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

Published on 12/10/2020

COVID-19 Genomics and Precision Public Health Weekly Update Content

Pathogen and Human Genomics Studies

- Variants in SARS-CoV-2 Associated with Mild or Severe (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=433)
  JD Voss et al, MEDRXIV, December 3, 2020

  In 155,958 SARS-CoV-2 genomes, we found that models that included viral genomic variants outperformed other models (AUC=0.91 as compared with 0.68 for age and gender alone; p<0.001). Among individual variants, we found 17 single nucleotide variants in SARS-CoV-2 have more than two-fold greater odds of being associated with higher severity and 67 variants associated with =0.5 times the odds of severity.

- Cold-chain transportation in the frozen food industry may have caused a recurrence of COVID-19 cases in destination: Successful isolation of SARS-CoV-2 virus from the imported frozen cod package surface. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=435)
  Liu Peipei et al. Biosafety and health 2020 Nov

  After two stevedores in Qingdao, China, developed COVID-19, packages of imported frozen cod in a shipment they had handled were found to be contaminated with closely related SARS-CoV-2 of apparent European origin. The authors postulate that transport at freezing temperatures maintained virus viability during transport.

- Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=436)
  DE Gordon et al, Science, December 4, 2020

  This study mapped the interactions between viral and human proteins for SARS-CoV-2, SARS-CoV-1, and MERS-CoV; analyzed the localization of viral proteins in human cells; and used genetic screening to identify host factors that enhance or inhibit viral infection. For a subset of interactions essential for the virus life cycle, the authors determined the cryo–electron microscopy structures and mined patient data to understand how targeting host factors may be relevant to clinical outcomes.

- A 6-mRNA host response whole-blood classifier trained using patients with non-COVID-19 viral infections accurately predicts severity of COVID-19 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=450)
  L Buturovic et al, MEDRXIV, December 8, 2020

  We developed a blood-based generalizable host-gene-expression-based classifier for the severity of viral infections and validated it in multiple viral infection settings including COVID-19. We selected 6 host mRNAs and trained a logistic regression classifier with a training AUROC of 0.90 for predicting 30-day mortality in viral illnesses. In validation cohorts the locked 6-mRNA classifier had an AUROC of 0.91.

Non-Genomics Precision Health Studies

- Variants in SARS-CoV-2 Associated with Mild or Severe (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=433)
  JD Voss et al, MEDRXIV, December 3, 2020

> In 155,958 SARS-CoV-2 genomes, we found that models that included viral genomic variants outperformed other models (AUC=0.91 as compared with 0.68 for age and gender alone; p<0.001). Among individual variants, we found 17 single nucleotide variants in SARS-CoV-2 have more than two-fold greater odds of being associated with higher severity and 67 variants associated with =0.5 times the odds of severity.

- Cold-chain transportation in the frozen food industry may have caused a recurrence of COVID-19 cases in destination: Successful isolation of SARS-CoV-2 virus from the imported frozen cod package surface. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=435)
  Liu Peipei et al. Biosafety and health 2020 Nov

  > After two stevedores in Qingdao, China, developed COVID-19, packages of imported frozen cod in a shipment they had handled were found to be contaminated with closely related SARS-CoV-2 of apparent European origin. The authors postulate that transport at freezing temperatures maintained virus viability during transport.

- Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=436)
  DE Gordon et al, Science, December 4, 2020

  > This study mapped the interactions between viral and human proteins for SARS-CoV-2, SARS-CoV-1, and MERS-CoV; analyzed the localization of viral proteins in human cells; and used genetic screening to identify host factors that enhance or inhibit viral infection. For a subset of interactions essential for the virus life cycle, the authors determined the cryo–electron microscopy structures and mined patient data to understand how targeting host factors may be relevant to clinical outcomes.

- A 6-mRNA host response whole-blood classifier trained using patients with non-COVID-19 viral infections accurately predicts severity of COVID-19 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=450)
  L Buturovic et al, MEDRXIV, December 8, 2020

  > We developed a blood-based generalizable host-gene-expression-based classifier for the severity of viral infections and validated it in multiple viral infection settings including COVID-19. We selected 6 host mRNAs and trained a logistic regression classifier with a training AUROC of 0.90 for predicting 30-day mortality in viral illnesses. In validation cohorts the locked 6-mRNA classifier had an AUROC of 0.91.

News, Reviews and Commentaries

- Variants in SARS-CoV-2 Associated with Mild or Severe (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=433)
  JD Voss et al, MEDRXIV, December 3, 2020

> In 155,958 SARS-CoV-2 genomes, we found that models that included viral genomic variants outperformed other models (AUC=0.91 as compared with 0.68 for age and gender alone; p<0.001). Among individual variants, we found 17 single nucleotide variants in SARS-CoV-2 have more than two-fold greater odds of being associated with higher severity and 67 variants associated with =0.5 times the odds of severity.

- Cold-chain transportation in the frozen food industry may have caused a recurrence of COVID-19 cases in destination: Successful isolation of SARS-CoV-2 virus from the imported frozen cod package surface. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=435)
  Liu Peipei et al. Biosafety and health 2020 Nov

  > After two stevedores in Qingdao, China, developed COVID-19, packages of imported frozen cod in a shipment they had handled were found to be contaminated with closely related SARS-CoV-2 of apparent European origin. The authors postulate that transport at freezing temperatures maintained virus viability during transport.

- Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=436)
  DE Gordon et al, Science, December 4, 2020

  > This study mapped the interactions between viral and human proteins for SARS-CoV-2, SARS-CoV-1, and MERS-CoV; analyzed the localization of viral proteins in human cells; and used genetic screening to identify host factors that enhance or inhibit viral infection. For a subset of interactions essential for the virus life cycle, the authors determined the cryo–electron microscopy structures and mined patient data to understand how targeting host factors may be relevant to clinical outcomes.

- A 6-mRNA host response whole-blood classifier trained using patients with non-COVID-19 viral infections accurately predicts severity of COVID-19 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=450)

L Buturovic et al, MEDRXIV, December 8, 2020

We developed a blood-based generalizable host-gene-expression-based classifier for the severity of viral infections and validated it in multiple viral infection settings including COVID-19. We selected 6 host mRNAs and trained a logistic regression classifier with a training AUROC of 0.90 for predicting 30-day mortality in viral illnesses. In validation cohorts the locked 6-mRNA classifier had an AUROC of 0.91.

Page last reviewed: Oct 1, 2020

Page last updated: Jan 18, 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)