

Name: \_\_\_\_\_

# ANALYSIS OF CORONAVIRUS EVOLUTION

Coronaviruses (CoV), like Severe Acute Respiratory Syndrome (SARS-CoV), are positive sense RNA viruses that have been circulating from animal populations into human populations for many years. Researchers collected complete genome sequences from several populations of viruses and constructed a phylogenetic tree to represent their evolutionary relatedness (Figure 1).

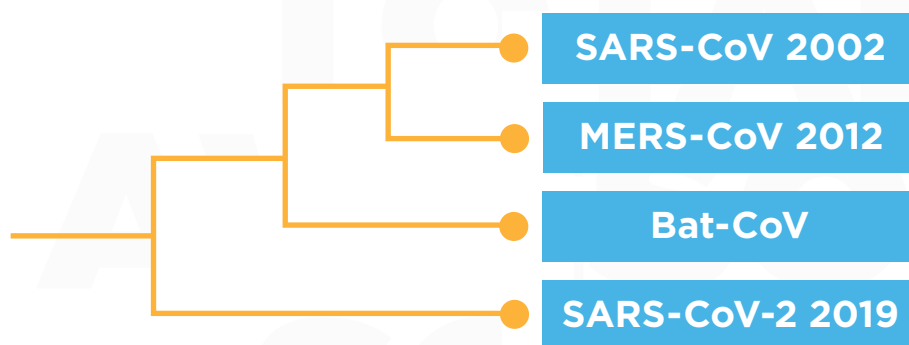


Figure 1. Phylogenetic tree representing evolutionary relatedness among corona virus strains based on whole viral genomes sequence comparison

A researcher studying adaptations in CoV sequenced the spike protein (S) in the human coronaviruses SARS, MERS, SARS-CoV-2, and Bat coronavirus. There are several substitutions found only in the SARS-CoV.

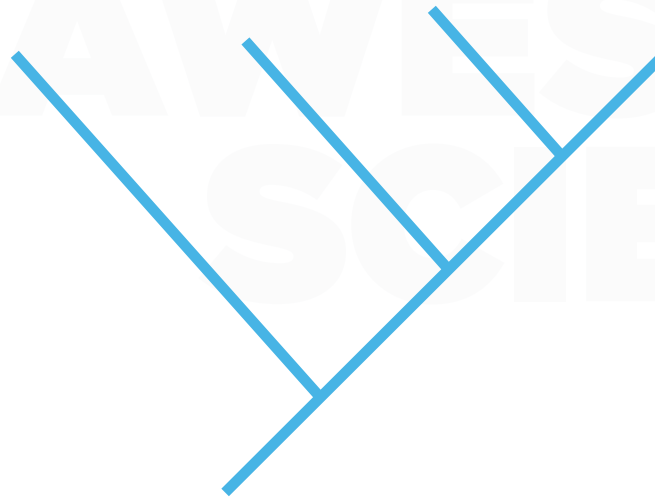
	Bat-CoV	MERS-CoV	SARS-CoV	SARS-CoV-2
Bat-CoV	-			
MERS-CoV	61.16%	-		
SARS-CoV	21.89%	58.76%	-	
SARS-CoV-2	2.12%	61.37%	22.53%	-

Table 1. Percentage of differences in the spike protein among CoV species

1. Identify the populations of virus to which SARS Cov-2 is most closely related.

2. Identify two populations whose position could be switched without affecting the relationships illustrated in the tree.

3. Construct a cladogram on the template to represent the model of the evolutionary relationship among the CoV species based on the differences in spike protein. Circle the out-group.



4. A student claims that spike protein amino acid sequences comparison provide a more accurate phylogeny of CoV species than do whole genome sequence comparisons. Provide one piece of reasoning to support the student claim.