

Online COVID-19 High School Curriculum - Solon Supplement 4. Sample Assessments from Teachers

Full assessment portfolio is available with downloaded curriculum materials

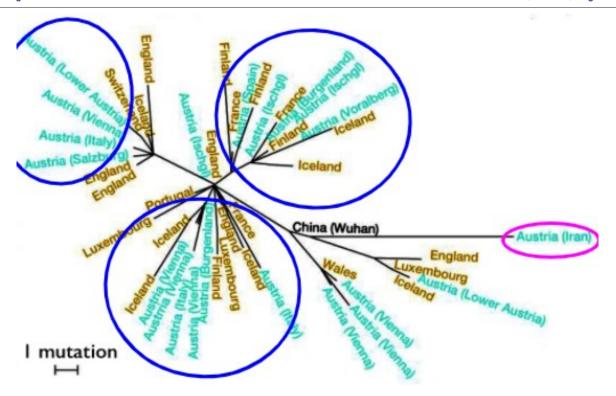
__Biomed_COVID Lesson 2.2 Quiz_20-21 SY

<u>Directions</u>: The following questions deal with COVID Lessons 2.2. Select the response/s that BEST answer/s the question. (Yes, some questions will have more than one correct response!) Read carefully!

- There are 16 questions and you will have 24 minutes to complete this quiz.
- This quiz is OPEN NOTE, but not open internet. You may use any notes that you have taken on COVID Unit 2, but do NOT use the internet to look up answers as this would be a violation of the academic integrity policy. (See below.)
- You will get three attempts. Your BEST score will be recorded in SIS.

<u>PLEASE NOTE</u>: By beginning this assessment, you are agreeing to follow the student handbook, which outlines academic integrity. Failure to maintain academic integrity will result in behavioral and academic consequences.

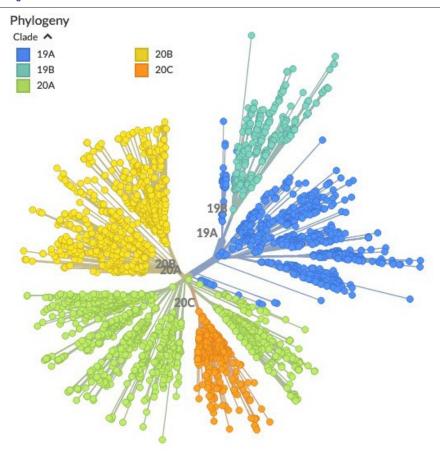
- 1. What does the phylogenetic analysis of viruses like SARS-CoV-2 involve? (Choose all that apply.) (1 point)
 - ☐ Tracking how many different animal species have been illegally trafficked through a specific region.
 - ☐ Comparing the protein structure of the Spike proteins of viral isolates to create a 'family tree' of how viruses have evolved over time.
 - Sequencing virus isolates collected in different places at different times.
 - ☑ Tracking how SARS-CoV-2 initially spread throughout the world.
 - ☑ Using the nucleotide sequences of viral isolates to create a 'family tree' of how a virus like SARS-CoV-2 evolves over time.
- 2. The picture below shows study that used viral isolates to investigate how SARS-CoV-2 might have evolved. Note (1 point) that the sequence of the Austria (Iran) isolate puts it off on its own, whereas most of the other Austrian isolates are in three clusters off to the left outlined in blue.



Which Austrian isolate is the common ancestor for these three clusters?

- Austria (Ischgl)
- O Austria (Iran)
- China (Wuhan)
- Austria (Vienna)

3. (1 point)

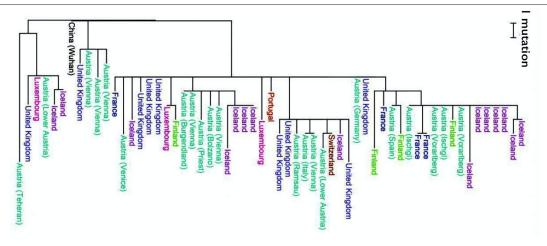


The picture above shows a clade map of SARS-CoV-2 from August 16, 2020. Groups of isolates with related sequences are called clades.

Clades colored the same are all derived from

- the same ancestor.
- () the same country.
- () the same lab.
- the same city.
- 4. TRUE or FALSE? A phylogenetic tree shows us definitively how various viral isolates are related. (1 point)
 - True A phylogenetic tree represents the final say in how various viral isolates are related. Evolution is a fixed process that does not change and always takes the same path. This is why phylogenetic trees are extremely reliable and predictable regardless of how many viral isolates are included.
 - False A phylogenetic tree represents a hypothesis of how various viral isolates are related, but the actual evolution of the isolates could have occurred in many ways. The reliability of any tree depends on the number of isolates it includes.
- 5. TRUE or FALSE? Grouping viral isolates into clades makes it easier to understand how they evolved. (1 point)
 - True A clade represents a group of isolates whose sequence of mutations indicates that they all originated from a common ancestor. Grouping viruses into clades makes identifying that ancestor easier.
 - False Clades are an outdated way of organizing viral isolates and can actually make it much harder to understand how they are grouped and how they evolved.
- 6. (1 point)

(1 point)



The labels at the end of a spike on the 'starburst', or a branch on the 'family tree' tell the country where the isolate was obtained, while the parentheses show

- the specific area the patient was planning to travel next.
- specific areas the patients traveled from.
- specific areas the patients traveled to after the isolate was discovered.
- the birthplace of the patient who carried the isolate.
- 7. The following nucleotide sequences were found in viral isolates. Which of the following phylogenetic trees shows a possible evolutionary relationship between the sequences? Assume only one nucleotide mutated each time. (Choose all that apply.)

