

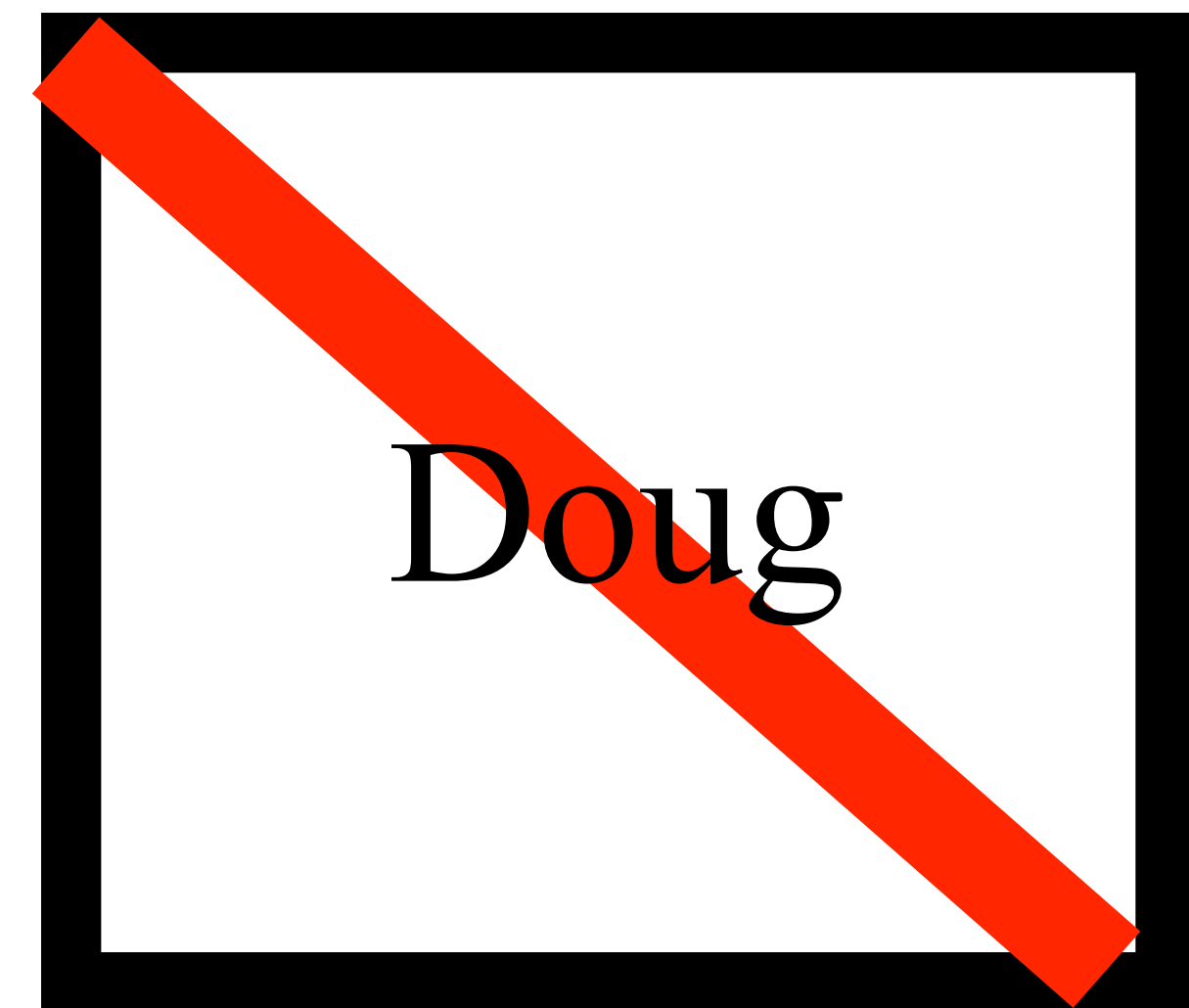
1. Clicker Attendance

- Launch your Top Hat app on your smart phone, or load the TopHat.com website, or text to the course phone number.

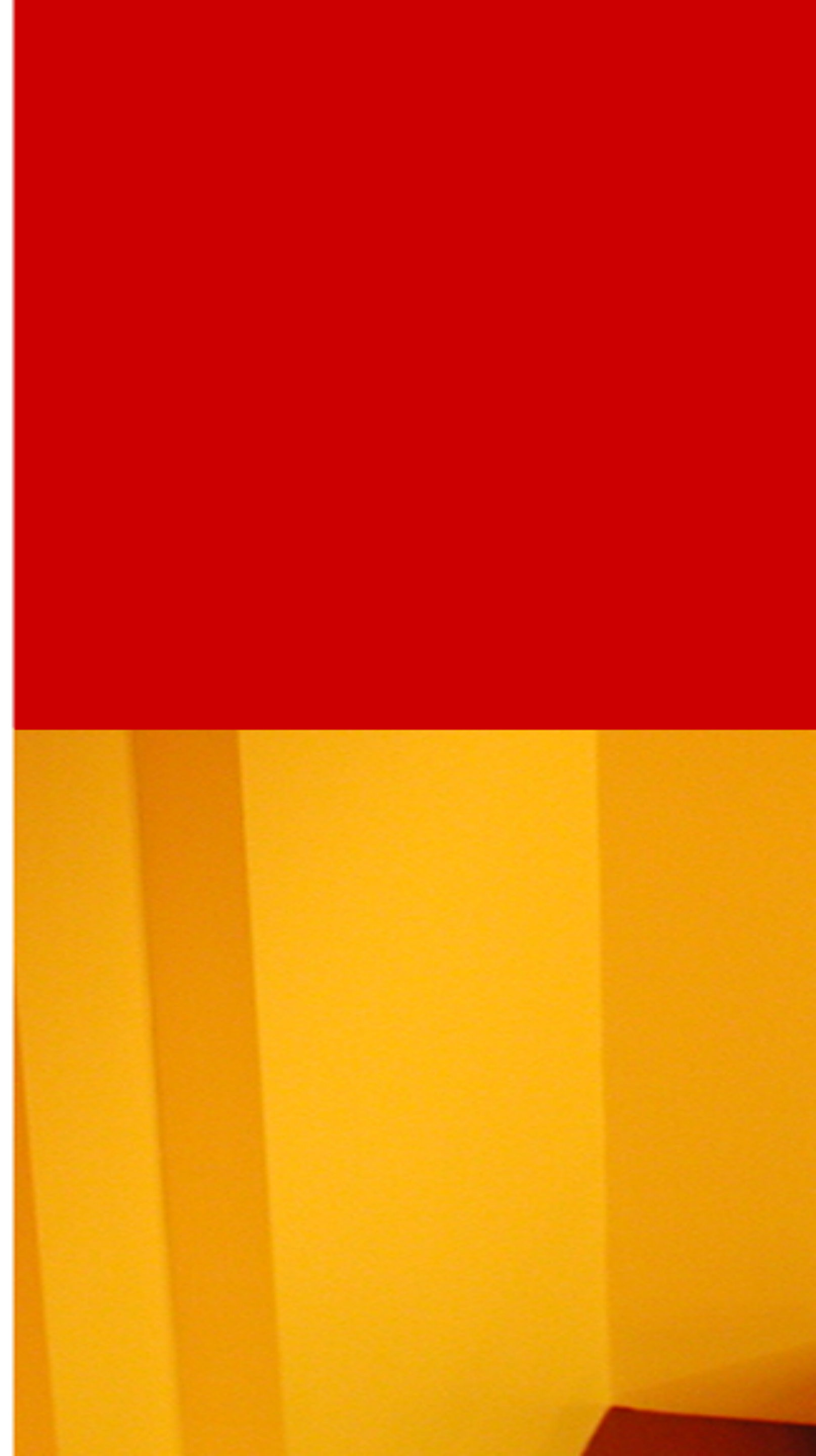
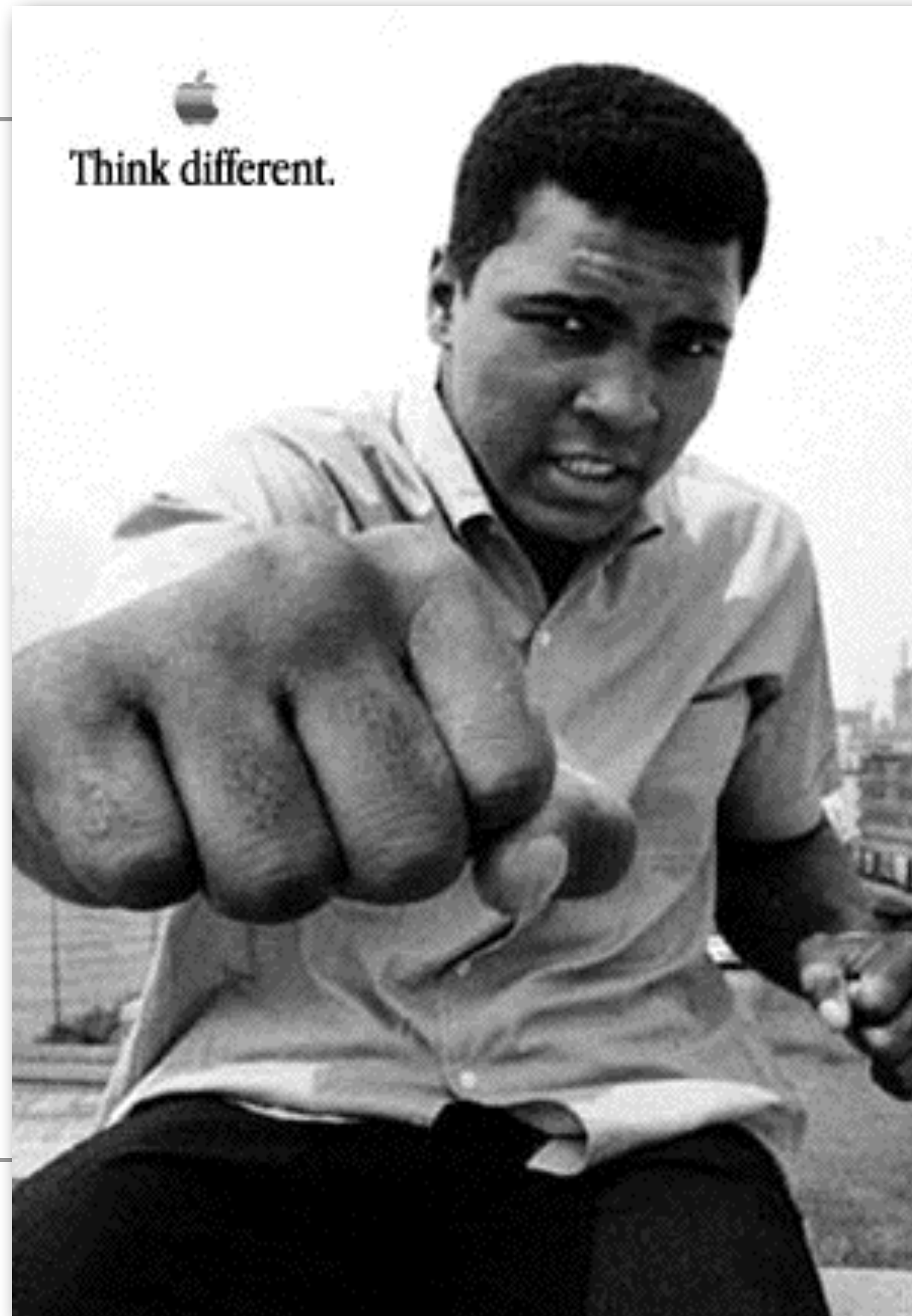
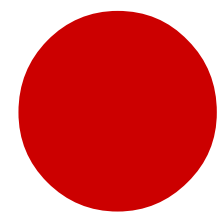
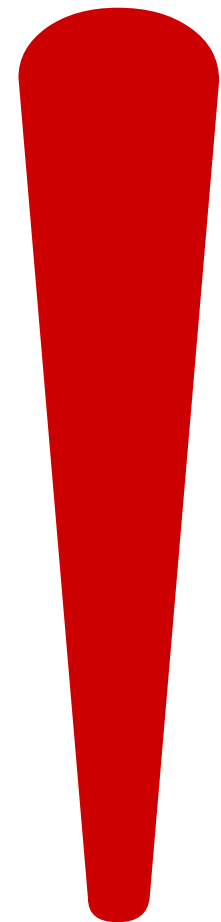
2. Sit with your group in lecture & lab

3. To Opt-OUT of being called upon

- Name Card with red stripe means you Opt-OUT (can Opt-OUT 3 times)



LB144-Pandemic 2022



Trifecta,
be Jedi
master

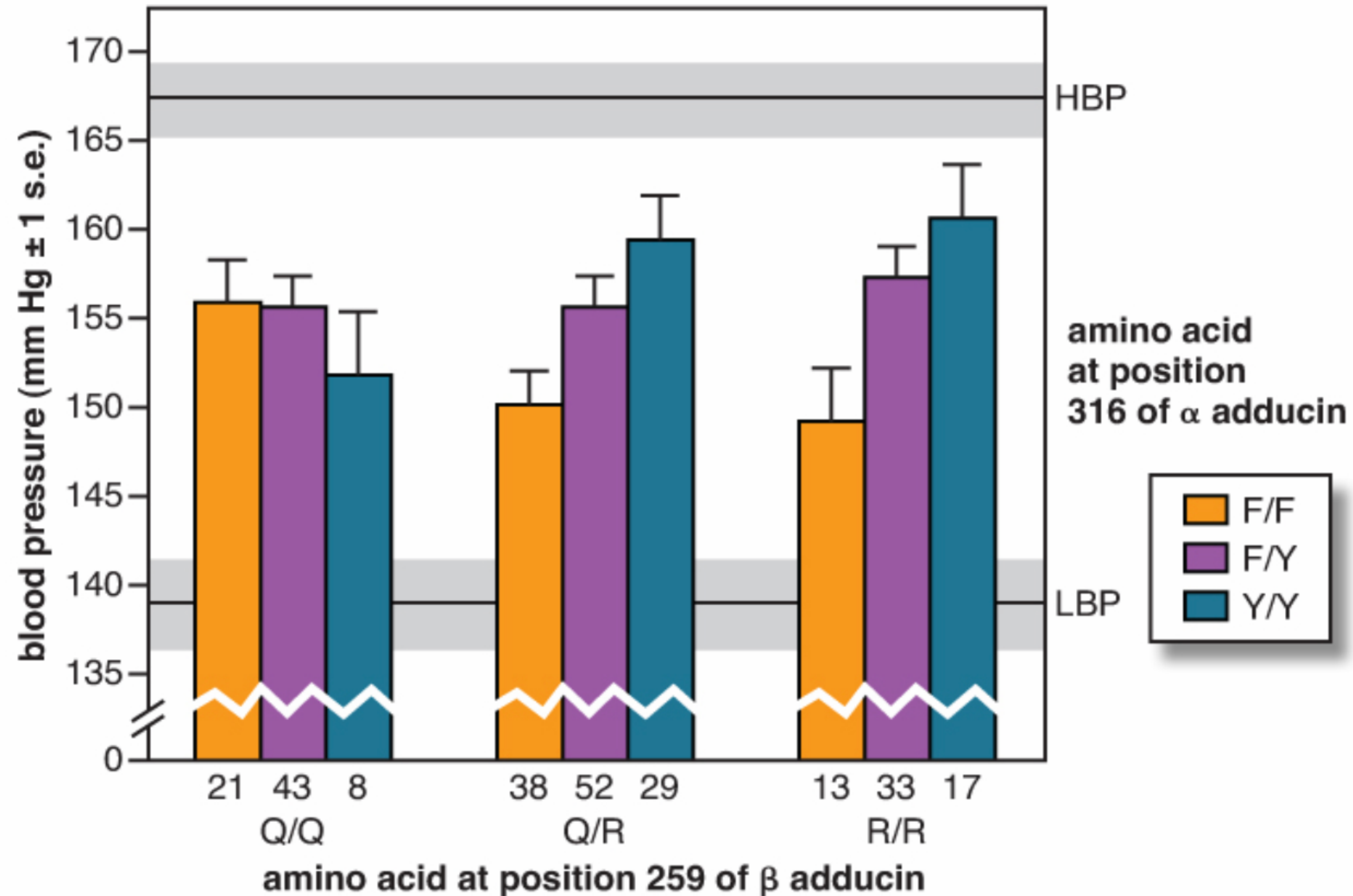
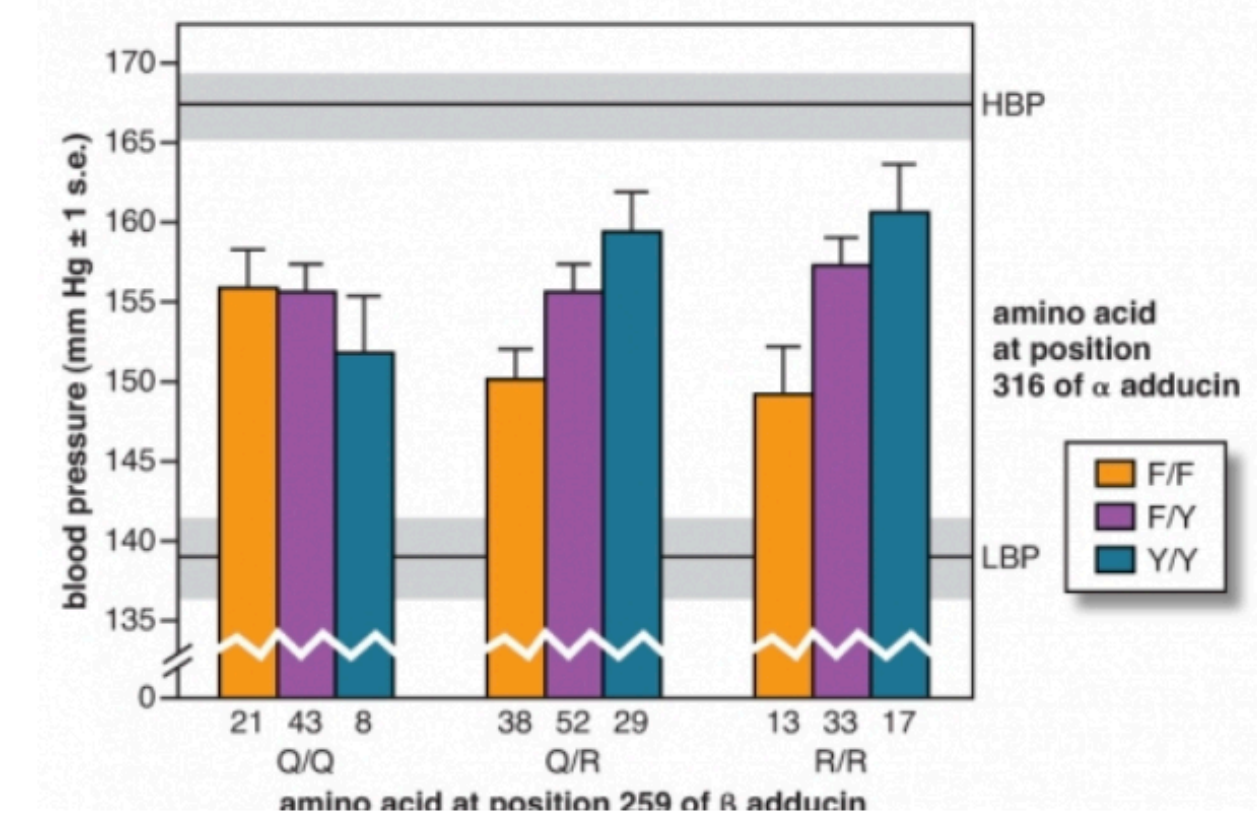


Figure 16.5 Mean blood pressures of the nine combinations of two versions of the α and β adducin genes in rats after two generations of breeding low and high blood pressure rats together. Error bars = 1 SE. Mean blood pressure (horizontal solid lines) \pm 1 SE (stippled areas) of 10 rats of each parental strain are included for comparison. HBP, High blood pressure; LBP, low blood pressure. From Bianchi et al., 1994, Figure 3, copyright (1994) National Academy of Sciences, U.S.A.

