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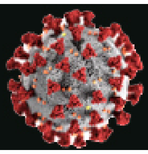

COVID-19 Weekly Update

Up to Date Genomics and Precision Health Information on COVID-19

Publication Date: Oct 28, 2021

Pathogen and Human Genomics Studies

Adverse Effects after BNT162b2 Vaccine and SARS-CoV-2 Infection, According to Age and Sex
(https://www.nejm.org/doi/full/10.1056/NEJMc2115045)
N Dagan et al, NEJM, October 27, 2021>

> The risk of myocarditis, which is considered to be the most potentially serious vaccine-associated adverse event, was increased after both vaccination and SARS-CoV-2 infection. After vaccination, the risk was increased mostly among young male adolescents and adults (16 to 39 years of age), with 8.62 excess events per 100,000 persons (95% confidence interval [CI], 2.82 to 14.35). After infection, the risk was increased in both age categories (<40 and =40 years) and in both male and female adolescents and adults, with 11.54 excess events per 100,000 persons (95% CI, 2.48 to 22.55) in young male adolescents and adults.

Rare Skin Reactions after mRNA Vaccination, Similar to Jones–Mote Basophil Responses
(https://www.nejm.org/doi/full/10.1056/NEJMc2111452)
P Askenase et al, NEJM, October 28, 2021>

> In a small group of recipients of messenger RNA (mRNA) vaccines against coronavirus disease 2019 (Covid-19), the occurrence of erythematous and indurated skin reactions has been reported at an average of 8 days after the first or second injection.

Waning Immunity after the BNT162b2 Vaccine in Israel
(https://www.nejm.org/doi/full/10.1056/NEJMoa2114228)
Y Goldberg et al, NEJM, October 27, 2021>

> Among persons 60 years of age or older, the rate of infection in the July 11–31 period was higher among persons who became fully vaccinated in January 2021 (when they were first eligible) than among those fully vaccinated 2 months later, in March (rate ratio, 1.6; 95% confidence interval [CI], 1.3 to 2.0). Among persons 40 to 59 years of age, the rate ratio for infection among those fully vaccinated in February (when they were first eligible), as compared with 2 months later, in April, was 1.7 (95% CI, 1.4 to 2.1). Among persons 16 to 39 years of age, the rate ratio for infection among those fully vaccinated in March (when they were first eligible), as compared with 2 months later, in May, was 1.6 (95% CI, 1.3 to 2.0).

Functional antibody and T cell immunity following SARS-CoV-2 infection, including by variants of concern, in patients with cancer: the CAPTURE study (https://www.nature.com/articles/s43018-021-00275-9)
A Fendler et al, Nature Medicine, October 27, 2021>

Of 357 patients with cancer, 118 were SARS-CoV-2 positive, 94 were symptomatic and 2 died of COVID-19. In this cohort, 83% patients had S1-reactive antibodies and 82% had neutralizing antibodies against wild type SARS-CoV-2, whereas neutralizing antibody titers against the Alpha, Beta and Delta variants were substantially reduced. S1-reactive antibody levels decreased in 13% of patients, whereas neutralizing antibody titers remained stable for up to 329?days.

Effectiveness of Covid-19 Vaccines in the United States Over 9 Months: Surveillance Data from the State of North Carolina (https://www.medrxiv.org/content/10.1101/2021.10.25.21265304v1)
D Lin et al, MEDRXIV, October 26, 2021>

The two mRNA vaccines are remarkably effective and durable in reducing the risks of hospitalization and death. The Janssen vaccine also offers a high level of protection against hospitalization and death. The Moderna vaccine is significantly more durable than the Pfizer vaccine in reducing the risk of Covid19. Waning vaccine effectiveness is caused primarily by declining immunity rather than emergence of new variants.

Neurological complications after first dose of COVID-19 vaccines and SARS-CoV-2 infection (https://www.nature.com/articles/s41591-021-01556-7)
M Patone et al, Nature Medicine, October 25, 2021 >

We undertook a self-controlled case series study to investigate hospital admissions from neurological complications in the 28?days after a first dose of ChAdOx1nCoV-19 (n?=?20,417,752) or BNT162b2 (n?=?12,134,782), and after a SARS-CoV-2-positive test (n?=?2,005,280). There was an increased risk of Guillain–Barré syndrome (incidence rate ratio (IRR), 2.90; 95% confidence interval (CI): 2.15–3.92 at 15–21?days after vaccination) and Bell's palsy (IRR, 1.29; 95% CI: 1.08–1.56 at 15–21?days) with ChAdOx1nCoV-19. There was an increased risk of hemorrhagic stroke (IRR, 1.38; 95% CI: 1.12–1.71 at 15–21?days) with BNT162b2. An independent Scottish cohort provided further support for the association between ChAdOx1nCoV and Guillain–Barré syndrome (IRR, 2.32; 95% CI: 1.08–5.02 at 1–28?days).

