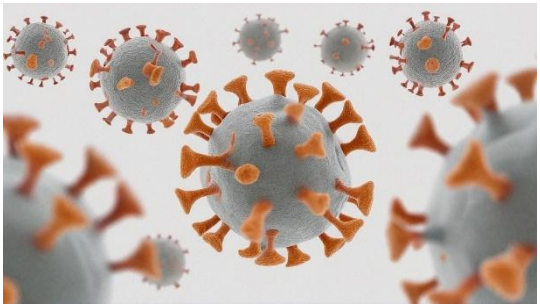
COVID-19 Risk Predicted by Nasal Protein Levels

A recent study determines the potential of measuring transmembrane serine protease 2 (TMPRSS2) and angiotensin-converting enzyme 2 (ACE2) levels in the nasal cavity to predict the risk of future coronavirus disease 2019 (COVID-19) and whether the host nasal microbiome modulates the expression of these proteins.



Study

Two retrospective case-control studies were conducted in Washington D.C. by utilizing 1,548 self-collected nasal swab samples. Nasal swabs were collected from population-based surveillance testing of community-dwelling adults.

The first retrospective case-control study a cross-sectional study with 111 cases and 343 controls and longitudinal study consisting of 97 cases and 286 controls. A nasal microbiome study of 428 cases was also conducted.

Cases, which included individuals who tested positive for SARS-CoV-2, were matched with controls based on test date and age. Pre-infection samples were analysed and reverse transcription qualitiative polymerase chain reaction (RT-qPCR) was used to estimate nasal ACE2/TMPRSS2 expression.

The nasal microbiome was characterized using 16S ribosomal ribonucleic acid (rRNA) gene-based qPCR and sequencing. Machine learning and regression analysis models were also used to determine whether TMPRSS2 and ACE2 expression in the nasal cavity could predict COVID-19.

Results

The test immediately before the positive SARS-CoV-2 test (t-1) occurred at an average of 12 days before the positive SARS-CoV-2 test (t0). Nasal ACE2 and TMPRSS2 levels among cases at t-1 were higher than controls.

Three regions were identified based on crossing point (Cp) values that predicted future SARS-CoV-2 infection. The low region did not exhibit any ACE2 or TMPRSS2 expression, whereas ACE2 was not detected and TMPRSS2 Cp values were over 32 in the medium region. High regions exhibited ACE2 expression or TMPRSS2 Cp values of 32 or less.

As compared to controls, elevated nasal levels of ACE2 and TMPRSS2 were associated with a 3.6-fold increased risk of SARS-CoV-2 infection. Males were also more likely to exhibit greater ACE2 and TMPRSS2 expression than females.

In the longitudinal study considering five time points (t-5 to t-1), cases expressed distinct longitudinal nasal ACE2/TMPRSS2 patterns before viral infection. Cases were more likely to switch between expression categories, exhibit persistently high expression categories across different time points, and have unstable ACE2/TMPRSS2 expression.

In the nasal microbiome study of 428 individuals, 27% belonged to the high category, 51% medium, and 22% low. A new nasal CST dominated by *Haemophilus influenzae* was identified, while Enterobacteriaceae-dominated CST was absent.

Corynebacterium-dominated CST was the most prevalent species, along with *Cutibacterium-, Staphylococcus epidermidis-, Dolosigranulum-, and S. aureus*-dominated CST. The least common CSTs were H. influenza-dominated CST and Moraxella catarrhalis/nonliquefaciens-dominated CST. CSTs did not significantly differ across nasal expression categories.

D. pigrum, M. catarrhalis/nonliquefaciens, H. influenzae, and S. aureus significantly affected nasal ACE2/TMPRSS2 gene expression.

High absolute abundance of *D. pigrum* was associated with lower nasal ACE2/TMPRSS2 expression. The beneficial impact of *D. pigrum* was likely driven by its absolute abundance, rather than its proportional abundance with other bacteria.

Comparatively, the abundance of M. *catarrhalis/nonliquefaciens, H. influenzae, and S. aureus* was associated with an increased risk of SARS-CoV-2 infection.

Conclusion

Adults with higher nasal ACE2 and TMPRSS2 expression levels were significantly more likely to contract SARS-CoV-2 infection in the near future. Future studies are needed to investigate the relationship between SARS-CoV-2 infection and the nasal microbiome to devise new strategies to prevent or treat COVID-19.

Source:

https://www.news-medical.net/news/20250416/Nasal-protein-levels-may-predict-COVID-19-risk.aspx