

COVID-19 OCULAR ASSOCIATIONS IN THE SCIENTIFIC LITERATURE:

SYNOPSIS 22

The COVID-19 pandemic began in December and has affected people in nearly every country in the world. We provide a summary of ocular-related associations with COVID-19 in the literature, and we plan to update this as we become aware of new manuscripts. Thus far, it appears that approximately 1-5% of COVID-19 patients experience conjunctivitis and very few COVID-19 patients exhibit virus in their tears.

Hamashima K Gautam P, Lau KA, et al. Potential modes of COVID-19 transmission from human eye revealed by single-cell atlas. bioRxiv. 2020

- Review paper (not peer reviewed)
 - SARS-CoV-2 viruses enter through ACE2 receptors after the S proteins of the virus are primed by proteases such as TMPRSS2
 - Earlier studies also indicate that SARS-CoV, which is closely related to SARSCoV-2, is able to enter the body via mucosal membranes in the eyes
 - A study by Hui et al. observed that SARS-CoV-2 was able to infect conjunctival cells ex vivo and undergo productive replication, implying that the ocular route may emerge as a significant mode of transmission of COVID-19
 - Tissues in the cornea express ACE2 and superficial conjunctival cells co-express ACE2 and TMPRSS2
 - BSG expression in corneal and conjunctival epithelium indicates that BSG could also serve as a receptor for SARS-CoV-2 entry into certain ocular cells
 - Viral entry via the ocular route could result in subsequent manifestation of respiratory disease
- via the nasolacrimal system, but it remains unclear whether this is a major mode of transmission of COVID-19 and which receptors are used by SARS-CoV-2 to infect ocular cells
 - ACE2 expression occurs in a few epithelial cells in the cornea and conjunctiva
 - Proteases, such as TMPRSS2, cathepsin B, and cathepsin L necessary for viral entry were also expressed in the conjunctiva
 - Conclusions: “We identified unique populations of corneal cells with high ACE2 expression, among which the conjunctival cells co-expressed both ACE2 and TMPRSS2, suggesting that they could serve as the entry points for the virus. Integrative analysis further models the signaling and transcription regulon networks involved in the infection of distinct corneal cells.”



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