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Review Article

# Human Coronaviruses: The Deadly Seven

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## Abstract

Coronaviruses belong to the Family Coronaviridae, which is a classification of enveloped virus pathogens that have a large positive RNA genome. Coronaviruses are known to cause a variety of debilitating ailments including gastroenteritis and diseases of the lower/upper respiratory track. Coronaviruses are known to infect bats, cats, camels, chickens, cows, dogs, ferrets, horses, mice, minks, pigs, rabbits, raccoons, rats, snakes, tigers, and turkeys. To date, at least seven known human coronaviruses exist including: HCoV-229E, HCoV-OC43, HCoV-HKU1, HCoV-NL63, MERS-COV, SARS-CoV and the most recently discovered, SARS-COV-2, also known as COVID-19. This manuscript is intended to identify the health concerns and molecular identification methods for all known human coronaviruses in order to combat the spread of SARS-COV-2.

**Keywords:** Coronavirus; SARS-COV-2; COVID-19; Virus; Virology; Public Health; Molecular Biology

## Introduction

Coronaviruses were first discovered in the 1960's and they belong to the Order Nidovirales, and Family Coronaviridae [5-9,26,34]. They are described to be enveloped virus pathogens that have the largest positive RNA genome of any viruses known to date [5-9,26,34]. The majority of coronaviruses are known to cause a variety of acute diseases including gastroenteritis and diseases of the upper/lower respiratory track [1-42]. Although coronaviruses are a major health concern for humans, coronaviruses are also known to infect bats, cats, camels, chickens, cows, dogs, ferrets, horses, mice, minks, pigs, rabbits, raccoons, rats, snakes, tigers, and turkeys [1-42]. All coronaviruses can have a major economic impact on the world economy due to the extensive trade agreements between nations on all the major continents.

Coronaviruses are divided into four sub-groups based upon their molecular sequence, which include: Alphacoronavirus, Betacoronavirus, Gammacoronavirus, Deltacoronavirus [5]. The term 'Human Coronaviruses' are a common term for Alphacoronaviruses and Betacoronaviruses that use humans as their main host for replication, but they can infect other organisms as alternate hosts [5,34]. As of 2020, at least seven known human coronaviruses exist, which include; HCoV-229E, HCoV-OC43, SARS-CoV, HCoV-NL63, MERS-COV, HCoV-HKU1, and the most recently discovered, SARS-COV-2, also known as COVID-19 [5,7,34]. Early genomic research revealed that the genome of human coronaviruses is incredibly large, complex and can exceed 30,000 nucleotides in length [32]. This manuscript is designed to address the major health concerns and molecular identification methods to detect the seven known human coronaviruses, including the most recently discovered SARS-COV-2, also known as COVID-19 by the World Health Organization (WHO). The seven known human coronaviruses will be presented in the order in which they were discovered.

One type of the 'Common Cold' is caused by the human coronavirus HCoV-229E which is closely related to viruses that infect insectivorous bats in Africa, Asia, Caribbean, Europe, and North America [26,34]. HCoV-229E was discovered in the 1960's and is known to cause mild upper respiratory infections for normally health adults but can cause severe symptoms in the elderly, HIV patients, and the young with underdeveloped immune systems [34,35]. Recent molecular dating methodologies suggest that HCov-229E evolved between the years 1346 B.C.E and 116 B.C.E. [26]. Villamil-Gómez., et al. suggests that the anti-viral drugs designed to treat HCoV-229E are unreliable and the only available treatments are to provide breathing support to the infected person [35]. Molecular identification methodologies to detect HCoV-229E have been provided by Stephensen and colleagues [31,34].

A second type of the 'Common Cold' is caused by the human coronavirus HCoV-OC43 which is closely related to HCoV-229E [4,34]. Like HCoV-229E, HCoV-OC43 was discovered in the 1960's and are closely related to viruses that infect insectivorous bats [19,34]. HCoV-OC43 causes acute upper respiratory infections in heathy adults, but can cause elevated symptoms in the elderly, the

immunocompromised, and infants [20,34]. It has also been shown that HCoV-OC43 is more likely to cause lower respiratory infections in children, than other human coronaviruses [4]. Infections from HCoV-OC43, like HCoV-229E, generally occur during the winter and early spring months [4,20]. Arnold and colleagues state that there is little research data related to the community spread of human coronaviruses [4]. Molecular identification methodologies to detect HCoV-OC43 have been provided by Stephensen and colleagues [31,34].

The last type of the 'Common Cold' is caused by the human coronavirus HCoV-NL63, which is a virus that is most closely related to HCoV-229E [25,33,37,41]. The human coronavirus HCoV-NL63 can also cause 'Croup' in children and is generally thought to cause more severe clinical symptoms than HCoV-229E and HCoV-OC43 [20]. HCoV-NL63 can also cause rhinorrhea, cough, tachypnea, and obstructive laryngitis [33]. Like HCoV-229E and HCoV-OC43, HCoV-NL63 causes acute upper respiratory infections in heathy adults, but can cause elevated symptoms in the elderly, the immunocompromised, and infants [25]. The genome of HCoV-NL63, like other coronavirus, is large, complex, and ranges from 28-32k base pairs [33]. Tsai and colleagues have recently shown anti-viral action of leaf extracts from Strobilanthes cusia [Nees], a plant belonging to the Acanthaceae family, which inhabits east Asia and the Indian subcontinent [33]. Although anti-viral drugs are being developed, there are currently no available cures of HCoV-NL63 to date [33]. Molecular identification methodologies to detect HCoV-NL63 have been provided by various research groups [31,33,34,41].

