amplification (SISPA) to amplify RNA randomly for the detection of SARS-CoV-2. We designed a classifier that corrects for barcode crosstalk between specimens. Our assay yielded 100% specificity and 95.2% sensitivity for specimens with a RT-qPCR cycle threshold value less than 30.

 Association of COVID-19 vaccines ChAdOx1 and BNT162b2 with major venous, arterial, and thrombocytopenic events: whole population cohort study in 46 million adults in England (https://www.medrxiv.org/content/10.1101/2021.08.18.21262222v1) W Whiteley et al, MEDRXIV, August 23, 2021

This study aimed to quantify associations of vaccination with ChAdOx1-S and BNT162b2 with major arterial, venous and thrombocytopenic events. Design: Cohort study based on linked electronic health records among adults registered with an NHS general practice in England. Increases in ICVT and thrombocytopenia after ChAdOx1-S vaccination in adults aged <70 years are small compared with its effect in reducing COVID-19 morbidity and mortality, although more precise estimates for adults <40 years are needed. For people aged =70 years, rates of arterial or venous thrombotic, events were generally lower after either vaccine.

- Model-based assessment of SARS-CoV-2 Delta variant transmission dynamics within partially vaccinated K-12 school populations (https://www.medrxiv.org/content/10.1101/2021.08.20.21262389v1)
 JR Head et al, MEDRXIV, August 23, 2021
- Superspreaders drive the largest outbreaks of hospital onset COVID-19 infections (https://elifesciences.org/articles/67308)
 Illingworth JR, et al. eLife, Aug 24, 2021.

To build their algorithm, Illingworth, Hamilton et al. collected SARS-CoV-2 genetic data from patients and staff in a hospital, and combined it with information about how SARS-CoV-2 spreads and how these people moved in the hospital. The algorithm showed that, for the most part, patients were infected by other patients (20 out of 22 cases), while staff were infected equally by patients and staff. By further probing these data, Illingworth, Hamilton et al. revealed that 80% of hospital-acquired infections were caused by a group of just 21% of individuals in the study, identifying a ?superspreader? pattern.

 Emergence and expansion of SARS-CoV-2 B.1.526 after identification in New York. (https://pubmed.ncbi.nlm.nih.gov/34428777)
 Annavajhala Medini K et al. Nature 2021 8

We report the emergence of variant lineage B.1.526 that contains E484K and its alarming rise to dominance in New York City in early 2021. This variant is partially or completely resistant to two therapeutic monoclonal antibodies in clinical use and less susceptible to neutralization by convalescent plasma or vaccinee sera, posing a modest antigenic challenge. The B.1.526 lineage has now been reported from all 50 states in the United States and numerous other countries.

 Clinical and virological features of SARS-CoV-2 variants of concern: a retrospective cohort study comparing B.1.1.7 (Alpha), B.1.315 (Beta), and B.1.617.2 (Delta).

(https://pubmed.ncbi.nlm.nih.gov/34423834)

Ong Sean Wei Xiang et al. Clinical infectious diseases : an official publication of the Infectious Diseases Society of America 2021 8

In this retrospective study, we compared outcomes of patients infected with B.1.1.7, B.1.351, and B.1.617.2 with those with wild-type strains from early 2020.... After adjusting for age and sex, B.1.617.2 was associated with higher odds of oxygen requirement, ICU admission, or death (adjusted odds ratio (aOR) 4.90, [95% CI 1.43-30.78]). 157 of these patients were admitted to our center. After adjusting for age, sex, comorbidities, and vaccination, aOR for pneumonia with B.1.617.2 was 1.88 [95% CI 0.95-3.76]) compared with wild-type. These differences were not seen with B.1.1.7 and B.1.351.

 Safety of the BNT162b2 mRNA Covid-19 Vaccine in a Nationwide Setting. (https://pubmed.ncbi.nlm.nih.gov/34432976)
 Barda Noam et al. The New England journal of medicine 2021 8

In this study in a nationwide mass vaccination setting in Israel, the BNT162b2 vaccine was not associated with an elevated risk of most of the adverse events examined. The vaccine was associated with an excess risk of myocarditis (1 to 5 events per 100,000 persons). The risk of this potentially serious adverse event and of many other serious adverse events was substantially increased after SARS-CoV-2 infection.

 Viral dynamics of SARS-CoV-2 variants in vaccinated and unvaccinated individuals (https://www.medrxiv.org/content/10.1101/2021.02.16.21251535v3)
 SM Kissler et al, MEDRXIV, AUgust 25, 2021

We measured the duration of viral proliferation and clearance and the peak viral concentration separately for individuals infected with alpha, delta, and non-variants of interest/variants of concern (non-VOI/VOC), and for vaccinated and unvaccinated individuals. We found that Alpha, delta, and non-VOI/VOC infections feature similar viral trajectories. Acute infections in vaccinated and unvaccinated people feature similar proliferation and peak Ct, but vaccinated individuals cleared the infection more quickly.

 Predominance of antibody-resistant SARS-CoV-2 variants in vaccine breakthrough cases from the San Francisco Bay Area, California (https://www.medrxiv.org/content/10.1101/2021.08.19.21262139v1)
 V Servellita et al MEDRXIV, August 25, 2021

Fully vaccinated were more likely than unvaccinated persons to be infected by variants carrying mutations associated with decreased antibody neutralization (L452R, L452Q, E484K, and/or F490S) (78% versus 48%, p = 1.96e-08), but not by those associated with increased infectivity (L452R and/or N501Y) (85% versus 77%, p = 0.092). Differences in viral loads were non-significant between unvaccinated and fully vaccinated persons overall (p = 0.99) and according to lineage (p = 0.09 - 0.78).

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: Sep 03, 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)