Genomic epidemiology and the role of international and regional travel in the SARS-CoV-2 epidemic in Zimbabwe: a retrospective study of routinely collected surveillance data (https://www.thelancet.com/journals/langlo/article/PIIS2214-109X(21)00434-4/fulltext)
T Mashe et al, Lancet Global Health, October 2021 >

Advances in SARS-CoV-2 sequencing have enabled identification of new variants, tracking of its evolution, and monitoring of its spread. We aimed to use whole genome sequencing to describe the molecular epidemiology of the SARS-CoV-2 outbreak and to inform the implementation of effective public health interventions for control in Zimbabwe. We found that initial public health interventions delayed onset of SARS-CoV-2 community transmission after the introduction of the virus from international and regional migration in Zimbabwe. Global whole genome sequence data are essential to reveal major routes of spread and guide intervention strategies.

Immunogenicity and efficacy of heterologous ChadOx1/BNT162b2 vaccination (https://www.nature.com/articles/s41586-021-04120-y)
B Pozzetto et al, Nature, October 21, 2021>

We conducted a longitudinal survey of the anti-spike immunity conferred by each vaccine combination. Both combinations induced strong anti-spike antibody (Ab) responses but sera from heterologous vaccinated individuals displayed a stronger neutralizing activity, regardless of the SARS-CoV-2 variant. This enhanced neutralizing potential was correlated with increased frequencies of switched and activated memory B cells recognizing the SARS-CoV-2 Receptor Binding Domain (RBD). The ChAdOx1-S-nCoV-19 vaccine induced a weaker IgG response but a stronger T cell response than the BNT162b2 vaccine after the priming dose, which could explain the complementarity of both vaccines when used in combination. The heterologous vaccination regimen could therefore be particularly suitable for immune compromised individuals.

Non-Genomics Precision Health Studiess

It’s complicated: characterizing the time-varying relationship between cell phone mobility and COVID-19 spread in the US (https://www.nature.com/articles/s41746-021-00523-3#Fig1)

S Jewell et al, NPJ Digital Medicine, October 27, 2021

> We propose an interpretable statistical model to identify spatiotemporal variation in the association between mobility and infection rates. Using 1 year of US county-level data, we found that sharp drops in mobility often coincided with declining infection rates in the most populous counties in spring 2020. However, the association varied considerably in other locations and across time. Our findings are sensitive to model flexibility, as more restrictive models average over local effects and mask much of the spatiotemporal variation. We conclude that mobility does not appear to be a reliable leading indicator of infection rates, which may have important policy implications.

Cryptic transmission of SARS-CoV-2 and the first COVID-19 wav (https://www.nature.com/articles/s41586-021-04130-w)
JT Davis et al, Nature, October 25,2021

> We use a global metapopulation epidemic model to provide a mechanistic understanding of the early dispersal of infections, and the temporal windows of the introduction and onset of SARS-CoV-2 local transmission in Europe and the United States. We find that community transmission of SARS-CoV-2 was likely in several areas of Europe and the United States by January 2020, and estimate that by early March, only 1 to 3 in 100 SARS-CoV-2 infections were detected by surveillance systems. The modelling results highlight international travel as the key driver of the introduction of SARS-CoV-2 with possible introductions and transmission events as early as December 2019–January 2020.

Who has long-COVID? A big data approach (https://www.medrxiv.org/content/10.1101/2021.10.18.21265168v1)
ER Plaff et al, MEDRXIV, October 22, 2021

News, Reviews and Commentaries

Insights from Zimbabwe's SARS-CoV-2 genomic surveillance (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&link=1974)

T Dzinamarira, Lancet Global Health, October 2021

> The emergence of SARS-CoV-2 variants pose a serious threat to national vaccination programs due to potential shifts in herd immunity thresholds. Frequent travel from South Africa as a result of close economic ties between the two countries presents a great risk of importing variants. The usefulness of genomic surveillance studies like the one discussed here as a tool to prevent the emergence and spread of emerging variants would depend on the intensity with which the findings are incorporated into policies by national public health programs.