Clicker points

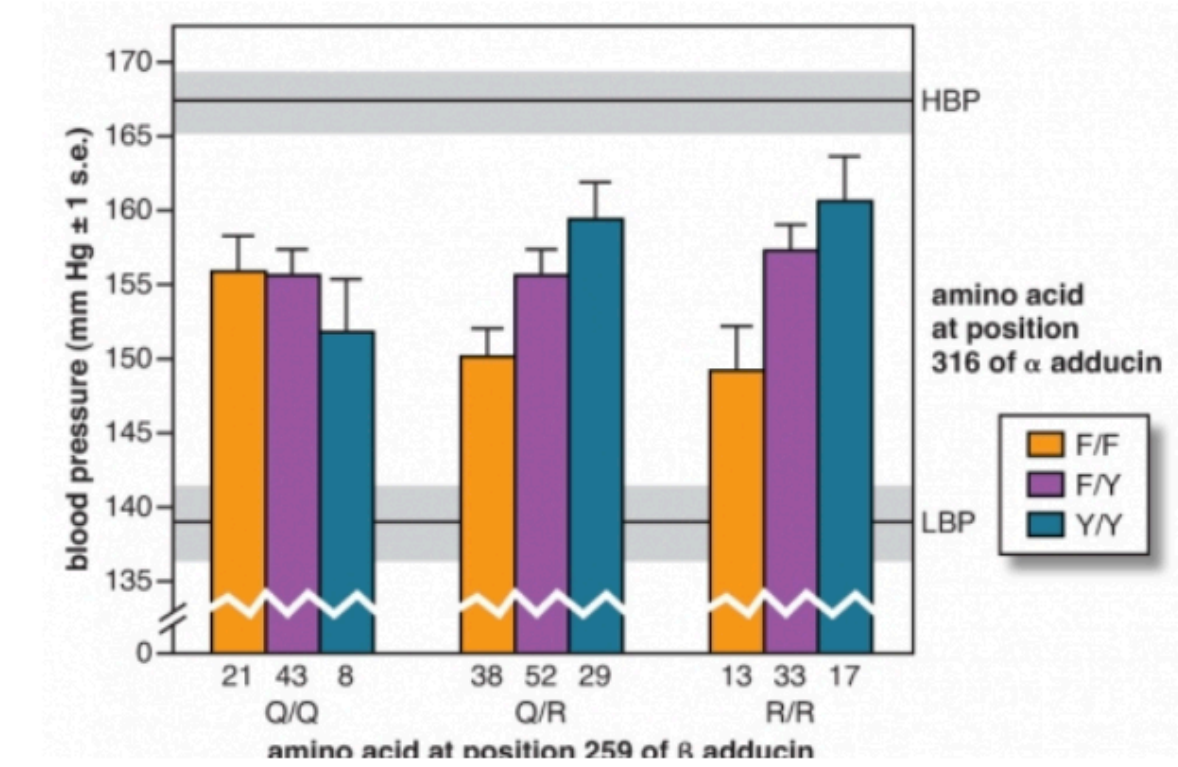
Check what you know!
(Rewards for preparation)

In this Figure, if ALL the orange bars were at 165 mmHg and ALL the purple bars were at 140 mmHg, which adducin protein, α or β , affects systolic blood pressure the most?



- A** α , as there is much more variation across the α alleles
- B** β , as there is much more variation across the β alleles.
- C** They affect blood pressure equally.
- D** Neither affect blood pressure as the offspring all have blood pressures in between the averages of their parents

In this figure, if ALL three Q/Q bars were at 165 mmHg, and all three R/R bars were at 140 mmHg, which adducin protein, α or β , affects systolic blood pressure the most?



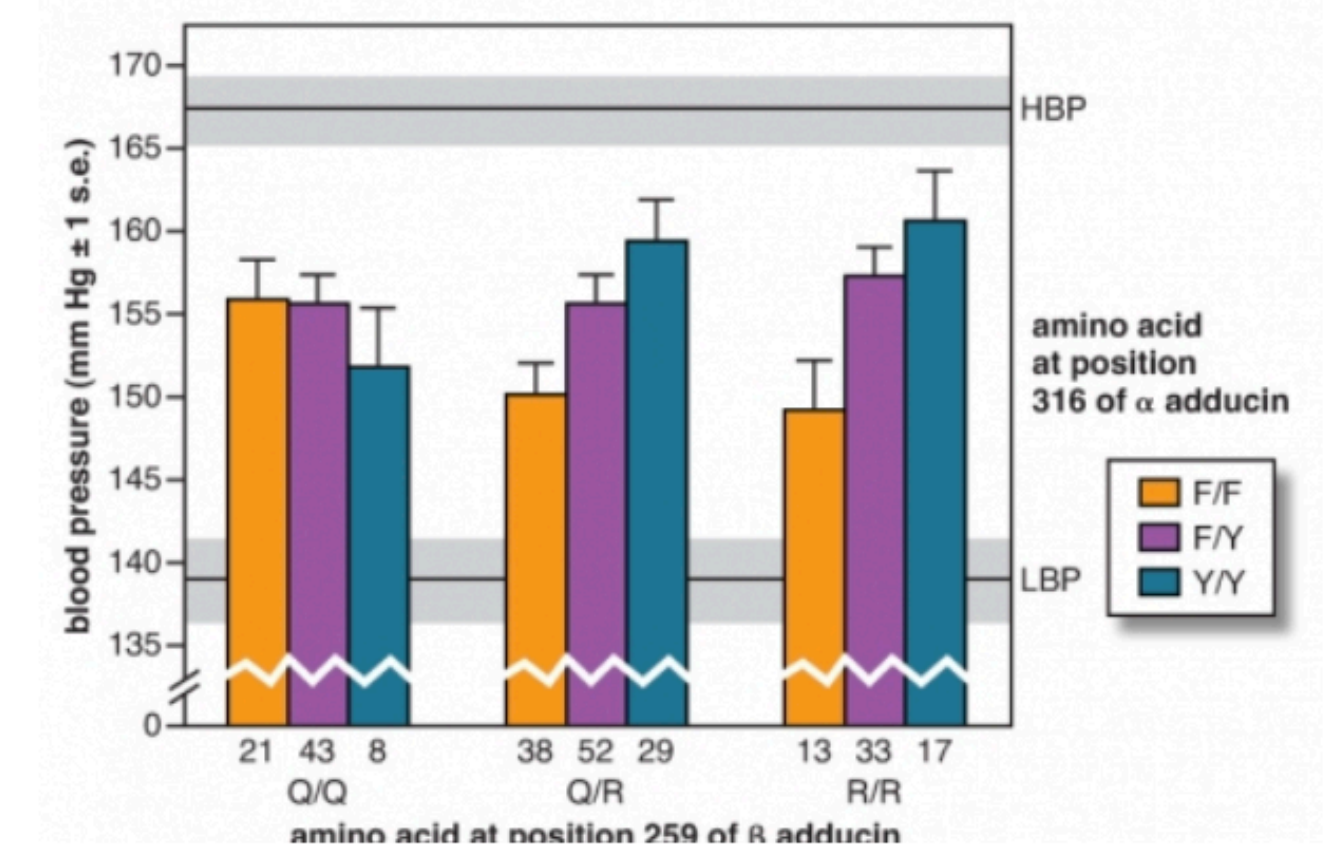
A α , as there is much more variation across the α alleles

B β , as there is much more variation across the β alleles.

C They affect blood pressure equally.

D Neither affect blood pressure as the offspring all have blood pressures in between the averages of their parents

Based on Figure 16.5 and the reading, which adducin protein, α or β , affects systolic blood pressure the most?



- A** α , as there is much more variation across the α alleles
- B** β , as there is much more variation across the β alleles.
- C** They affect blood pressure equally.
- D** Neither affect blood pressure as the offspring all have blood pressures in between the averages of their parents

Researchers discover a new virus. They determine that it is capable of using the host cell's machinery to manufacture proteins, but it does not need its genome to be transcribed first; its genome is translated into a protein immediately after it enters the host cell. **Predict into which of the following groups should this new discovery be placed?**

- A. double-stranded DNA (dsDNA) viruses
- B. double-stranded RNA (dsRNA) viruses
- C. single-stranded RNA (ssRNA) viruses
- D. RNA reverse-transcribing viruses

In late 2019 researchers discover a new virus (SARS-CoV-2). It becomes the largest pandemic since 1918. In the USA in the first six months it killed 200,000 people, more than the 1918 Spanish flu in the same span. **Which of these statements is TRUE?**

- A. A full 50% of all Covid-19 serious hospitalizations in the USA were people under 50 yrs.
- B. The greatest age group under 50 yrs to be seriously sickened were in their 40 yrs.
- C. The vast majority of serious cases (80%+) were found in those over 65 years of age.
- D. The SARS-CoV-2 is far more lethal to lives and livelihoods in the USA than the 1918 Spanish flu.

END

Pop Quiz!

What do you prefer (Be Jedi?)

 Random calling?

 1:00

Which method would you prefer we use to gain answers from students in this course among: Volunteering (raise hand), random picking (deck of cards) or cold-calling (just ask someone).

All results ▾

A Pick only from volunteers (I know I will have the lowest learning if we do that, but I'm cool with that)

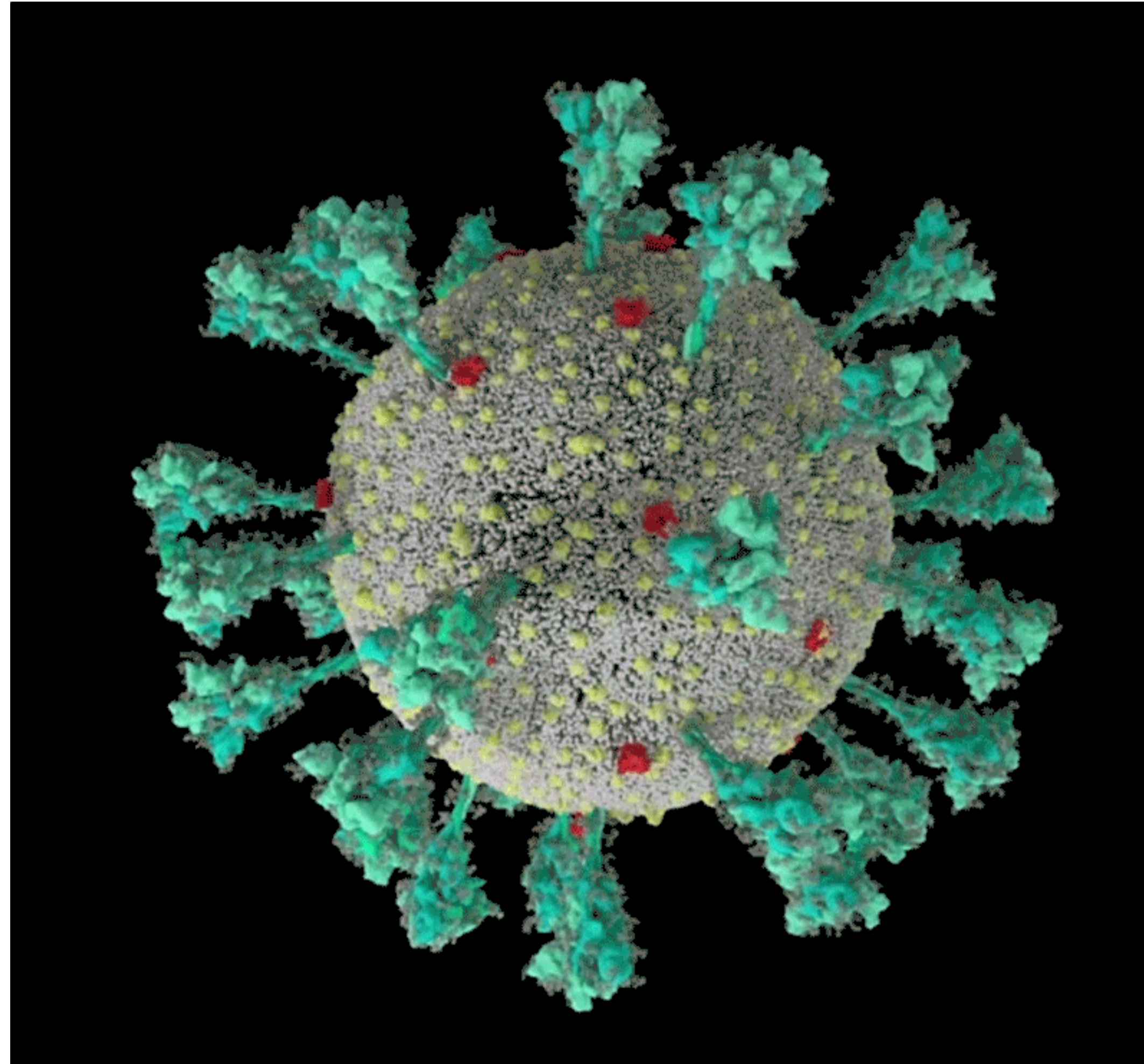
B Pick names from the deck of cards (learning is MUCH higher and feels more fair that way)

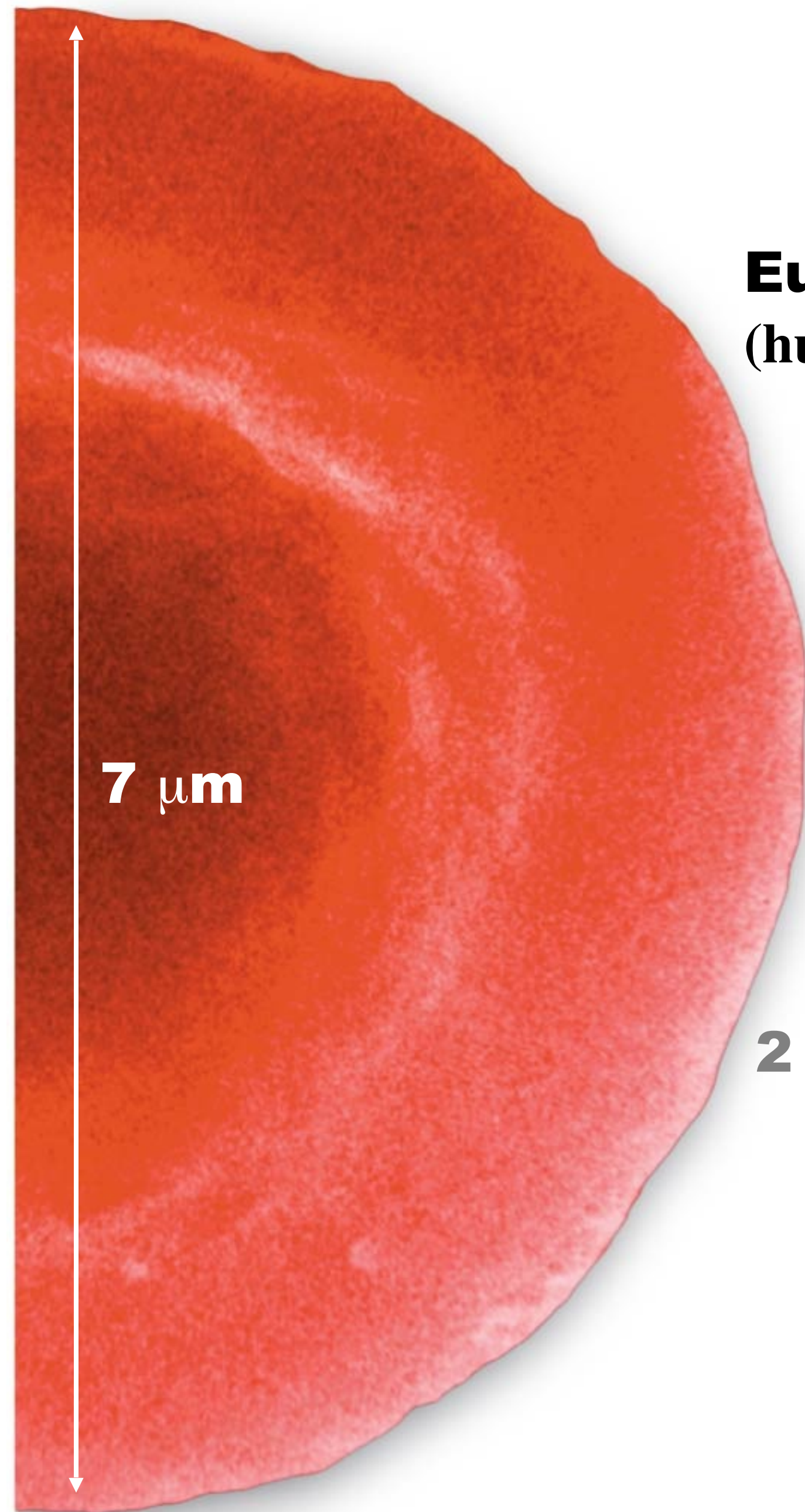
C Use Cold-calling (I want THE maximum learning, MSU charged us a lot of \$ for this, and I really need to get high grades in my future biology classes)

Budgeting homework time (40 min): Read section 16.3 " Non-Mendelian genetics: Why do we need annual flu vaccines?". This is just 1889 words with 3 figures. Just reading the text will take 8 minutes. The figures do not contain data, thus, when done properly, when you pause to decipher each figure, try Integrating Questions, and take notes, this assignment will take you more like 40 minutes.

