

Human coronavirus 229E

Human coronavirus 229E (*HCoV-229E*) is a species of coronavirus which infects humans and bats.^[1] It is an enveloped, positive-sense, single-stranded RNA virus which enters its host cell by binding to the APN receptor.^[2] Along with Human coronavirus OC43 (a member of the *Betacoronavirus* genus), it is one of the viruses responsible for the common cold.^{[3][4]} HCoV-229E is a member of the genus *Alphacoronavirus* and subgenus *Duvinacovirus*.^{[5][6]}

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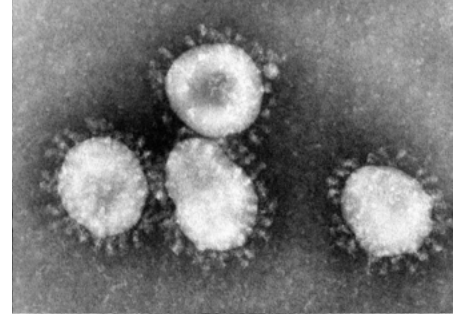
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Transmission electron micrograph of human coronavirus 229E

Virus classification

(unranked): Virus

Realm: Riboviria

Kingdom: Orthornavirae

Phylum: Pisuviricota

Class: Pisoniviricetes

Order: Nidovirales

Family: Coronaviridae

Genus: Alphacoronavirus

Subgenus: Duvinacovirus

Species: ***Human coronavirus 229E***

Transmission

HCoV-229E transmits via droplet-respiration and fomites.

Signs and symptoms

HCoV-229E is associated with a range of respiratory symptoms, ranging from the common cold to high-morbidity outcomes such as pneumonia and bronchiolitis. However, such high morbidity outcomes are almost always seen in cases with co-infection with other respiratory pathogens; there is a single published case report to date of a 229E infection that caused acute respiratory distress syndrome (ARDS) in an otherwise healthy patient having no detectable co-infection with another pathogen.^[7] HCoV-229E is also among the coronaviruses most frequently codetected with other respiratory viruses, particularly with human respiratory syncytial virus (HRSV).^{[8][9][10]}

Epidemiology

HCoV-229E is one of the seven human coronaviruses which include HCoV-NL63, HCoV-OC43, HCoV-HKU1, MERS-CoV, SARS-CoV-1, and SARS-CoV-2 and are globally distributed.^{[11][12]} However, the viruses were detected in different parts of the world at different times of the year.^[13]^{[14][15]} A NCBI-study found a previous HCoV-229E infection in 42.9% – 50.0% of children of 6–12 months of age and in 65% of those 2.5–3.5 years of age.^[16]

Virology

HCoV-229E is one of seven known coronaviruses to infect humans. The other six are:^[17]

- Human coronavirus NL63 (HCoV-NL63)
- Human coronavirus OC43 (HCoV-OC43)
- Human coronavirus HKU1 (HCoV-HKU1)
- Middle East respiratory syndrome-related coronavirus (MERS-CoV)
- Severe acute respiratory syndrome coronavirus (SARS-CoV-1)
- Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)

Research

Chloroquine, a zinc ionophore, inhibits the replication of Human coronavirus 229E in cell culture.^[18]

Human HCoV-229E, and human HCoV-NL63, likely originated from bats.^[19]

History

A researcher at the University of Chicago, Dorothy Hamre, first identified 229E in 1965.^{[20][21]}

See also

- Virulence
- Outbreak
- RNA virus
- Human coronavirus HKU1
- Positive/negative-sense

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External links

- [CDC \(https://www.cdc.gov/coronavirus/about/\)](https://www.cdc.gov/coronavirus/about/)
 - [Virology online \(http://virology-online.com/viruses/CORZA4.htm\)](http://virology-online.com/viruses/CORZA4.htm)
 - [Coronaviruses \(https://web.archive.org/web/20070309144307/http://www-micro.msb.le.ac.uk/3035/Coronaviruses.html\)](https://web.archive.org/web/20070309144307/http://www-micro.msb.le.ac.uk/3035/Coronaviruses.html)
 - [Viralzone: Alphacoronavirus \(http://viralzone.expasy.org/viralzone/all_by_species/766.html\)](http://viralzone.expasy.org/viralzone/all_by_species/766.html)
 - [Virus Pathogen Database and Analysis Resource \(ViPR\): Coronaviridae \(http://www.viprbrc.org/brc/home.do?decorator=corona\)](http://www.viprbrc.org/brc/home.do?decorator=corona)
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