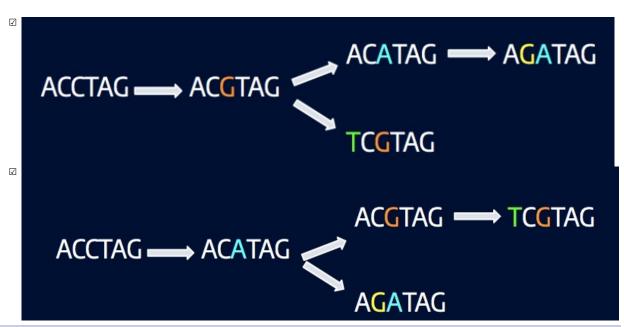
ACCTAG

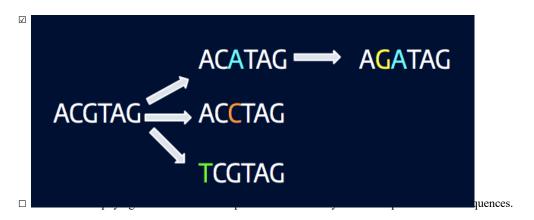
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ACGTAG

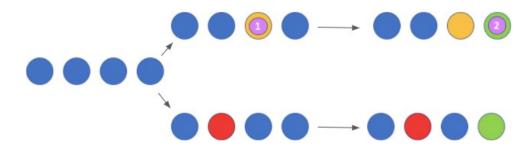
AGATAG

TCGTAG





8. Here is a cartoon of what a phylogenetic tree for a virus would look like. Each circle represents one nucleotide in a sequence of 4 nucleotides. If a nucleotide mutates, its color changes.

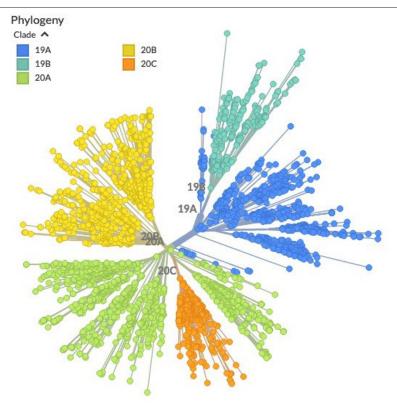


Mutations in the top branch are labeled with numbers to show when they appear.

If SARS CoV-2 mutates about twice a month (it does!) how long does the top branch of the diagram represent?

- The top branch represents evolution over 1 month.
- The top branch represents evolution over 2 months.
- It is impossible to tell how much time it has taken to create the isolates seen in the top branch.
- The top branch represents evolution over half a month.
- 9. TRUE or FALSE? You calculate the number of mutations an isolate has undergone by counting the number of branch points from the original isolate. (1 point)
 - True Each branch point is equal to one mutation. If an isolate is 5 branch points away from the original isolate, then it has acquired 5 mutations.
 - False There is a set distance along each branch that is equivalent to one mutation. The number of mutations is calculated by measuring the length of the isolate branch and dividing it by this set distance.

10. (1 point)



The picture above shows a clade map of SARS-CoV-2 from August 16, 2020. Groups of isolates with related sequences are called clades. How many clades are shown in this clade map?

 $\bigcirc 6$

5

2980

 \bigcirc 8

11. Matching Directions - Match the definitions on the left with the vocabulary words on the right. (3 points)

_3 A sample of virus that is obtained from an infected person, not grown in a laboratory situation.

1. phylogenetic analysis

2 A diagram showing evolutionary relationships.

2. phylogenetic tree

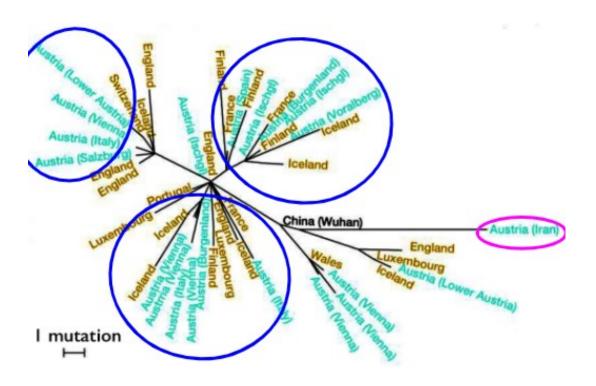
1 Using random mutations a virus undergoes over time to track how it evolves.