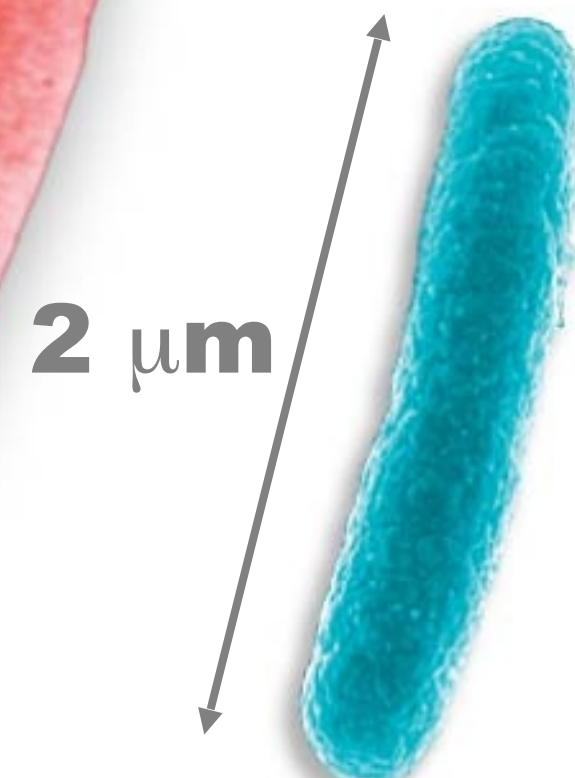
1. _____ **For Thursday's lecture, slowly** read section 16.3 " Non-Mendelian genetics: Why do we need annual flu vaccines?". And please take handwritten notes.
2. _____ Try to answer some **Integrating Questions** and **Review Questions**. As you read the ICB textbook always attempt to test yourself a little, answer at least one of each set.
3. _____ **Prepare to explain (aloud) Figures 16.12, 16.13, 16.14 in class.**
4. _____ **Advanced:** Check the CDC website and determine the strains of flu we currently face.

What is a virus?





Eukaryotic cell
(human red blood cell)



Bacterial cell
(*E. coli*)



Virus particles
(HIV)

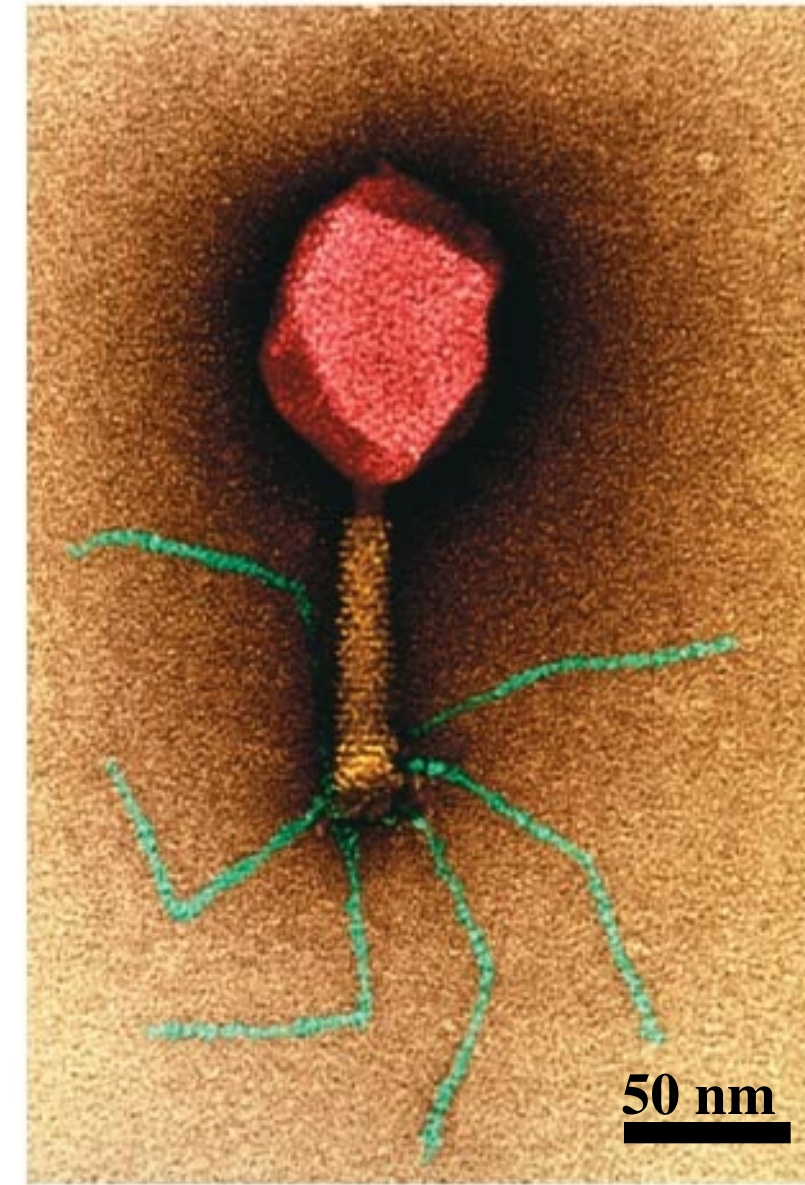
(a) Tobacco mosaic virus



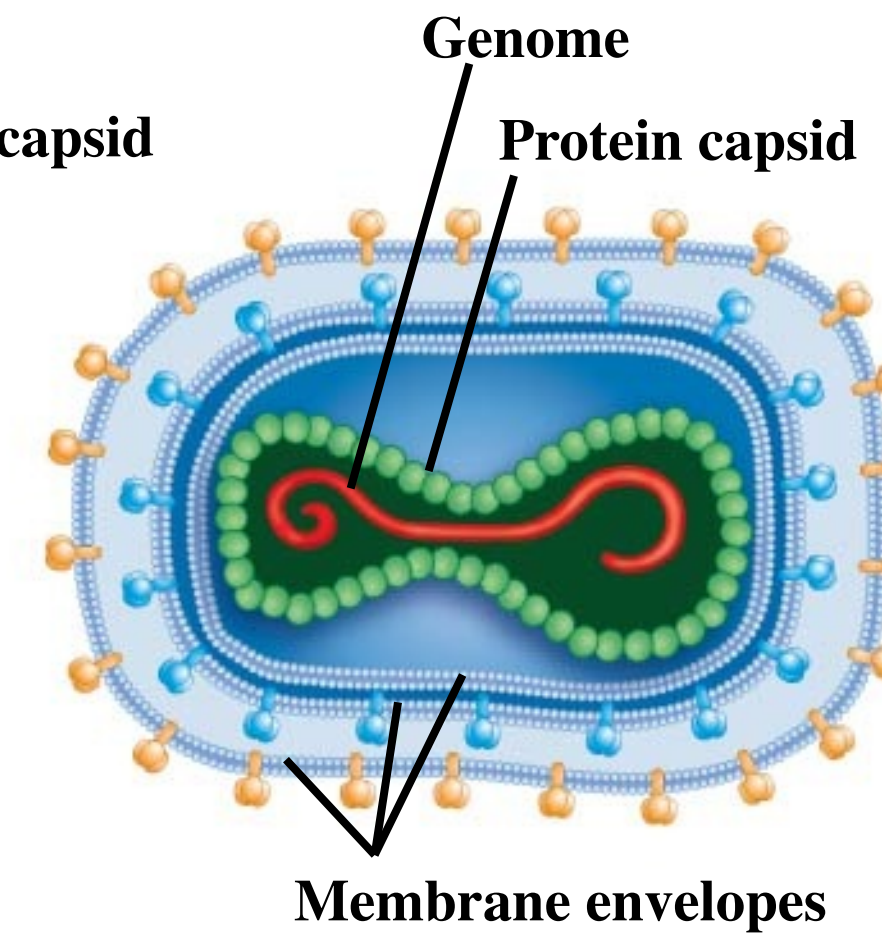
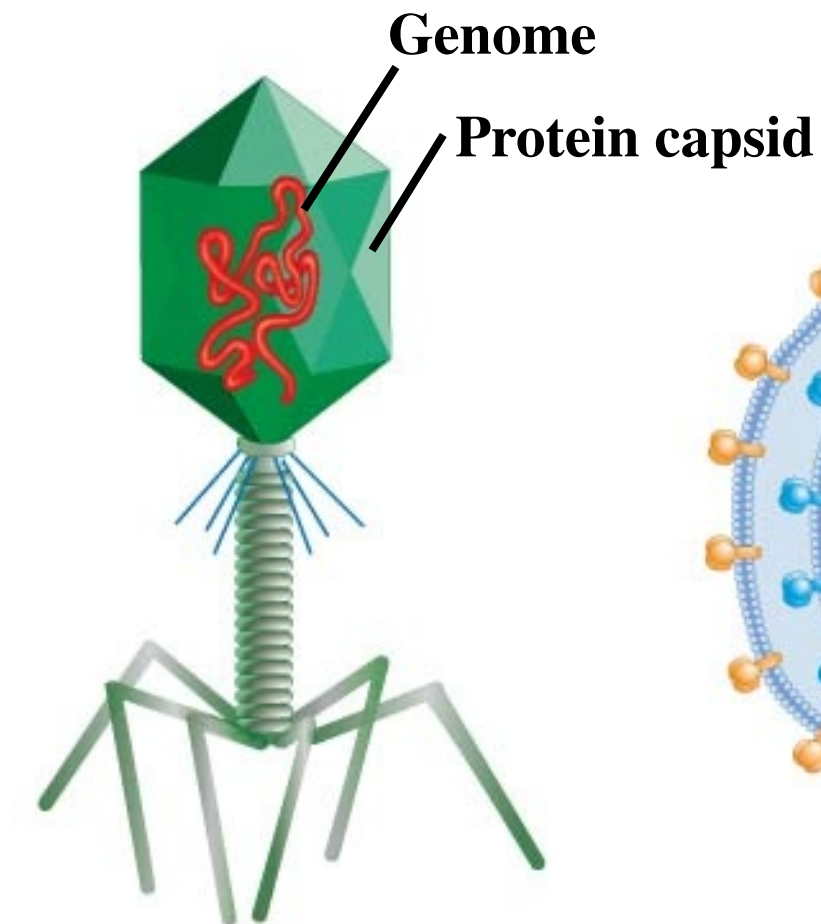
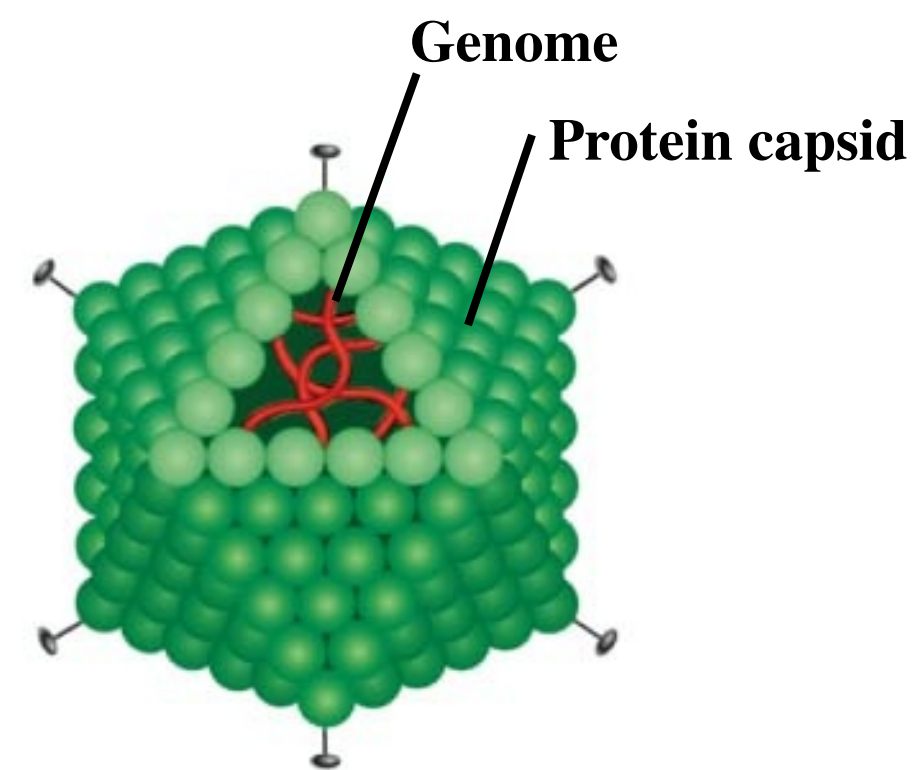
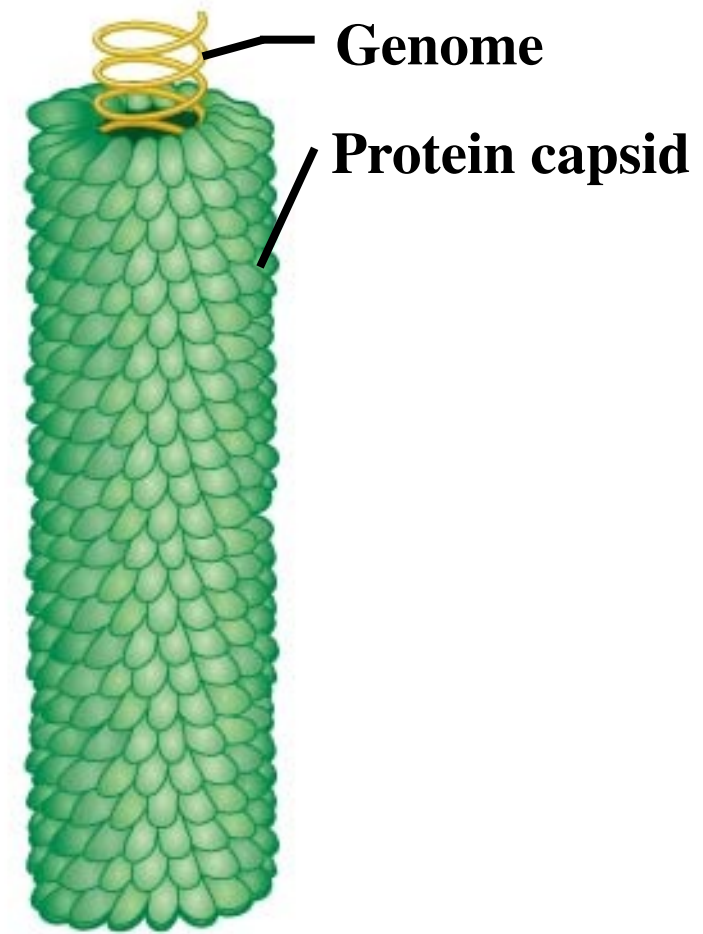
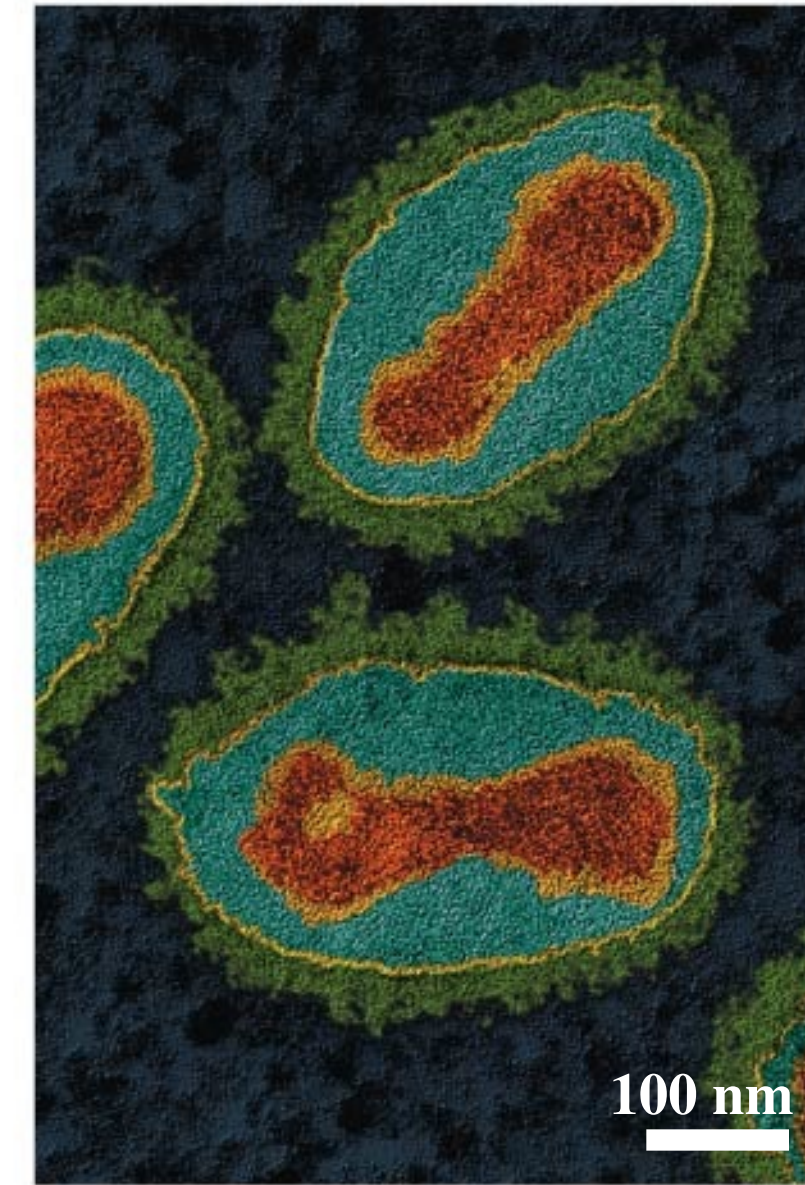
(b) Adenovirus



(c) Bacteriophage T4



(d) Smallpox virus



Introduction

- A **virus** is an obligate, intracellular parasite
- Viruses enter a **host cell** and use the host's biosynthetic machinery to reproduce and synthesize its proteins
- Most biologists would argue that viruses are **not alive**, because they depend on their host cell to satisfy the key attributes of life

Math

How long after recovering from COVID-19
do you continue to exhale virus particles?

