

Obese people found to be at increased risk of COVID-19

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A new study led by researchers at Queen Mary University of London uses a novel approach to investigate the effects of cardiovascular risk factors on the risk of COVID-19 infection.



Several <u>observational studies</u> have reported the link between cardiovascular risk factors (such as obesity, <u>high blood pressure</u>, diabetes and <u>high cholesterol</u>) and COVID-19 severity. However, these studies could not ascertain the cause and effect relationship due to the observational design.

The new study, published in the science journal *Frontiers in Genetics*, used a novel approach called 'Mendelian Randomisation', which leveraged on the individual genetic information, to investigate the effects of cardiovascular risk factors on the risk of COVID-19 infection.

Lead author Dr. Nay Aung from Queen Mary University of London said: "Our results show that individuals with high body mass index (BMI), a marker of obesity, and high low-density lipoprotein (LDL) cholesterol (also known as 'bad' cholesterol) are at an increased risk of getting COVID-19. Other <u>cardiovascular risk factors</u> (high blood pressure and diabetes) do not appear to elevate the COVID-19 risk.

"Our findings support the use of BMI and LDL cholesterol as important metrics alongside other known characteristics (such as age and ethnicity) in the risk assessment of vulnerability to COVID-19 infection."

The findings may have an impact on public health policy, whereby those who fall in the at risk obese category or those with extreme hyperlipidemia in the general population may require more rigorous social distancing or shielding. Furthermore, studies assessing the role for cholesterol modification therapy during illness or hospital admission could be undertaken to assess potential impact on outcomes.

More information: Nay Aung et al. Causal Inference for Genetic Obesity, Cardiometabolic Profile and COVID-19 Susceptibility: A Mendelian Randomization Study, *Frontiers in Genetics* (2020). DOI: 10.3389/fgene.2020.586308



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