3. viral isolate

12. What is an epidemic?

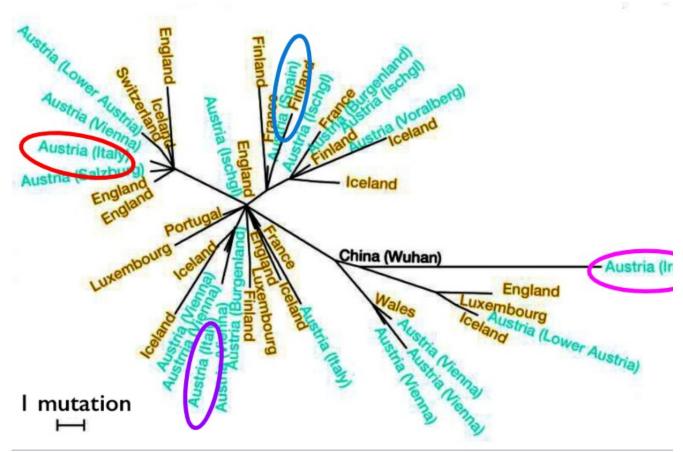
(1 point)

- An infection that is transmitted from an animal to a human.
- A disease outbreak that shows up in a couple of patients then quickly goes away.
- A disease outbreak confined to one region.
- A disease of short duration but with symptoms that are typically severe.
- A disease outbreak that is more widespread across several regions.
- 13. The picture below shows study that used viral isolates to investigate how SARS-CoV-2 might have evolved. Note (1 point) that the sequence of the Austria (Iran) isolate puts it off on its own, whereas most of the other Austrian isolates are in three clusters off to the left outlined in blue.



What does the diagram suggest about community transmission in Austria? (Choose all that apply.)

- ☐ The isolates outlined in blue arise from the China (Wuhan) sample suggesting that the China (Wuhan) sample led to community transmission.
- ☑ The isolates outlined in blue arise from the Austria (Ischgl) sample and not the Austria(Iran) sample, meaning the Austria (Iran) sample did not lead to community transmission.
- ☑ Community transmission is shown by isolates from patients who did not travel outside Austria.
- □ The isolates outlined in blue arise from the Austria (Iran) sample suggesting that the Austria (Iran) sample led to community transmission.
- 14. The picture below shows study that used viral isolates to investigate how SARS-CoV-2 might have evolved. Three isolates fro patients who had come from Europe, plus one that came from Iran, are circled.

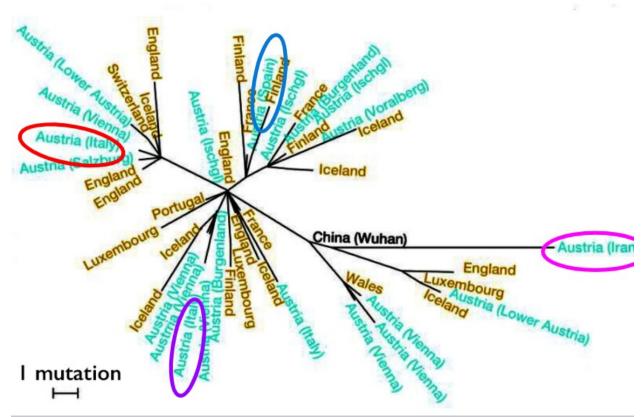


The number of mutations that each isolate has acquired compared to the Wuhan original is listed the table below (second column). The amount of time (in months) that each isolate would have taken to develop is listed in the third column.

Austria (Iran)	10	5
Austria (Spain)	8	4
Austria (Italy)	8	4
Austria (Italy)	7	3.5

Given the data in the table and phylogenetic tree above, which isolate is most likely Austria's "patient zero" (the first Austri infected)?

- Austria (Iran) in pink. It has the most mutations, and has been around the longest amount of time after the original Wuhan isolate was found.
- Austria (Italy) in red. It has the least mutations, and has been around the shortest amount of time after the original Wuhan isolate was found.
- Austria (Spain) in blue. It has the most mutations, and has been around the longest amount of time after the original Wuhan isolate was found.
- Austria (Italy) in purple. It has the least mutations, and has been around the shortest amount of time after the original Wuhan isolate was found.
- 15. The picture below shows study that used viral isolates to investigate how SARS-CoV-2 might have evolved. Three isolates from patients who had come from Europe, plus one that came from Iran, are circled.



The number of mutations that each isolate has acquired compared to the Wuhan original is listed the table below (second column). The amount of time (in months) that each isolate would have taken to develop is listed in the third column.

Austria (Iran)	10	5
Austria (Spain)	8	4
Austria (Italy)	8	4
Austria (Italy)	7	3.5

Given the information in the table above, about how often does SARS-CoV-2 mutate?

- It is impossible to tell how often SARS-CoV-2 mutates.
- About every 4 weeks.
- About every week.
- About every 2 weeks.

16. What is a pandemic?

(1 point)

- An infection that is transmitted from an animal to a human.
- \bigcirc A disease outbreak that shows up in a couple of patients then quickly goes away.
- A disease outbreak confined to one region.
- A disease outbreak that is more widespread across several regions.

A disease of short duration but with symptoms that are typically severe.