CDC Yearly Lab Work on Flu Viruses

More than 1 million patient specimens are tested in clinical labs participating in CDC domestic disease surveillance.*

About 100,000 specimens are tested in 93 state/local public health labs.

CDC conducts full genetic sequencing on about 7,000 flu viruses each year.

CDC tests about 2,000 flu viruses to determine their immune properties.

CDC prepares as many as 50 viruses for possible use in vaccine production.

*2017-2018 influenza data as reported by CDC's Influenza Division, National Center for Immunization and Respiratory Diseases (NCIRD)



What you want to talk about next?

- A. Influenza, 1918, and the Spanish Flu pandemic
- B. SARS-CoV-2, 2020, and COVID-19 disease pandemic

16.3 Non-Mendelian genetics: Why do we need annual flu vaccines?

Biology Learning Objectives

- Explain why we need annual flu vaccines and how that relates to information.
- Distinguish viral mechanisms for genetic diversity from cellular mechanisms.

?

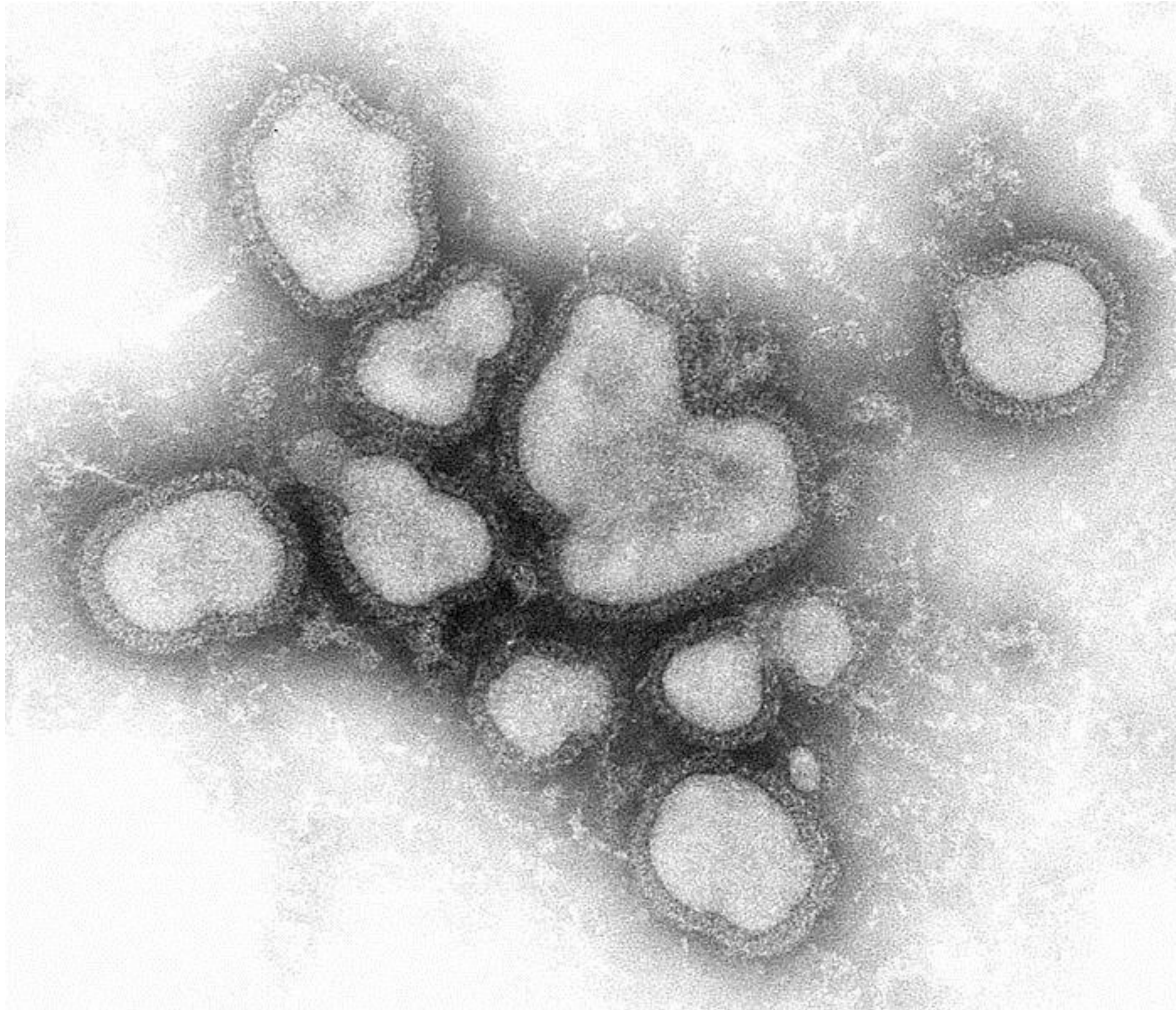
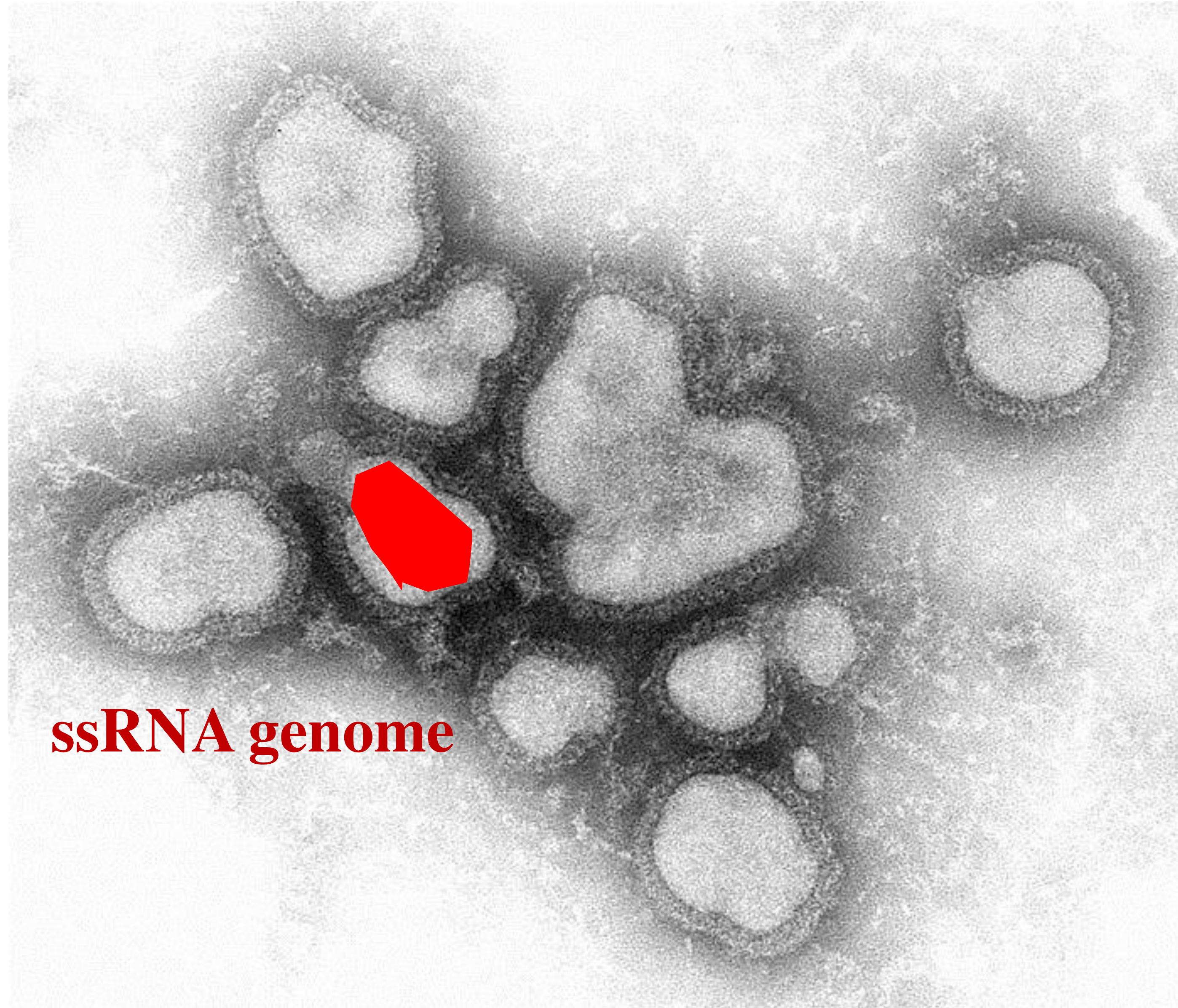


Figure 16.12

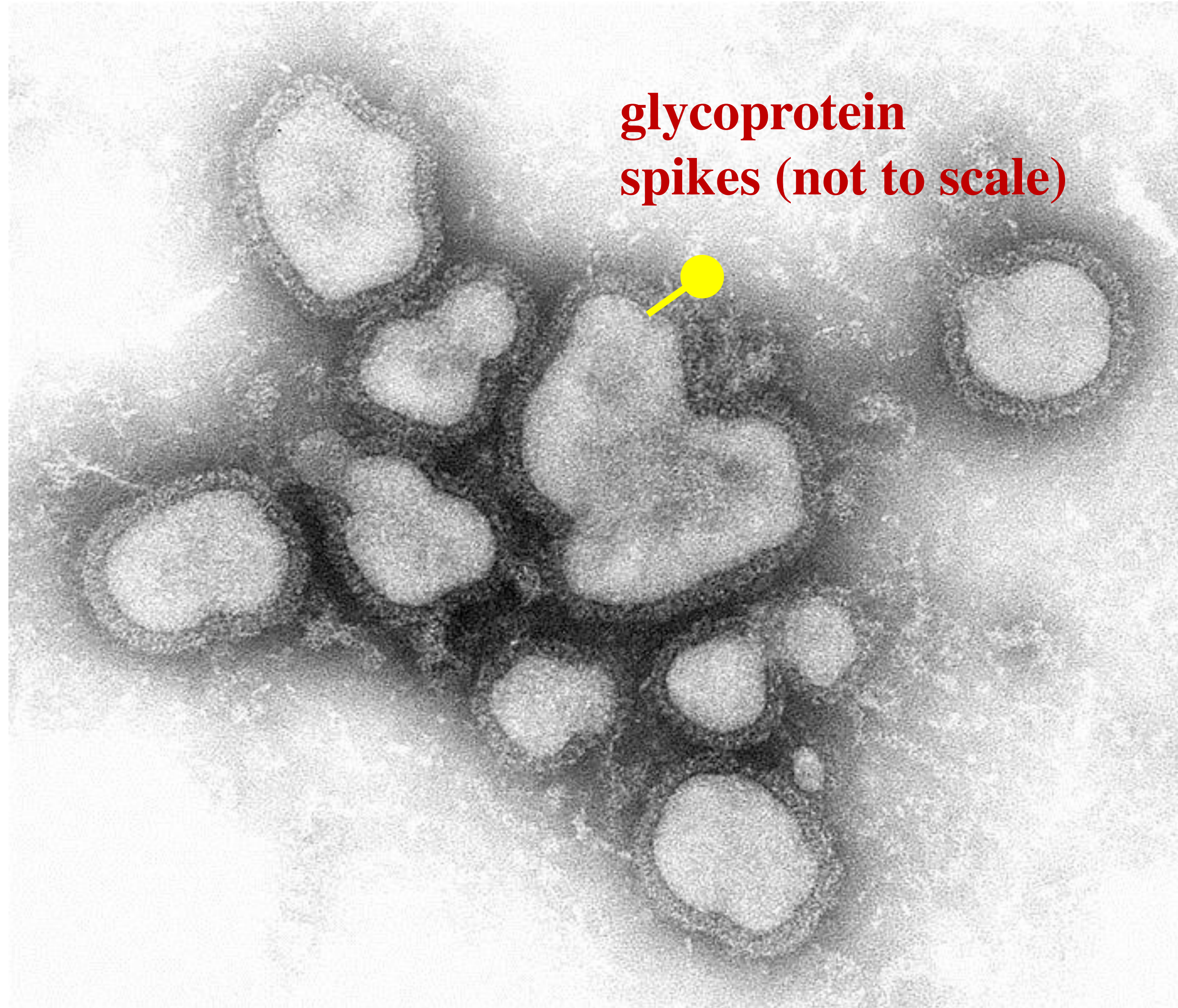
Image from CDC. Public Domain.

Influenza A Virus



ssRNA genome

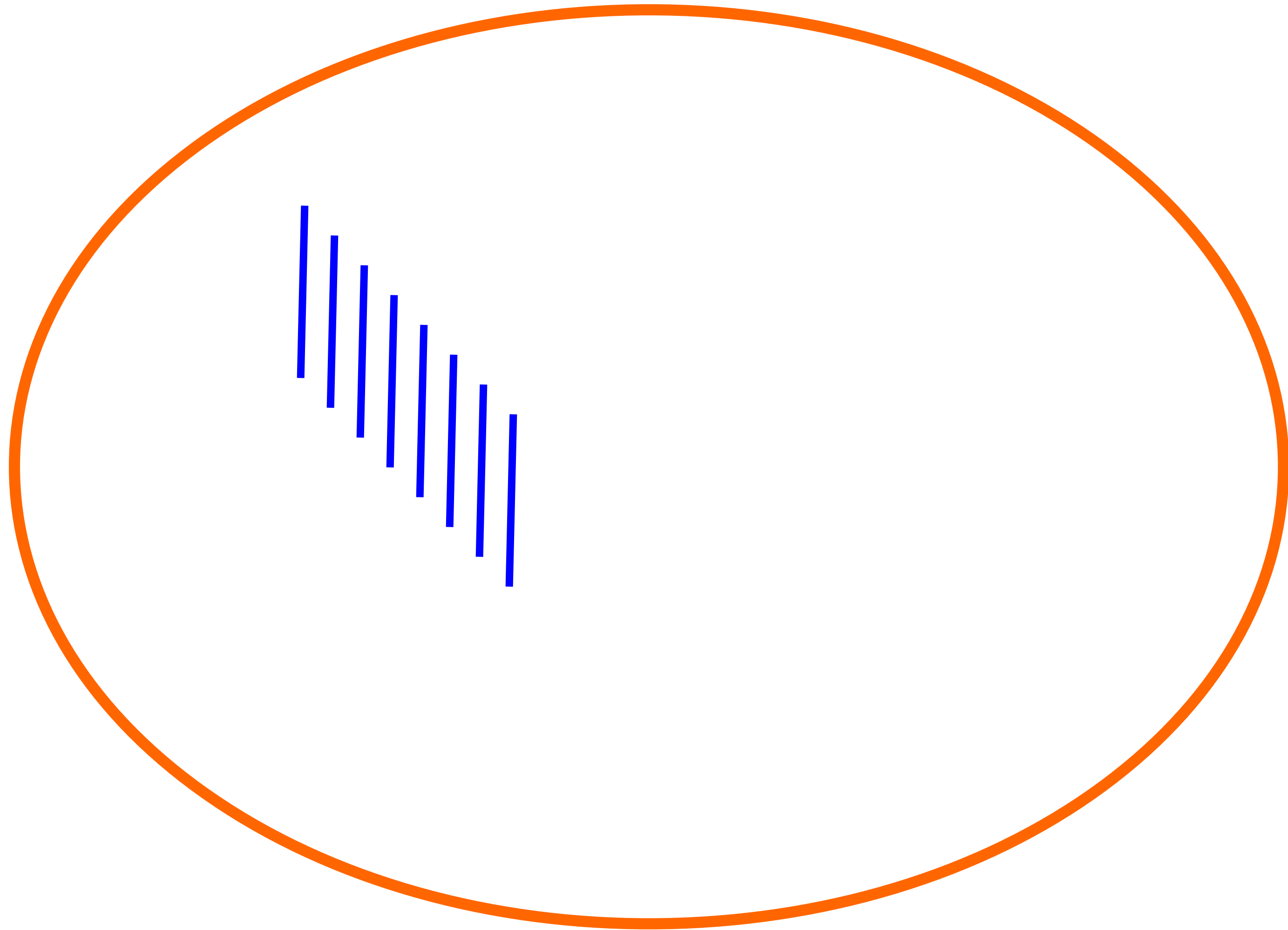
Influenza A Virus



Some Emerging Viruses Arise from Genome Reassortment

- **Influenza** has a single-stranded RNA genome consisting of eight segments
 - Most segments encode only one protein
- If two viruses infect the same cell, replicated genomic segments are randomly shuffled
 - Progeny often have segments from each parent virus

