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COVID-19 Genomics and Precision Public Health Weekly Update Content

- Pathogen and Human Genomics Studies
- Non-Genomics Precision Health Studies
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Pathogen and Human Genomics Studies

• Impact of body composition on COVID-19 susceptibility and severity: a two-sample multivariable Mendelian randomization study

D Freuer et al, MEDRXIV, October 24,2020

Using Mendelian randomization, we investigated the causal impact of body composition on the susceptibility and severity of COVID-19. Genetically predicted BMI was strongly associated with both, susceptibility (OR=1.31 per 1 SD increase) and hospitalization (OR=1.62 per 1 SD increase) even after adjustment for genetically predicted visceral obesity traits. These associations were neither mediated substantially by T2D nor by CVD.

Z Daniloski et al, Cell, October 24, 2020

Identification of required host factors for SARS-CoV-2 infection in human cells

We performed a genome-scale CRISPR loss-of-function screen to identify host factors required for SARS-CoV-2

JA Plante et al, Nature, October 26, 2020

viral infection of human alveolar epithelial cells. Top-ranked genes cluster into distinct pathways, including the vacuolar ATPase proton pump, Retromer, and Commander complexes. Given the key role of the ACE2 receptor in the early stages of viral entry, we show that loss of RAB7A reduces viral entry by sequestering the ACE2 receptor inside cells. Spike mutation D614G alters SARS-CoV-2 fitness

not lungs, confirming clinical evidence that the D614G mutation enhances viral loads in the upper respiratory

tract of COVID-19 patients and may increases transmission.

 A large national outbreak of COVID-19 linked to air travel, Ireland, summer 2020. Murphy Nicola et al. Euro surveillance: bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin 2020 10 (42)

An outbreak of 59 cases of coronavirus disease (COVID-19) originated with 13 cases linked by a 7 h,

Hamsters infected with the G614 variant produced higher infectious titers in the nasal washes and trachea, but

17% occupancy flight into Ireland, summer 2020. The flight-associated attack rate was 9.8?17.8%. Spread to 46 non-flight cases occurred country-wide. Asymptomatic/pre-symptomatic transmission in-flight from a point source is implicated by 99% homology across the virus genome in five cases travelling from three different continents. Restriction of movement on arrival and robust contact tracing can limit propagation post-flight.

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