In 2002, Severe Acute Respiratory Syndrome Coronavirus, also known as SARS-CoV, became a world heath problem as it spread throughout China and other countries in east-Asia [6,11,25,34]. By 2003, the World Health Organization identified over 2353 cases of SARS-COV and reported a 4.0% mortality rate [11]. As of 2020, 8098 cases of SARS-COV was reported, and of those infected with the virus, 774 fatalities occurred, resulting in a 9.5% mortality rate [42]. Genetically, SARS-COV belongs to the genus betacoronavirus and is classified into the subgenera of Sarbecovirus [6]. Recently, Kampf and colleagues reviewed the persistence of SARS-COV on inanimate surfaces ranging from disposable gowns, to surgical gloves, to metal surfaces, showing that this virus can last on some surfaces for up to 9 days [12]. Anti-viral drugs have been developed for SARS-COV, although the success of these drugs has not resulted in a cure for this disease [42]. Identification methodologies are provided by Drosten and colleagues [11,42].

HCoV-HKU1 is a human coronavirus first isolated and described from a pneumonia patient in January of 2005 [30]. Although this coronavirus does not have a common name, it has been shown to cause upper and lower respiratory tract infections in east-Asia, North America, as well as in Australia [4,25,30]. Sloots and colleagues revealed that 3.1% of upper/lower respiratory tract infections in Australia were caused by HCoV-HKU1 [30]. Sloots and colleagues also show that HCoV-HKU1 can be categorized into two sub-categories: type A, and type B [30]. It has also been shown by Sloots., et al. that HCoV-HKU1 is more likely to occur in the absents of other microbes and is most likely to affect children under the age of two [30]. Recently, Arnold., *et al.* has shown nine infections of HCoV-HKU1 in Louisville Kentucky, which accounted for less than 0.5% of the human coronavirus infections sampled from nine hospitals [4]. Molecular identification methodologies to detect HCoV-HKU1 have been provided by Sloots research group [30].

In 2012, a novel human coronavirus first named HCoV-EMC, was re-named MERS-COV, was isolated from two infected patients from Saudi Arabia [8,25,37]. By 2013, thirteen patients had been infected with MERS-COV and seven of those patients have died, showing a mortality rate of 53.84% [27]. In 2014, 635 laboratory confirmed cases of MERS-COV existed and 193 of these cases resulted in a fatality, proving a mortality rate of 30.39% [1]. In 2015, MERS-COV spread to South Korea, causing 186 cases and 36 related deaths [21]. By 2020, 2500 cases of MERS-COV had been reported with a mortality rate of around 35% [10]. Symptoms of MERS-COV include severe respiratory distress and, in some cases, chronic renal disfunction, diabetes mellitus, hypertension, chronic kidney disease, and chronic cardiac disease had been reported [2,27]. About 9.8% of infect patients of MERS-COV were recognized as asymptomatic through screening processes [3]. After molecular characterization MERS-COV, it is reported to be most related to European bat coronaviruses HCoV-HKU4 and HCoV-HKU5, isolated from samples collected in the Netherlands [27]. Investigation into carriers of MERS-COV reveal numerous non-human hosts [6]. Various anti-viral drugs have been researched for their efficacy against MERS-COV, but none of these treatments provided immunity to MERS-COV [14,29]. Identification methodologies to detect MERS-COV has been provided by numerous research groups [8,27].

In December of 2019, a novel coronavirus, officially named SARS-CoV-2 by the International Committee of Taxonomy of Viruses, first appeared in Wuhan China then subsequently disseminated through-out Australia, the rest of Asia, Europe, North America, and South America [3,7,9,12-18,22-24,28,38,39,41,42]. The World Health Organization named unofficially named this novel coronavirus COVID-19, while other research groups refer to this virus as 2019-nCOV, or Wuhan CoV [3,5,9,12,24,38,39]. The physiological effects of SARS-COV-2 very greatly, from asymptomatic patients, to patients that experiences pneumonia-like symptoms, to complete respiratory failure and death [3,39]. To date, no anti-viral drugs have been developed to specifically combat SARS-COV-2, so anti-viral treatments designed to treat MERS-COV infections are currently being tested as a therapy for SARS-CoV-2 [14]. Identification methodologies are provided by various research groups [9,38].

As of March 2020, the World Health Organization has declared that SARS-COV-2, also known as COVID-19, has reached pandemic stages, and the fate of millions of people's lives is unknown. Tsai and colleagues have shown the anti-viral properties of *Strobilanthes cusia* [Nees], which could be studied to combat SARS-COV-2 [33]. This manuscript is intended to provided health care and public health professionals sufficient background information on all 7 known coronaviruses, in order to educate the public on the social concerns related to this virus outbreak [1-42]. The information provided in this manuscript is also intended to clarify terminology associated with human coronaviruses and provide a clear distinction between all of the known human coronaviruses [1-42]. Continued research on SARS-COV-2 will take place until the virus is contained, cured, or has run its course through the world's populations.

## Conclusion

Human Coronaviruses are a group of viruses that infect humans and alternate hosts. To date, only seven coronaviruses are known to infect humans, and only a few of these are of serious consequence at the present time. This review is intended to provided background information on all seven known coronaviruses and to provided identification methods for every virus in this study. This study also mentions possible treatments for SARS-COV-2, which has become a worldwide pandemic.

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## Conflict of Interest

No conflict of interest is declared.

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