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COVID-19 Genomics and Precision Public Health Weekly Update Content

Pathogen and Human Genomics Studies

- The major genetic risk factor for severe COVID-19 is inherited from Neanderthals.
  Zeberg Hugo et al. Nature 2020 Sep

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- A Comparison of Five SARS-CoV-2 Molecular Assays With Clinical Correlations.
  Procop Gary W et al. American journal of clinical pathology 2020 Oct

  We compared five SARS-CoV-2 assays using nasopharyngeal and nasal swab specimens submitted in transport media; we enriched this cohort for positive specimens, since we were particularly interested in the sensitivity and false-negative rate. Performance of each test was compared with a composite standard. The sensitivities and false-negative rates of the 239 specimens that met inclusion criteria were, respectively, as follows: Centers for Disease Control and Prevention 2019 nCoV Real-Time RT-PCR Diagnostic Panel, 100% and 0%; TIB MOLBIOL/Roche z 480 Assay, 96.5% and 3.5%; Xpert Xpress SARS-CoV-2 (Cepheid), 97.6% and 2.4%; Simplexa COVID-19 Direct Kit (DiaSorin), 88.1% and 11.9%; and ID Now COVID-19 (Abbott), 83.3% and 16.7%.
- Analysis of Genomic Characteristics and Transmission Routes of Patients With Confirmed SARS-CoV-2 in Southern California During the Early Stage of the US COVID-19 Pandemic
  W Zang et al, JAMA Network Open, October 7, 2020

  This case series of 192 patients found that 82% of SARS-CoV-2 isolates from Los Angeles shared closest similarity to those originating in Europe vs those from Asia (15%). Using the variation signature of the viral genomes, 2 main clusters were identified, with the top variants sharing genomic features from European SARS-CoV-2 isolates, and several subclusters of SARS-CoV-2 outbreaks represented trackable community spread in Los Angeles.
- Comprehensive Genome Analysis of 6,000 USA SARS-CoV-2 Isolates Reveals Haplotype Signatures and Localized Transmission Patterns by State and by Country.
  Shen Lishuang et al. Frontiers in microbiology 2020 573430

  Genomic analysis of SARS-CoV-2 sequences is crucial in determining the effectiveness of prudent safer at home measures in the United States (US). By haplotype analysis of 6,356 US isolates, we identified a pattern of strongly localized outbreaks at the city-, state-, and country-levels, and temporal transmissions.

Non-Genomics Precision Health Studies

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News, Reviews and Commentaries

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