Name: **Date:**

HANDS-ON ACTIVITY

Modeling Viral Mutations

Although viruses can vary in shape, most of them include the same general components. Viruses all contain a capsid made of proteins. Inside the capsid is the genetic material—either DNA or RNA. The capsid is sometimes covered in a lipid envelope. Virus structures are usually formed by a small number of protein types arranged in a repeating pattern. Surface proteins on the outside of the capsid help the virus find and infect a host cell. The surface proteins can be responsible for connecting with proteins of the host cell and merging with them like a "lock and key," or they may serve other functions that impact the virus life cycle.

Influenza A virus provides an example of a virus for which changes in a single protein can have a significant impact on infectivity. Historically (and recently with the H1N1 pandemic), influenza outbreaks have begun with virus strains that infect non-human animals. Over generations, spontaneous mutations and genome reassortment events have caused changes in surface proteins that have enabled these viruses to infect humans. Some of these strains have mutated in a way that has given them excellent infectivity, which means they are much more easily passed from person to person, possibly causing significant outbreaks.

In this lab, you will design and construct two different virus models to illustrate changes that could occur by mutation.

POSSIBLE MATERIALS

- bag, resealable plastic sandwich
- ball, foam (tennis ball or softball size)
- foam rubber
- glue, white
- knife (serrated) or scalpel
- nails, small (1 box)
- pins, straight (1 box)
- pipe cleaners, assorted colors
- plastic wrap
- sequins and/or beads, assorted colors
- tape, masking (1 roll)
- thumbtacks (1 box)
- toothpicks (1 box)
- yarn (1 ball)

PREDICT

What virus will you model? How will you model the differences between the "original" and the mutated virus?

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PROCEDURE

1. Perform research on the methods that different viruses use to infect a host cell, as well as mutations that enable a particular virus to become a more efficient pathogen (for example, becoming better able to infect a host cell, making more new viruses, or improving immune system evasion).
2. Choose one type of virus that infects humans and select a mutation to model. Have your teacher approve your virus and mutation selection.
3. Brainstorm materials or methods that might be best for developing three-dimensional cross-sections of the virus you have chosen, both before and after the chosen mutation.
4. Come up with a plan. Design your models so that you can use the same or similar materials to represent similar structures in each viral strain. Consult with your teacher to make sure that the designs and materials you have chosen are appropriate.

5. Write out a set of blueprints for each of your models. As you plan the procedure, take the following steps:
   - Decide what materials you will use from those provided to the class. Consult with your teacher if you would like to use any additional materials.
   - Decide how you will evaluate the models.
   - Decide what safety procedures are necessary.
6. Have your teacher approve your plan.
7. Obtain the necessary materials and set up any apparatus you will need.
8. Take appropriate safety precautions.
9. Make labeled models, trying to keep to scale as much as possible.
10. Share your models with other teams, being sure to explain how the mutation allows the new strain to become a more efficient pathogen. Elicit their feedback on your designs.
11. Make objective observations.
12. Improve your designs.
13. Clean your lab station and return any equipment that you have used to its proper storage area. Take apart your models and store reusable materials.

ANALYZE

1. Summarize your findings and observations, including an analysis of what materials worked best and what ones did not work as well.

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2. How are the different viral structures that you modeled involved in the infection process? How does the mutation allow the new strain to become a more efficient pathogen?

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3. Share your results with your classmates. Which models were the best? Why?

CONCLUDE

1. What conclusions can you draw from your models? from your classmates' models?

2. Did your virus models show how a change in viral structure can lead to a strain with greater ability to infect humans? Explain why or why not, and give examples of what might be missing from your designs.