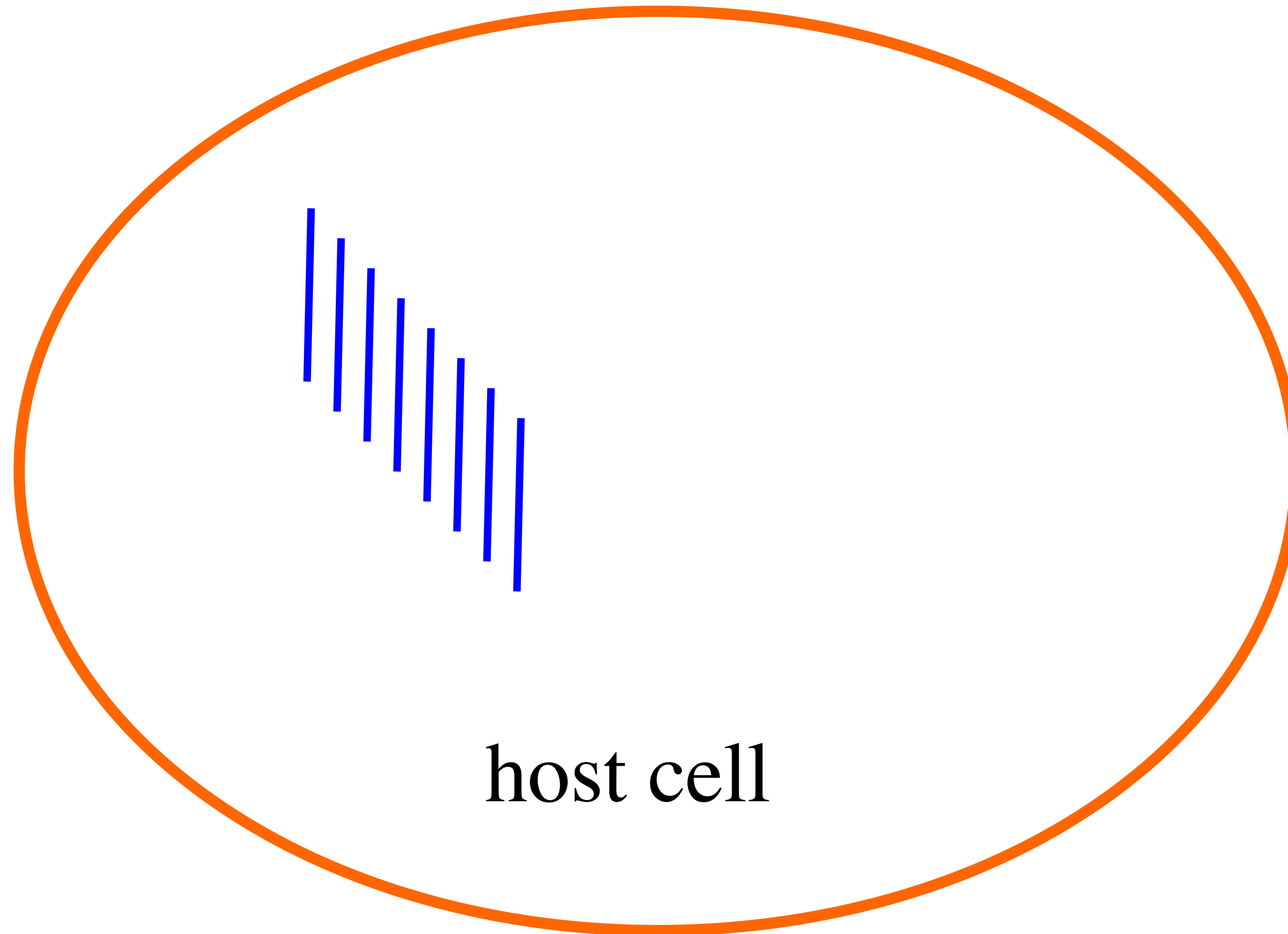
?



Recombination of Genomes

virus #1 infects a cell

?

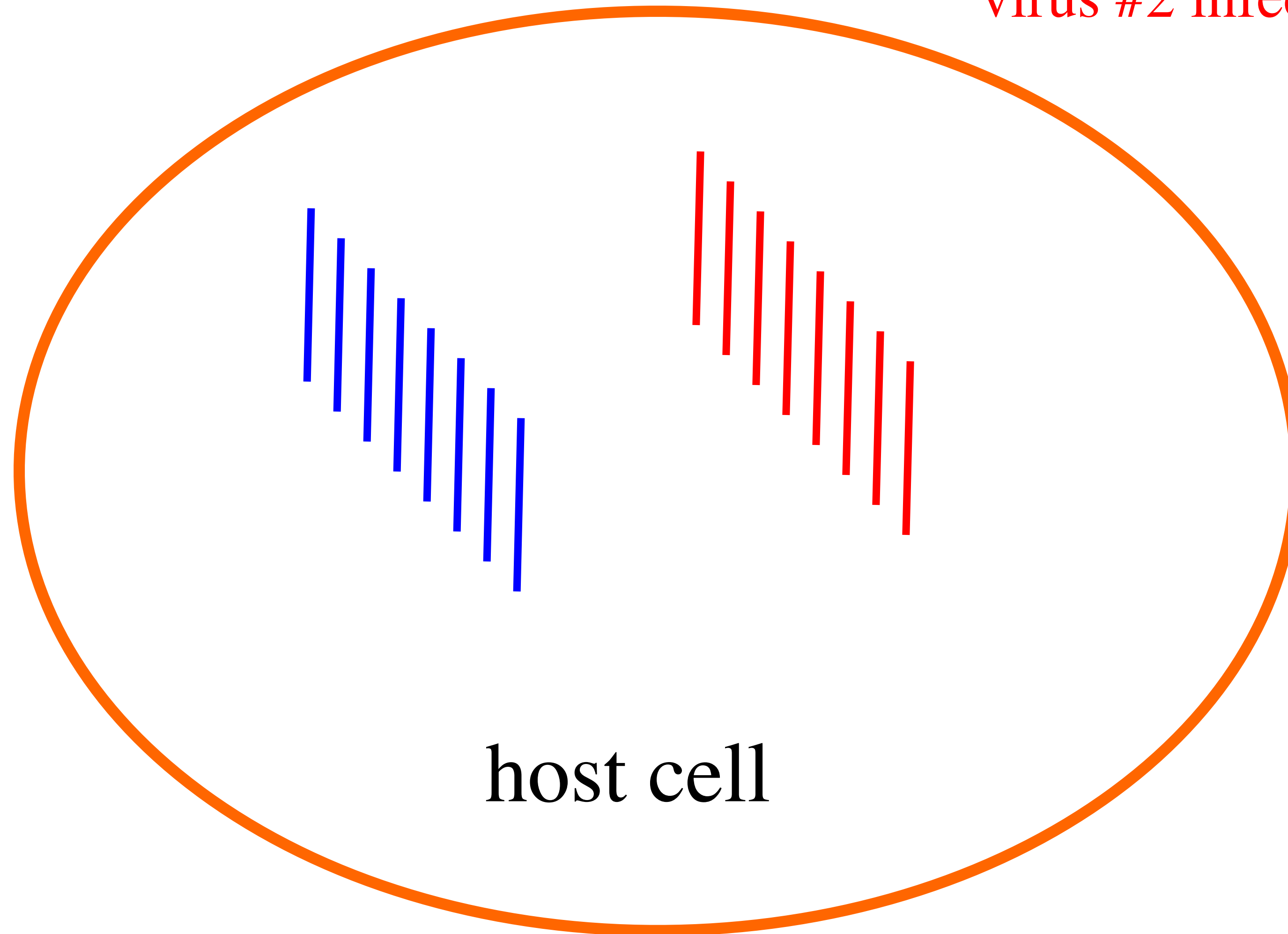


Extra Figure

Recombination of Genomes

virus #1 infects a cell

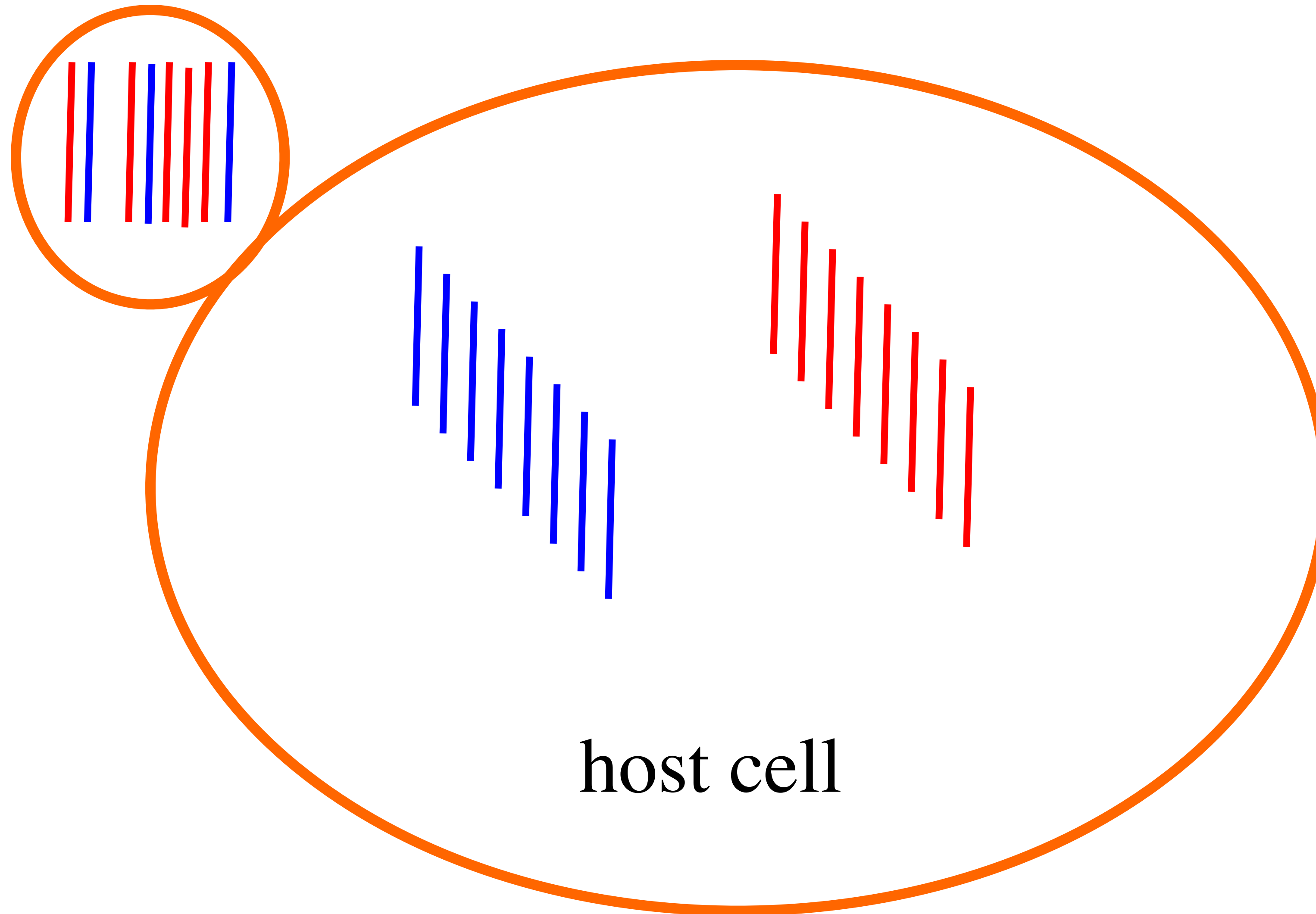
virus #2 infects a cell



Extra Figure

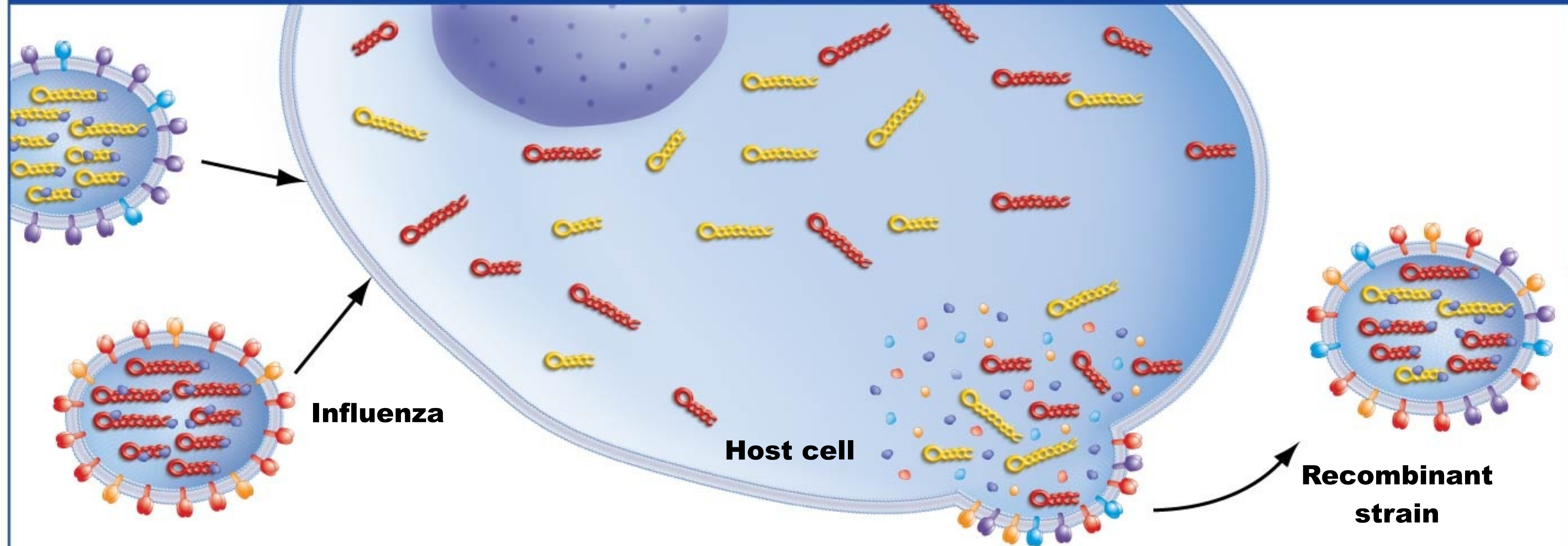
Recombination of Genomes

new virus buds with novel combination of ssRNA chromosomes



Extra Figure

PROCESS: GENOMIC REASSORTMENT GENERATES NEW INFLUENZA STRAINS

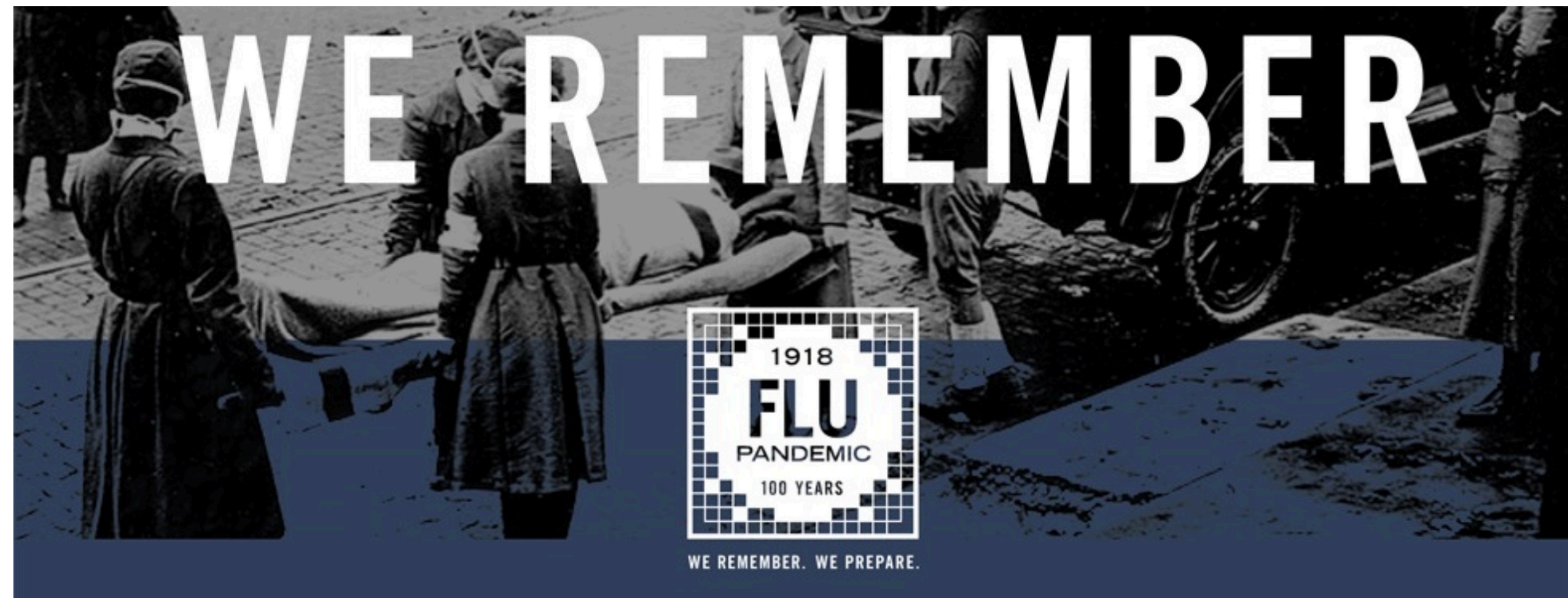


1. Two different strains of influenza infect the same cell.

2. Replication produces a mix of strain-specific genomic segments inside host.

3. Reassortment of segments generates new, recombinant strains.

The 1918 influenza pandemic occurred in three waves and was the most severe pandemic in history.



