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

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COVID-19 Genomics and Precision Public Health Weekly Update Content

Pathogen and Human Genomics Studies

- Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=406)
  Popa A, et al. Sci Transl Med, 2020 Nov 23;eabe2555.

  "Phylogenetic-epidemiological analysis enabled the reconstruction of superspreading events and charts a map of tourism-related viral spread originating from Austria in spring 2020.... Time-resolved virus sequencing unveiled viral mutation dynamics within individuals with COVID-19, and epidemiologically validated infector-infectee pairs enabled us to determine an average transmission bottleneck size of 103 SARS-CoV-2 particles. In conclusion, this study illustrates the power of combining epidemiological analysis with deep viral genome sequencing to unravel the spread of SARS-CoV-2, and to gain fundamental insights into mutational dynamics and transmission properties."
- Mining a GWAS of Severe Covid-19 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=409)
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  The COVID-19 genetic risk variant rs657152-A at the ABO locus is strongly associated with increased levels of the CD209 antigen. This dendritic cell-surface protein has been found to facilitate infection by SARS-CoV-2 and other viruses.
- Association of Toll-like receptor 7 variants with life-threatening COVID-19 disease in males (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=414)
  C Fallerini et al, MEDRXIV, November 27, 2020

  Recently, two families in which COVID-19 segregates like an X-linked recessive monogenic disorder have been reported leading to identification of variants in TLR7. We sought to determine whether the two families represent the tip of the iceberg of a subset of COVID-19 male patients. In 1178 SARS-CoV-2-infected subjects (<60y, 79 severe cases versus 77 control cases). Missense mutations in TLR7 disorder may contribute to disease susceptibility in up to 4% of severe COVID-19.
- Clonal hematopoiesis is associated with risk of severe Covid-19 (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=420)
  KL Bolton et al, MEDRXIV, NOvember 27, 2020

  Among 515 individuals with Covid-19 we found that CH was associated with severe Covid-19 outcomes (OR=1.9, 95%=1.2-2.9, p=0.01). We further explored the relationship between CH and risk of other infections in 14,211 solid tumor patients at MSK. CH was significantly associated with risk of Clostridium Difficile and Streptococcus/Enterococcus infections. These findings suggest a relationship between CH and risk of severe infections that warrants further investigation.
- Virus genomics as a clinical and epidemiological tool. (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=431)
  Petrone Mary et al. EBioMedicine 2020 Nov 103141

  A recent article presents an apt case study on the role of virus genomics in epidemiology and clinical practice. The D614G substitution is one example of how SARS-CoV-2 is evolving. Continuing to use whole genome sequencing as an epidemiological tool will facilitate the rapid detection and monitoring of new SARS-CoV-2 variants when they emerge.
- Computational Immune Proteomics Approach to Target COVID-19. (/PHGKB/phgHome.action?

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Tilocca Bruno et al. Journal of proteome research 2020 11 (11) 4233-4241

Non-Genomics Precision Health Studies

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News, Reviews and Commentaries

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