Will GWAS eventually allow the identification of genomic biomarkers for COVID-19 severity and mortality? (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&link=1972)
Colona Vito Luigi et al. The Journal of clinical investigation 2021 10

Genome-wide association studies (GWAS) involve testing genetic variants across the genomes of many individuals to identify genotype-phenotype associations. GWAS have enabled the identification of numerous genomic biomarkers in various complex human diseases including infectious ones. However, few of these studies are relevant for clinical practice or at the bedside.

A global effort to dissect the human genetic basis of resistance to SARS-CoV-2 infection. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&link=1970)
Andreakos Evangelos et al. Nature immunology 2021 10

Following the discovery that autosomal recessive deficiency in the DARC chemokine receptor confers resistance to Plasmodium vivax, autosomal recessive deficiencies of chemokine receptor 5 (CCR5) and the enzyme FUT2 were shown to underlie resistance to HIV-1 and noroviruses, respectively. Along the same lines, we propose a strategy for identifying, recruiting, and genetically analyzing individuals who are naturally resistant to SARS-CoV-2 infection.

Editorial: Global Initiatives Support the Use and Regulation of Digital Health Technology During the COVID-19 Pandemic. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&link=1969)
Parums Dinah V et al. Medical science monitor : international medical journal of experimental and clinical research 2021 10 e935123

In 2021, the WHO published a global strategy on digital health (eHealth) and mobile health (mHealth) for 2020 to 2025. The US Food and Drug Administration (FDA) Center for Devices and Radiological Health (CDRH) now evaluates software as a medical device (SaMD) and software that is in a medical device (SiMD) through the International Medical Device Regulators Forum (IMDRF). This Editorial aims to discuss how the COVID-19 pandemic has driven global initiatives to support the use and regulation of digital health technology and the requirements for digital health evidence frameworks and new approaches to regulatory approvals.

Application of machine learning in the prediction of COVID-19 daily new cases: A scoping review. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&link=1968)
Ghafouri-Fard Soudeh et al. Heliyon 2021 10 (10) e08143

We review studies which used these strategies to predict the number of new cases of COVID-19. Adaptive neuro-fuzzy inference system, long short-term memory, recurrent neural network and multilayer perceptron are among the mostly used strategies in this regard. We compared the performance of several machine learning methods in prediction of COVID-19 spread. Root means squared error (RMSE), mean absolute error (MAE), R2 coefficient of determination (R2), and mean absolute percentage error (MAPE) parameters were selected as performance measures for comparison of the accuracy of models. R2 values have ranged from 0.64 to 1 for artificial neural network (ANN) and Bidirectional long short-term memory (LSTM), respectively.

Artificial Intelligence for COVID-19: A Systematic Review. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&link=1966)
Wang Lian et al. Frontiers in medicine 2021 10 704256

We included 78 studies: 46 articles discussed AI-assisted diagnosis for COVID-19 with total accuracy of 70.00 to 99.92%, sensitivity of 73.00 to 100.00%, specificity of 25 to 100.00%, and area under the curve of 0.732 to 1.000. Fourteen articles evaluated prognosis based on clinical characteristics at hospital admission, such as clinical, laboratory and radiological characteristics, reaching accuracy of 74.4 to 95.20%, sensitivity of 72.8 to 98.00%, specificity of 55 to 96.87% and AUC of 0.66 to 0.997 in predicting critical COVID-19. Nine articles used AI models to predict the epidemic of the COVID-19, such as epidemic peak, infection rate, number of infected cases, transmission laws, and development trend.

Eight articles used AI to explore potential effective drugs, primarily through drug repurposing and drug development.

COVID vaccine makers brace for a variant worse than Delta- Companies are updating vaccines and testing them on people to prepare for whatever comes next in the pandemic. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&link=1964)
E Waltz, Nature, October 20, 2021

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- Search COVID-19 GPH database (/PHGKB/coVInfoStartPage.action)
- Visit CDC Office of Genomics and Precision Public Health website (http://www.cdc.gov/genomics/)

About Weekly Scan (/PHGKB/phgHome.action?action=about)

This weekly update contains the latest information and publications on the impact of genomics and precision health technologies on the investigation and control of COVID-19. Items are selected by staff from the CDC Office of Genomics and Precision Public Health daily from the COVID-19 GPH (/PHGKB/coVInfoStartPage.action).

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