**FIRST
WAVE
SPRING
1918**



The first outbreak of flu-like illnesses was detected in the U.S. in March, with more than 100 cases reported at Camp Funston in Fort Riley, Kansas.



During 1918, the U.S. was engaged in WWI. Hundreds and thousands of U.S. soldiers traveled across the

Atlantic to deploy for war. The mass troop movement contributed to the global spread of flu.

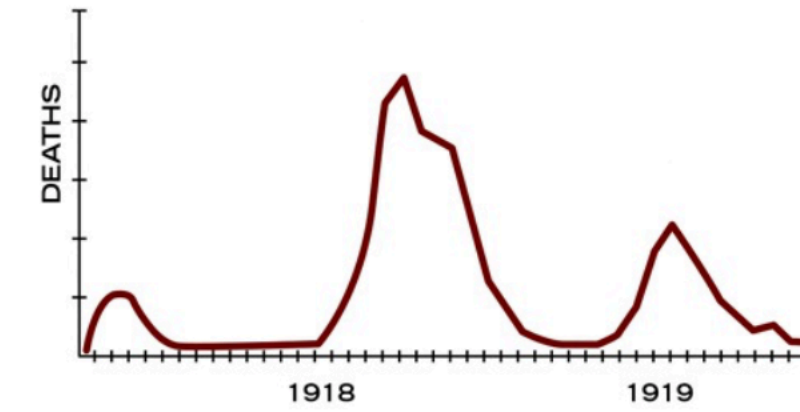
More people died during the 1918 pandemic than the total number of military and civilian deaths that resulted from World War I.

SECOND WAVE

FALL 1918



In 1918, many health professionals served in the U. S. military during WWI, resulting in shortages of medical personnel around the U.S. The economy suffered as businesses and factories were forced to close due to sickness amongst workers.



There were 3 different waves of illness during the pandemic, starting in March 1918 and subsiding by summer of 1919. The pandemic peaked in the U.S. during the second wave, in the fall of 1918. This highly fatal second wave was responsible for most of the U.S. deaths attributed to the pandemic.

THIRD WAVE

WINTER 1918

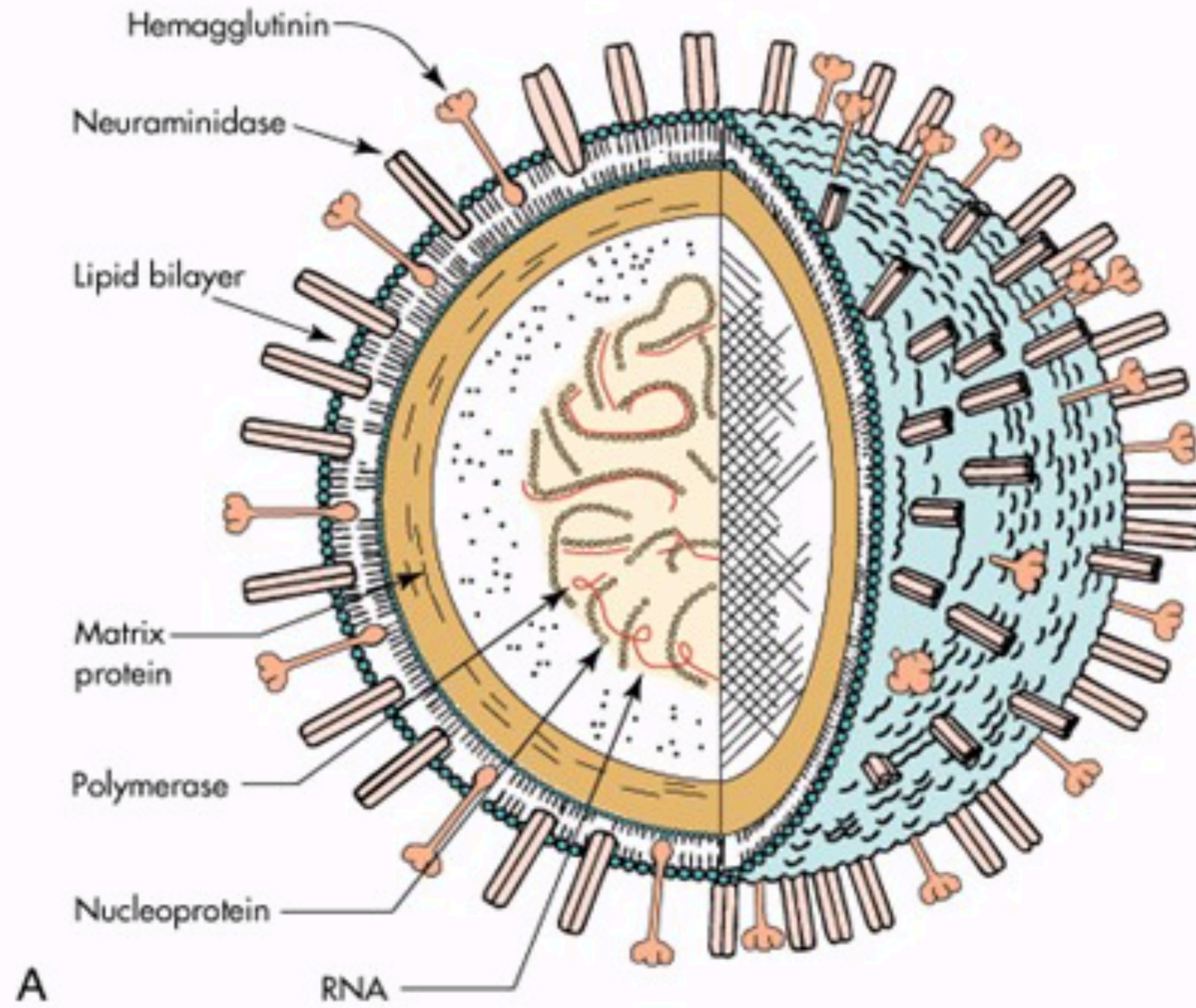


The Motor Corps of St. Louis chapter of the American Red Cross on ambulance duty during the influenza epidemic, October 1918.

A third wave of illness occurred during the winter and spring of 1919, adding to the pandemic death toll. The third wave of the pandemic subsided during the summer of 1919.

An estimated 1/3 of the world's population was infected with the 1918 flu virus – resulting in at least 50 million deaths worldwide.

Influenza Virion



A



B

Influenza Virus

- ✦ **RNA, enveloped**

- ✦ **Viral family**
Orthomyxoviridae

- ✦ **Size:**

80-200nm or .08 – 0.12 μm
(micron) in diameter

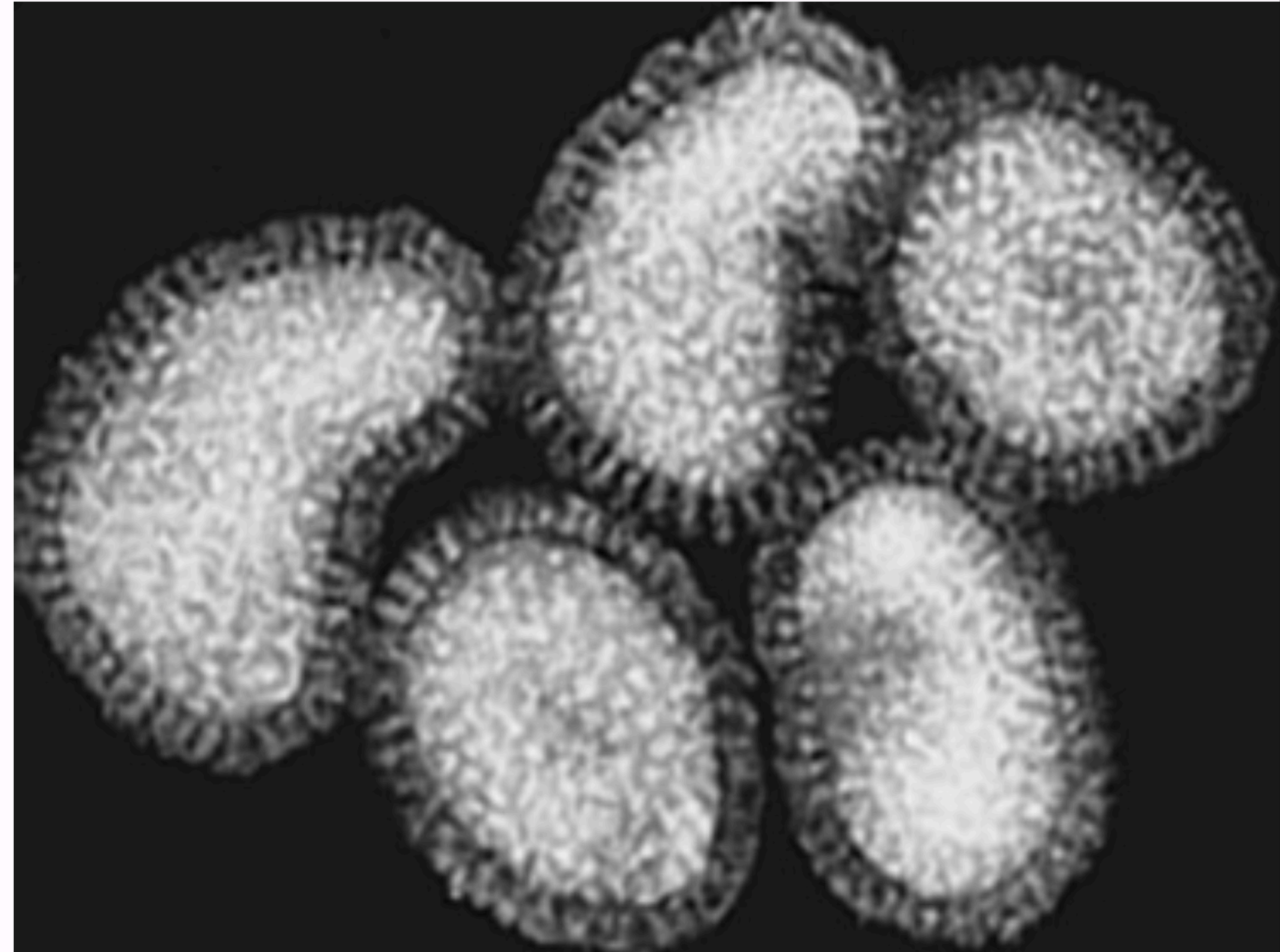
- ✦ **Three types**

- ✦ A, B, C

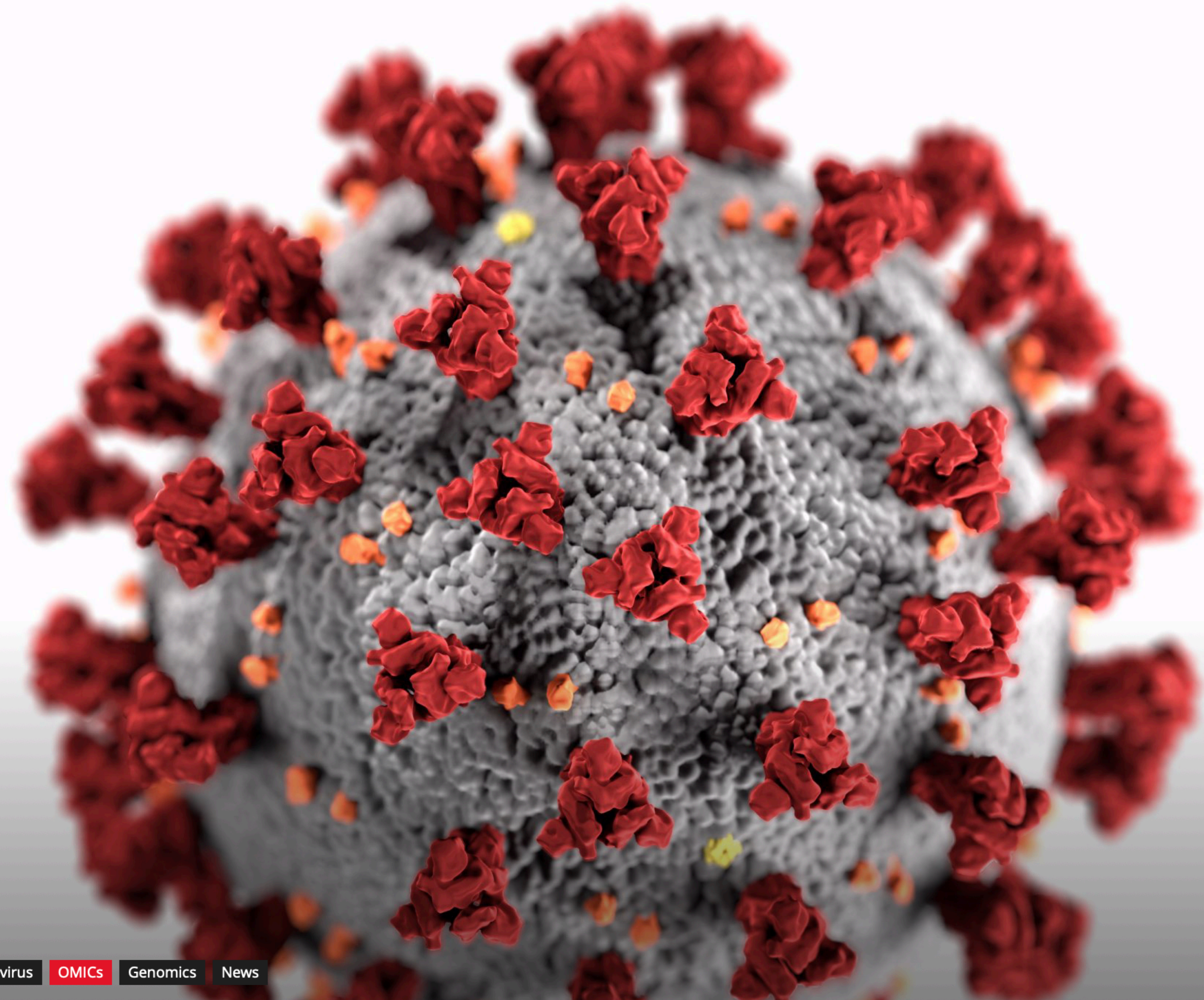
- ✦ **Surface antigens**

- ✦ H (haemagglutinin)

- ✦ N (neuraminidase)

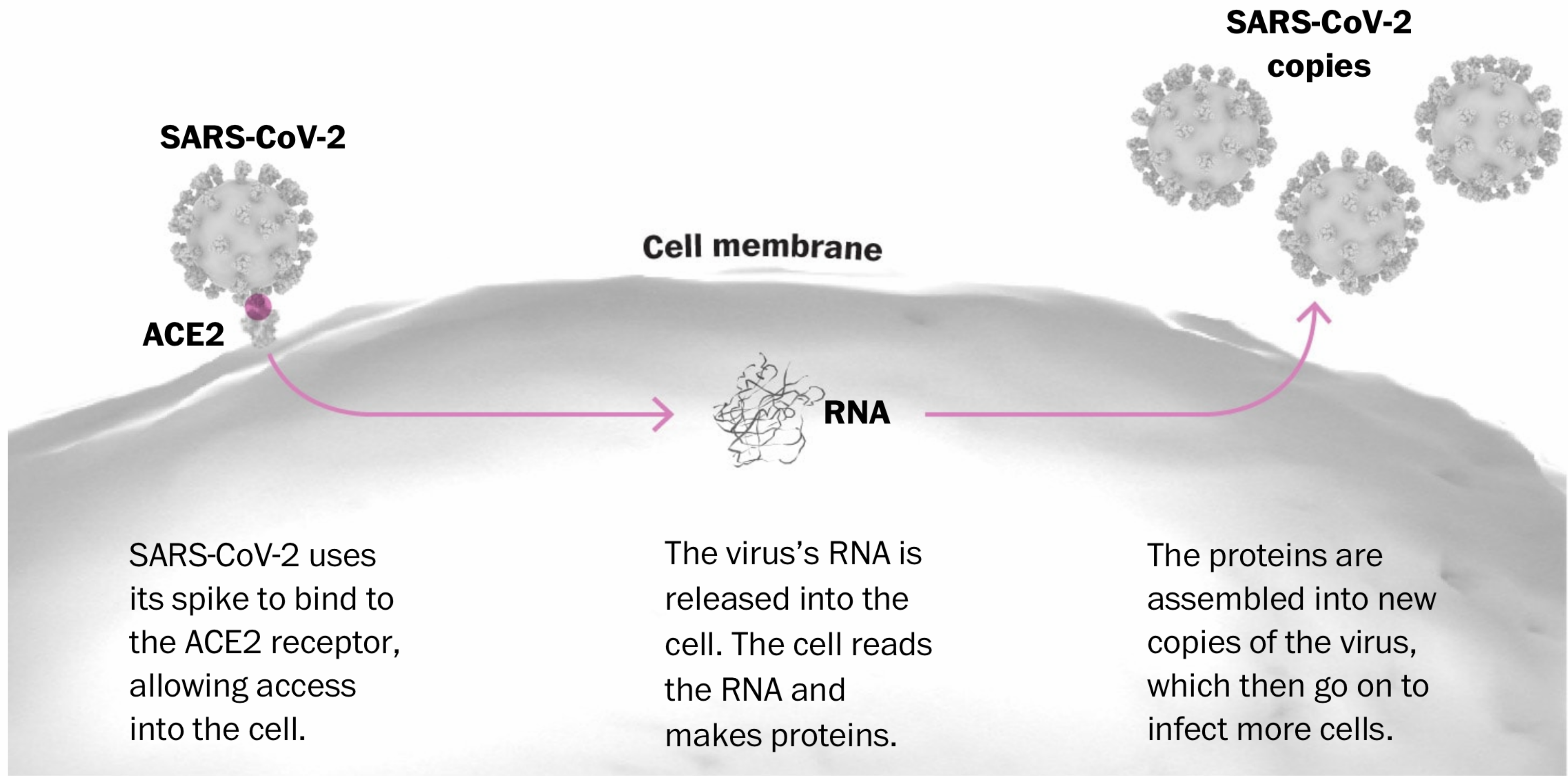


Credit: L. Stammard, 1995





<https://vimeo.com/414984186>



SARS-CoV-2 uses its spike to bind to the ACE2 receptor, allowing access into the cell.

