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# Novel Coronavirus COVID-19 related genes

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Coronaviruses (CoVs) are named after the crown-like spikes present on their surface. The coronaviruses that affect humans were first identified in the 1960s. The human coronaviruses identified so far are: **SARS-CoV** (Severe Acute Respiratory Syndrome Coronavirus); **NL63** (Human Coronavirus NL63 Amsterdam 1); **OC43** (Organ Culture 43); 229E (Human Coronavirus 229E); **MERS-CoV** (Middle East Respiratory Syndrome Coronavirus); and the novel coronavirus, **COVID-19** (Coronavirus Disease 2019). (1)

People around the globe typically get infected with human coronaviruses NL63, OC43, and 229E. However, as is in the case of SARS-CoV, MERS-CoV, and COVID-19 some viruses that only affect animals can evolve to infect humans. (2) This assignment is to discover similar genes to the novel coronavirus.

The number of animal coronaviruses (CoVs) quickly grew, including viruses causing diseases in several bird, and mammal species, with manifestations in the respiratory and gastrointestinal tracts, central nervous system, liver, reproductive tract, and other locations. Through sequencing studies, the animal coronaviruses were classified. (3; 1)

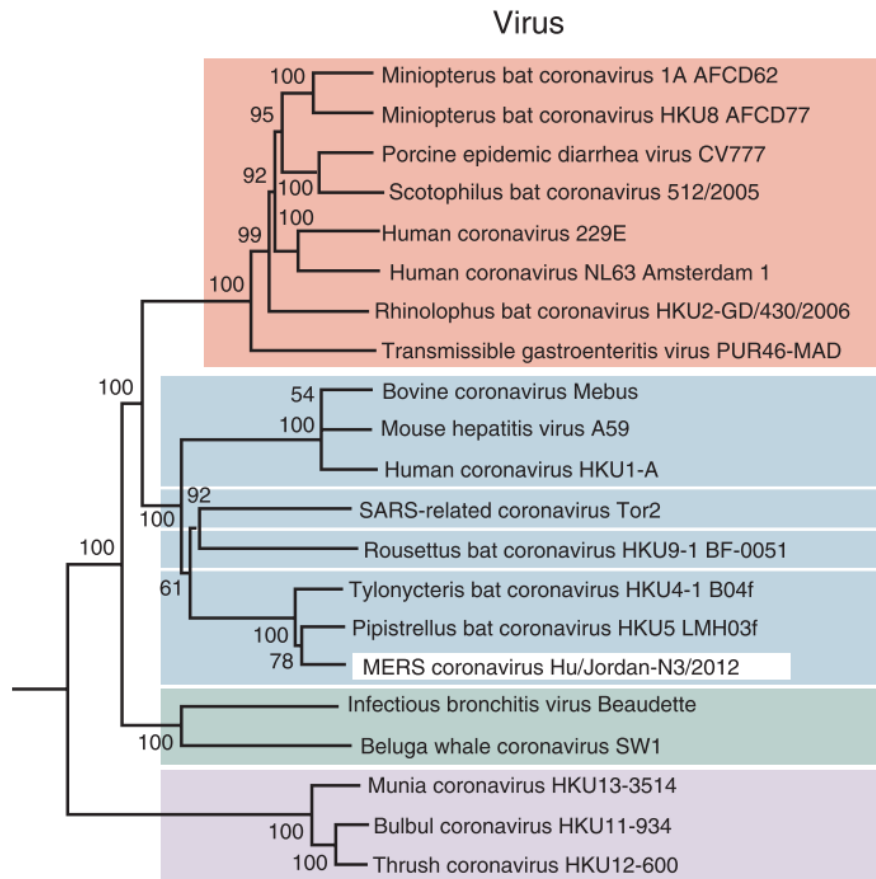
McIntosh et. al (4) generated a rooted neighbor-joining tree (Figure 1) from sequence alignments of 21 coronaviruses. The known human coronaviruses are indicated in the figure. The tree shows the four color coded clusters, corresponding to Alpha- (orange), Beta- (blue), Gamma- (green), and Delta- (purple) coronavirus classification.

It is expected to find similarities between the known human CoVs as all coronavirus genomes share the same baseline structure. (5) The human CoVs genome is compared using the NCBI-BLAST (National Center for Biotechnology Information Basic Local Alignment Search Tool), results are summarized in Table 1. As shown in the table, NL63, OC43, 229E, and MERS share about 50% of 'identities' and about 15% of 'gaps' with COVID-19; whereas SARS is the most similar to the novel coronavirus with 80% 'identities' and 1% 'gaps'.

On the other hand, several media sources have reported the COVID-19 to be from bat provenance. The origin of the novel coronavirus can be confirmed by running a 'Global Alignment' of

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**FIGURE 1**

Rooted neighbor-joining tree

COVID-19 against the bat coronavirus RaTG13. The alignment reports 96% 'identities' with 0% 'gaps', as shown in Table 1. The high percentage of identities and low gaps infers that COVID-19 comes from bats.

**TABLE 1**

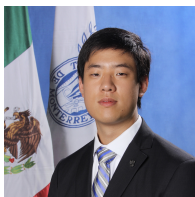
BLAST Global Alignment of the known human CoVs against the novel coronavirus COVID-19

Query ID	Virus	NW Score	Identities	Gaps
NC_045512	COVID-19	59806	29903/29903(100%)	0/29903(0%)
NC_004718	SARS	29084	23940/30067(80%)	480/30067(1%)
KF530114	NL63	-11628	17073/31015(55%)	4717/31015(15%)
KX344031	OC43	-10792	18197/32531(56%)	4446/32531(13%)
KF514433	229E	-12678	16938/31140(54%)	5212/31140(16%)
KT225476	MERS	-8741	18173/31984(57%)	4256/31984(13%)
MN996532	RaTG13	53877	28717/29905(96%)	52/29905(0%)

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## Author biography



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