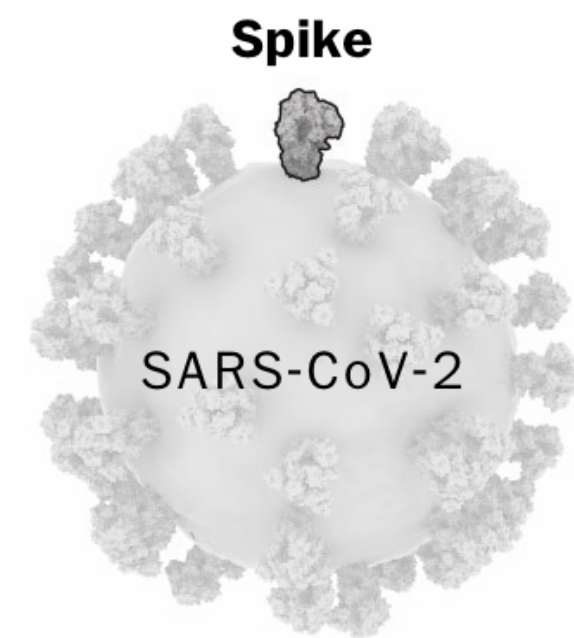
The virus's RNA is released into the cell. The cell reads the RNA and makes proteins.

The proteins are assembled into new copies of the virus, which then go on to infect more cells.

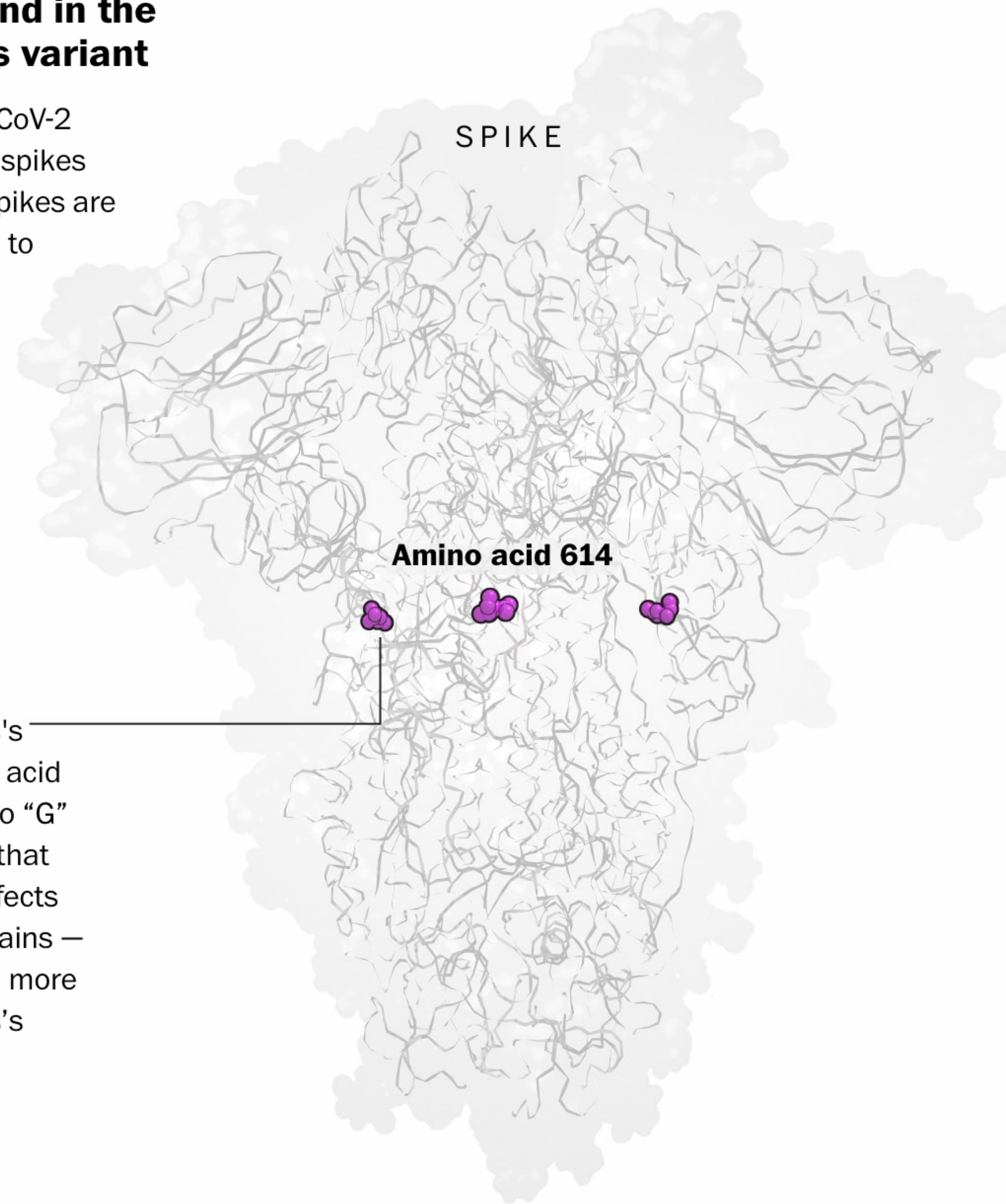
AARON STECKELBERG/THE WASHINGTON POST

The tiny mutation found in the dominant coronavirus variant

Like all coronaviruses, SARS-CoV-2 has a series of characteristic spikes surrounding its core. These spikes are what allow the virus to attach to human cells.



A mutation affecting the virus's spike protein changed amino acid 614 from "D" (aspartic acid) to "G" (glycine). Research suggests that this small change — which affects three identical amino acid chains — might make the spike protein more effective, enhancing the virus's infectiousness.



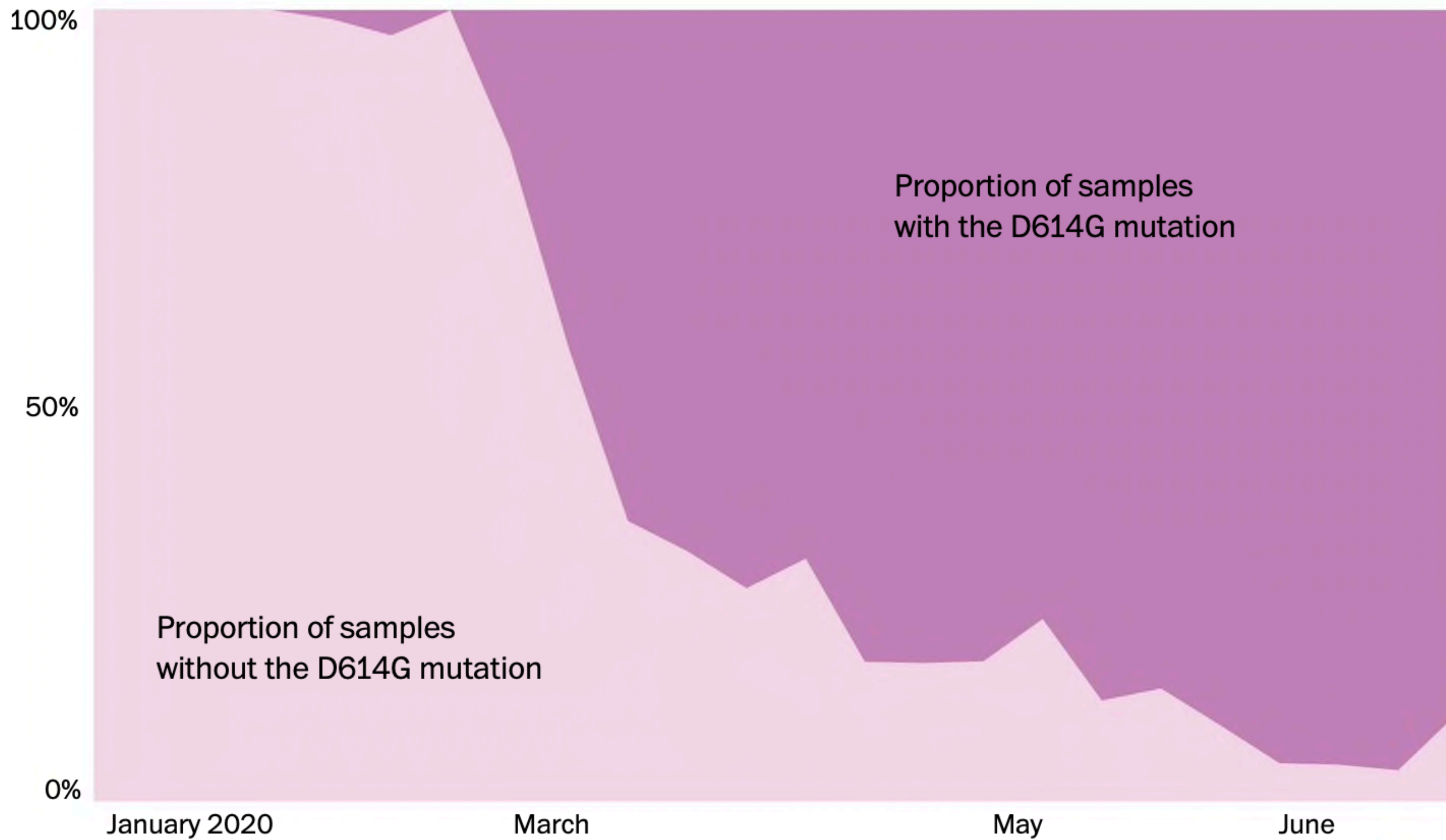
Source: GISAID, Post reporting

AARON STECKELBERG/THE WASHINGTON POST

Spike protein mutation takes over

A mutation in the spike protein of the SARS-CoV-2 virus changes just one amino acid in a chain of about 1,300, but it might make a difference in how the virus attacks human cells. The mutation (called D614G), which first appeared in January, is found in what has become the dominant variant of the coronavirus.

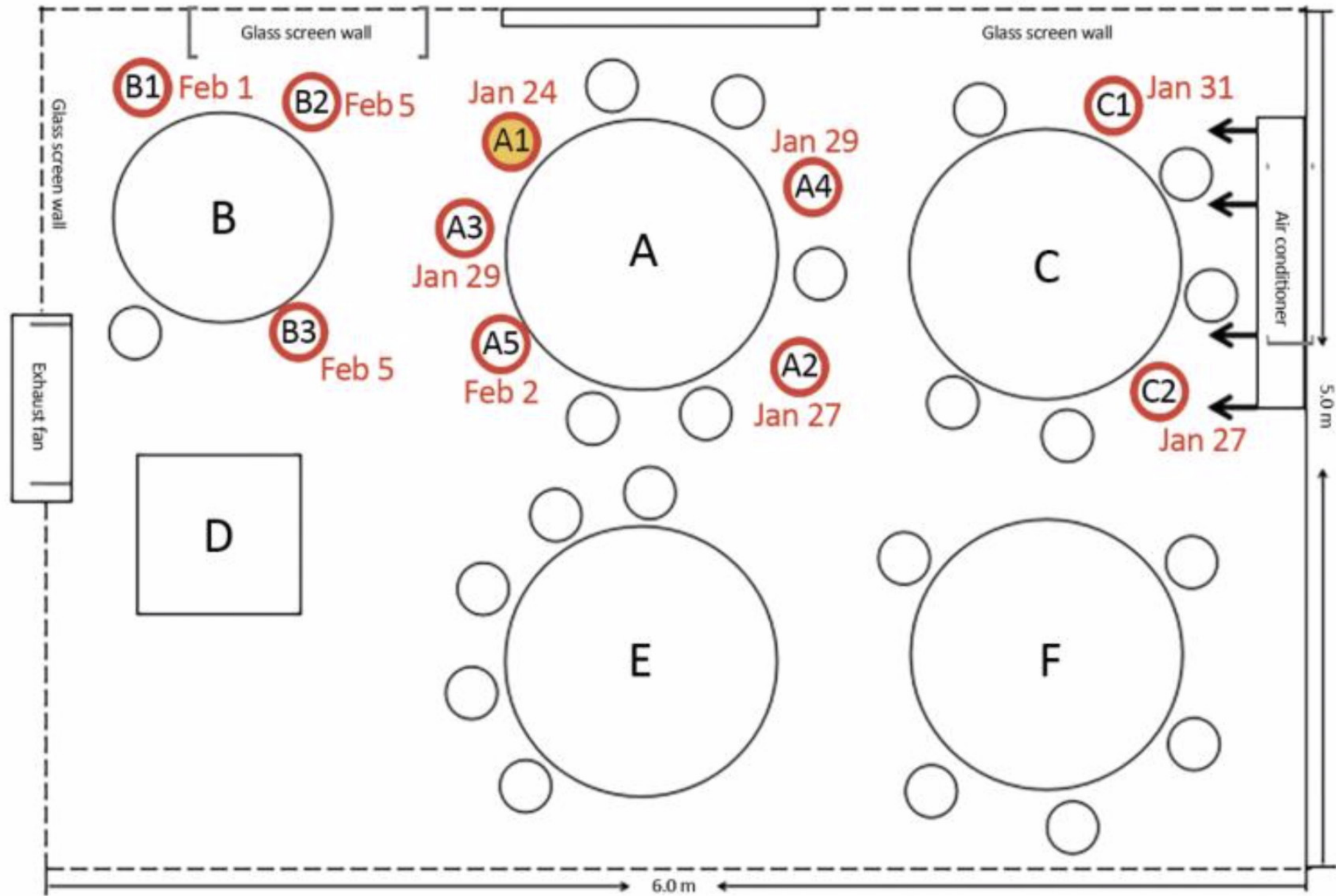
New weekly samples in Nextstrain's global subset of GISAID samples



Data includes 3,006 samples acquired June 24.

Source: Nextstrain, GISAID

JOE FOX/THE WASHINGTON POST



during January 28–February 6, 2020, and intravenous immunoglobulin therapy (20 g/d) during January 28–February 1. In addition, we administered glucocorticoid therapy with methylprednisolone (20–60 mg 2×/d by intravenous drip) during January 29–February 1. The patient's fever abated on January 29. He tested negative for SARS-CoV-2 on February 4 and again on February 6. During the progression of his recovery, we observed gradual reduction of the white patches in the lung caused by SARS-CoV-2 infection (Appendix Figure 2). On January 28 and January 31, we observed multiple ground-glass-like high-density shadows on both lungs with blurred edges and interstitial changes. On February 3, high-density shadows were slightly absorbed in the upper lobe of the bilateral lungs. On February 6, some lesions in the lower lobe of both lungs were slightly absorbed, and we observed the same situation on February 8. The index patient was discharged to home on February 9.

In summary, our epidemiologic study demonstrates asymptomatic and human-to-human transmission of SARS-CoV-2 infection through close contacts in both familial and hospital settings. In addition, the laboratory test results, together with course of medical therapies described, can provide a practical reference for COVID-19 diagnosis and treatment.

About the Author

Dr. Li specializes in infectious diseases and works as a clinical doctor at the Department of Infectious Disease at the Affiliated Hospital of Xuzhou Medical University, Xuzhou, Jiangsu Province, China. His primary research interests included clinical microbiologic detection and emerging infectious diseases.

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COVID-19 Outbreak Associated with Air Conditioning in Restaurant, Guangzhou, China, 2020

Jianyun Lu,¹ Jieni Gu,¹ Kuibiao Li,¹ Conghui Xu,¹ Wenzhe Su, Zhisheng Lai, Deqian Zhou, Chao Yu, Bin Xu, Zhicong Yang

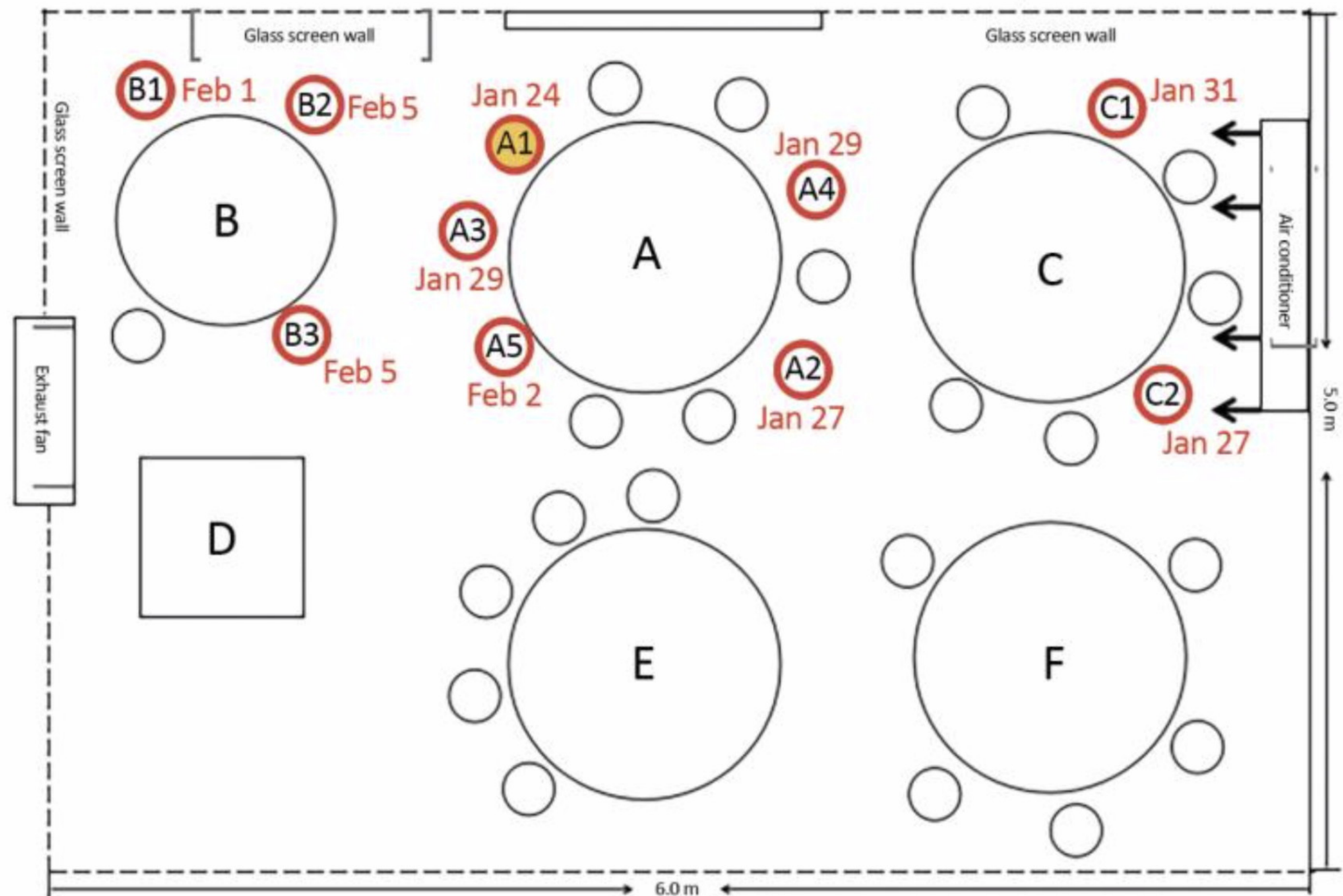
Author affiliations: Guangzhou Center for Disease Control and Prevention, Guangzhou, China (J. Lu, K. Li, C. Xu, W. Su, C. Yu, Z. Yang); Guangzhou Yuexiu District Center for Disease Control and Prevention, Guangzhou, China (J. Gu, Z. Lai, D. Zhou, B. Xu)

DOI: <https://doi.org/10.3201/eid2607.200764>

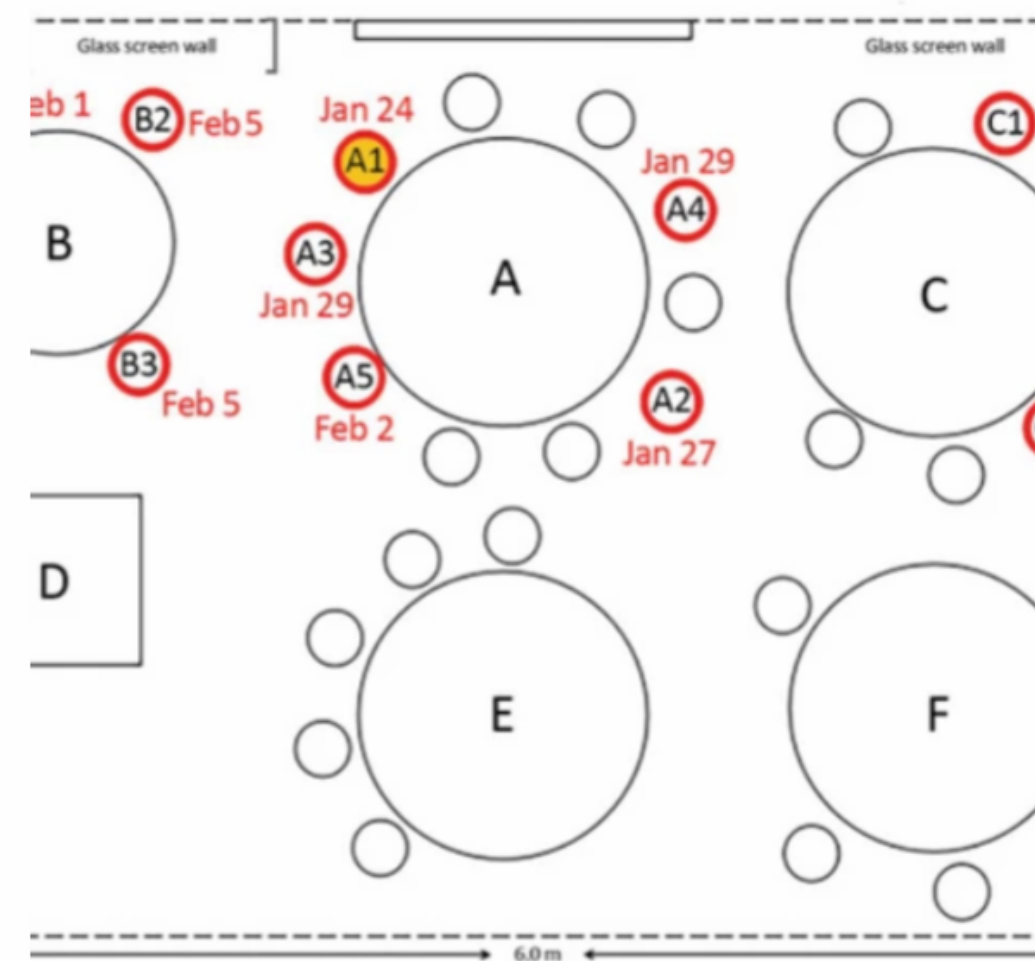
During January 26–February 10, 2020, an outbreak of 2019 novel coronavirus disease in an air-conditioned restaurant in Guangzhou, China, involved 3 family clusters. The airflow direction was consistent with droplet transmission. To prevent the spread of the virus in restaurants, we recommend increasing the distance between tables and improving ventilation.

From January 26 through February 10, 2020, an outbreak of 2019 novel coronavirus disease (COVID-19) affected 10 persons from 3 families (families A–C)

¹These authors contributed equally to this article.



Restaurants: Some really great shoe-leather epidemiology demonstrated clearly the effect of a single asymptomatic carrier in a restaurant environment (see below). The infected person (A1) sat at a table and had dinner with 9 friends. Dinner took about 1 to 1.5 hours. During this meal, the asymptomatic carrier released low-levels of virus into the air from their breathing. Airflow (from the restaurant's various airflow vents) was from right to left. Approximately 50% of the people at the infected person's table became sick over the next 7 days. 75% of the people on the adjacent downwind table became infected. And even 2 of the 7 people on the upwind table were infected (believed to happen by turbulent airflow). No one at tables E or F became infected, they were out of the main airflow from the air conditioner on the right to the exhaust fan on the left of the room. ([Ref](#))





Absence of Apparent Transmission of SARS-CoV-2 from Two Stylists After Exposure at a Hair Salon with a Universal Face Covering Policy — Springfield, Missouri, May 2020

M. Joshua Hendrix, MD¹; Charles Walde, MD²; Kendra Findley, MS³; Robin Trotman, DO⁴

On July 14, 2020, this report was posted as an MMWR Early Release on the MMWR website (<https://www.cdc.gov/mmwr>).

On May 12, 2020 (day 0), a hair stylist at salon A in Springfield, Missouri (stylist A), developed respiratory symptoms and continued working with clients until day 8, when the stylist received a positive test result for SARS-CoV-2, the virus that causes coronavirus disease 2019 (COVID-19). A second hair stylist (stylist B), who had been exposed to stylist A, developed respiratory symptoms on May 15, 2020 (day 3), and worked with clients at salon A until day 8 before seeking testing for SARS-CoV-2, which returned a positive result on day 10. A total of 139 clients were directly serviced by stylists A and B from the time they developed symptoms until they took leave from work. Stylists A and B and the 139 clients followed the City of Springfield ordinance* and salon A policy recommending the use of face coverings (i.e., surgical masks, N95 respirators,[†] or cloth face coverings) for both stylists and clients during their interactions. Other stylists at salon A who worked closely with stylists A and B were identified, quarantined, and monitored daily for 14 days after their last exposure to stylists A or B. None of these stylists reported COVID-19 symptoms. After stylist B received a positive test result on day 10, salon A closed for 3 days to disinfect frequently touched and contaminated areas. After public health contact tracings and 2 weeks of follow-up, no COVID-19 symptoms were identified among the 139 exposed clients or their secondary contacts. The citywide ordinance and company policy might have played a role in preventing spread of SARS-CoV-2 during these exposures. These findings support the role of source control in preventing transmission and can inform the development of public health policy during the COVID-19 pandemic. As stay-at-home orders are lifted, professional and social interactions in the community will present more opportunities for spread of SARS-CoV-2. Broader implementation of masking policies could

was recommended after testing on day 6, stylist A continued to work until the test returned a positive result, at which time stylist A was excluded from work by salon A. On day 3, after working with stylist A, stylist B developed respiratory symptoms. During Stylist A's symptomatic period, the two stylists interacted while neither was masked during intervals between clients. Stylist B worked from day 3 to day 8 while symptomatic before self-isolating and seeking PCR testing, which returned a positive result for SARS-CoV-2 on day 10. Stylist A worked with clients for 8 days while symptomatic, as did stylist B for 5 days. During all interactions with clients at salon A, stylist A wore a double-layered cotton face covering, and stylist B wore a double-layered cotton face covering or a surgical mask.

The Greene County Health Department (Missouri) conducted contact tracing for all 139 exposed clients back to the dates that stylists A and B first developed symptoms. The 139 clients were monitored after their last exposure at salon A. Clients were asked to self-quarantine for 14 days and were called or sent daily text messages to inquire about any symptoms; none reported signs or symptoms of COVID-19. Testing was offered to all clients 5 days after exposure, or as soon as possible for those exposed >5 days before contact tracing began. Overall, 67 (48.2%) clients volunteered to be tested, and 72 (51.8%) refused; all 67 nasopharyngeal swab specimens tested negative for SARS-CoV-2 by PCR. Telephone interviews were attempted 1 month after initial contact tracings to collect supplementary information. Among the 139 exposed clients, the Greene County Health Department interviewed 104 (74.8%) persons.

Among the 139 clients, the mean age was 52 years (range = 21–93 years); 79 clients (56.8%) were male (Table 1). Salon appointments ranged from 15 to 45 minutes in length (median = 15 minutes; mean = 19.5 minutes). Among the 104 interviewed clients, 102 (98.1%) reported wearing face coverings for their entire appointment, and two (1.9%) reported



TABLE 1. Characteristics* of clients (N = 139) who visited hair salon A and were exposed to stylists A and B with COVID-19 —Springfield, Missouri, May 2020

Characteristic	Value
Demographic characteristic	
Male, no. (%)	79 (56.8)
Age, yrs. mean (range)	52 (21–93)
Encounter information	
Appointment date range	May 12–20 (days 0–8 [†])
Exposure to stylist A, no. (%)	84 (60.4)
Exposure to stylist B, no. (%)	55 (39.6)
Appointment duration, mins, median (range)	15 (15–45)
Client testing	
Clients tested, no. (%)	67 (48.2)
Negative tests, no. (%) [§]	67 (100)

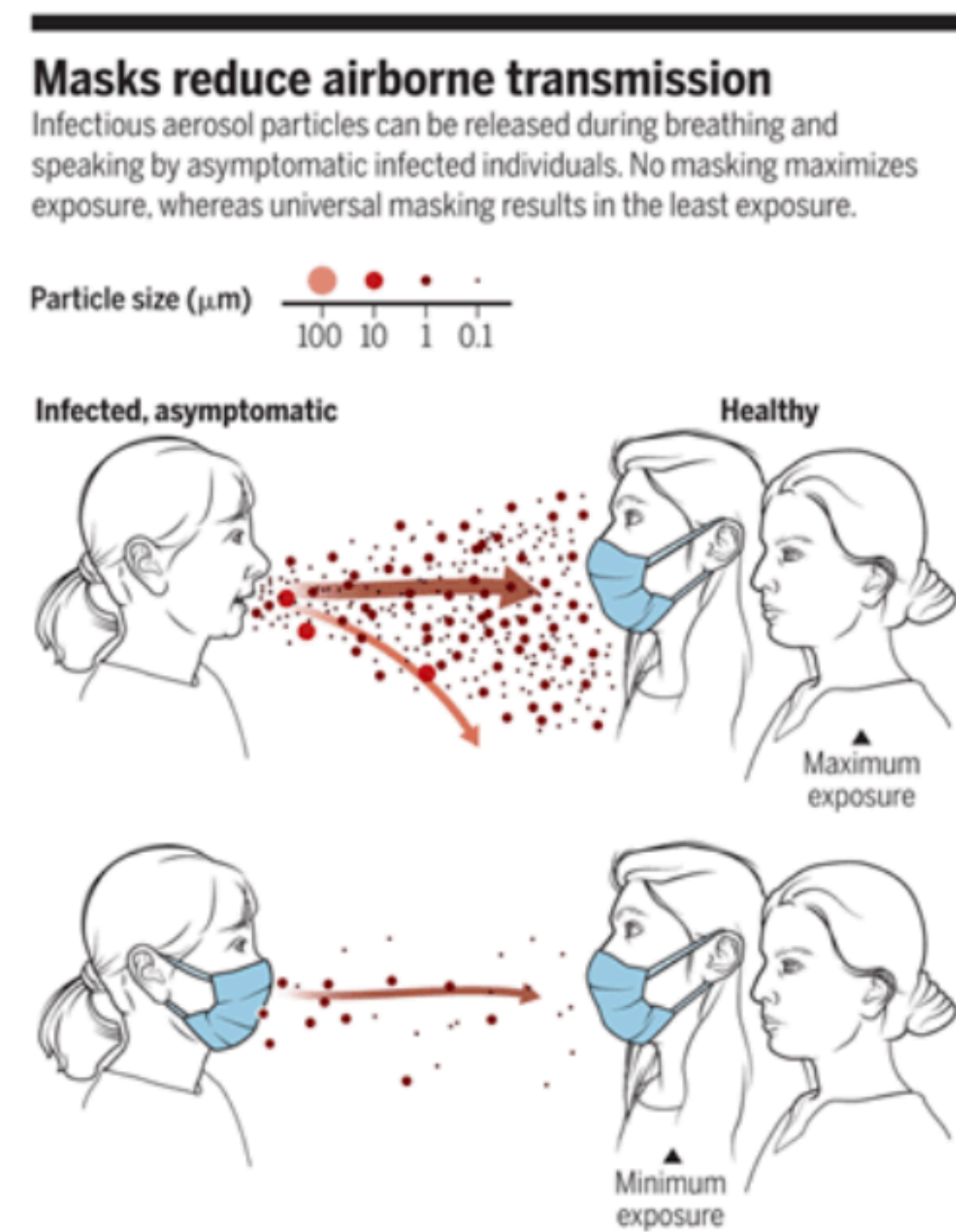
Abbreviation: COVID-19 = coronavirus disease 2019.

* All interviews were conducted via telephone by the Greene County Health Department.

[†] After onset of symptoms in stylist A.

[§] Among those tested.

The U.S. Centers for Disease Control and Prevention (CDC) recommendations for social distancing of 6 feet and hand washing to reduce the spread of SARS-CoV-2 are based on studies of respiratory droplets carried out in the 1930s. These studies showed that large, ~100 μm droplets produced in coughs and sneezes quickly underwent gravitational settling (1). However, when these studies were conducted, the technology did not exist for detecting submicron aerosols. As a comparison, calculations predict that in still air, a 100- μm droplet will settle to the ground from 8 feet in 4.6 s, whereas a 1- μm aerosol particle will take 12.4 hours (4). Measurements now show that intense coughs and sneezes that propel larger droplets more than 20 feet can also create thousands of aerosols that can travel even further (1). Increasing evidence for SARS-CoV-2 suggests the 6 feet CDC recommendation is likely not enough under many indoor conditions, where aerosols can remain airborne for hours, accumulate over time, and follow airflows over distances further than 6 feet (5, 10).



Masks reduce airborne transmission

Infectious aerosol particles can be released during breathing and speaking by asymptomatic infected individuals. No masking maximizes exposure, whereas universal masking results in the least exposure.

GRAPHIC: V. ALTOUNIAN/SCIENCE

A Cough: A single cough releases about 3,000 droplets and droplets travel at 50 miles per hour. Most droplets are large, and fall quickly (gravity), but many do stay in the air and can travel across a room in a few seconds.

A Sneeze: A single sneeze releases about 30,000 droplets, with droplets traveling at up to 200 miles per hour. Most droplets are small and travel great distances (easily across a room).

If a person is infected, the droplets in a single cough or sneeze may contain as many as 200,000,000 (two hundred million) virus particles which can all be dispersed into the environment around them.

A breath: A single breath releases 50 - 5000 droplets. Most of these droplets are low velocity and fall to the ground quickly. There are even fewer droplets released through nose-breathing. Importantly, due to the lack of exhalation force with a breath, viral particles from the lower respiratory areas are not expelled.

Unlike sneezing and coughing which release huge amounts of viral material, the respiratory droplets released from breathing only contain low levels of virus. We don't have a number for SARS-CoV2 yet, but we can use influenza as a guide. *Studies have shown that a person infected with influenza can release up to 33 infectious viral particles per minute.* But I'm going to use 20 to keep the math simple.

Remember the formula: Successful Infection = Exposure to Virus x Time

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