



# VIROLOGY LIVE

WITH VINCENT RACANIELLO

## The Infectious Cycle

Session 2

Virology Live

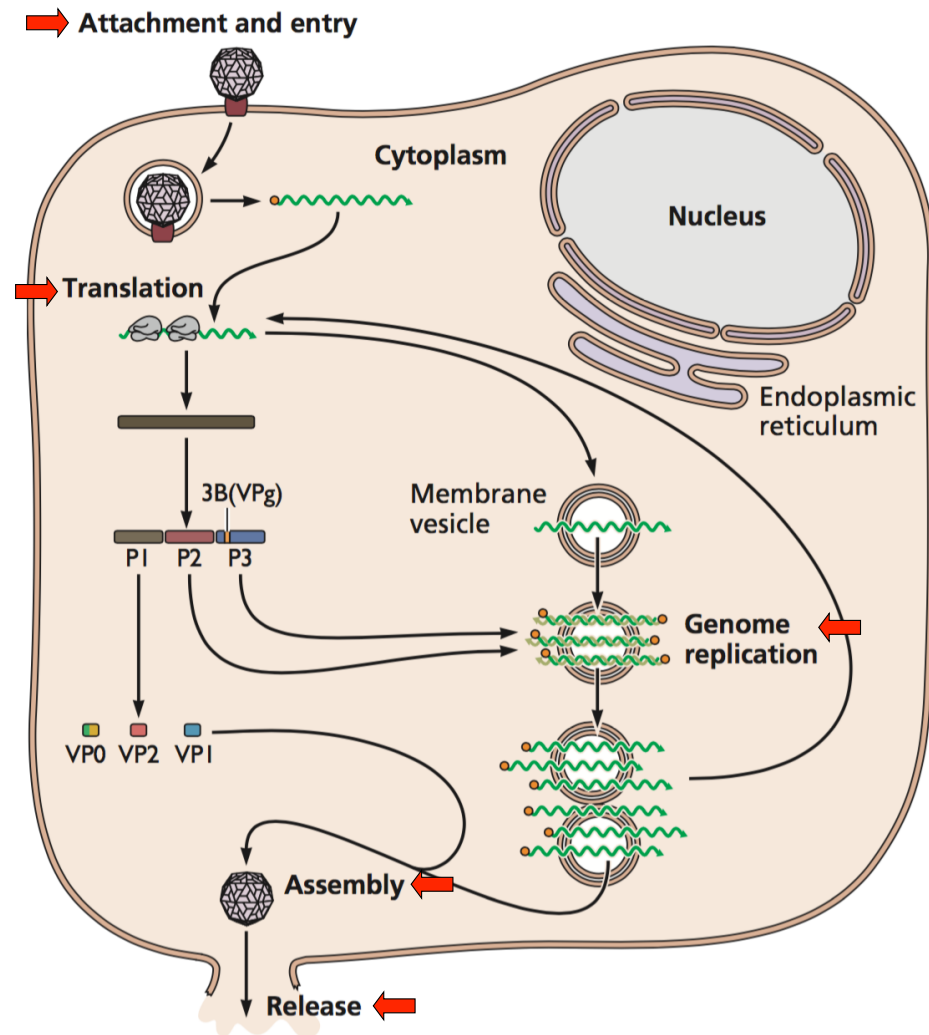
Fall 2021

*"You know my methods, Watson"*

--SIR ARTHUR CONAN DOYLE

# The Infectious Cycle

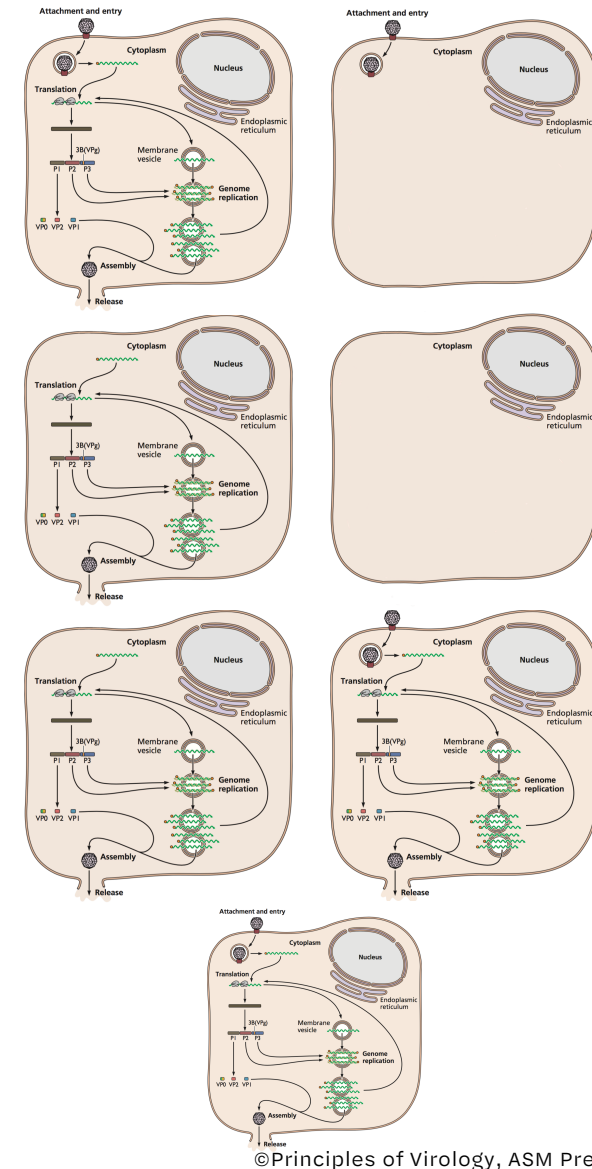
Virologists divide the infectious cycle into steps to facilitate their study, but no such artificial boundaries occur





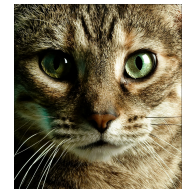
## Some important definitions

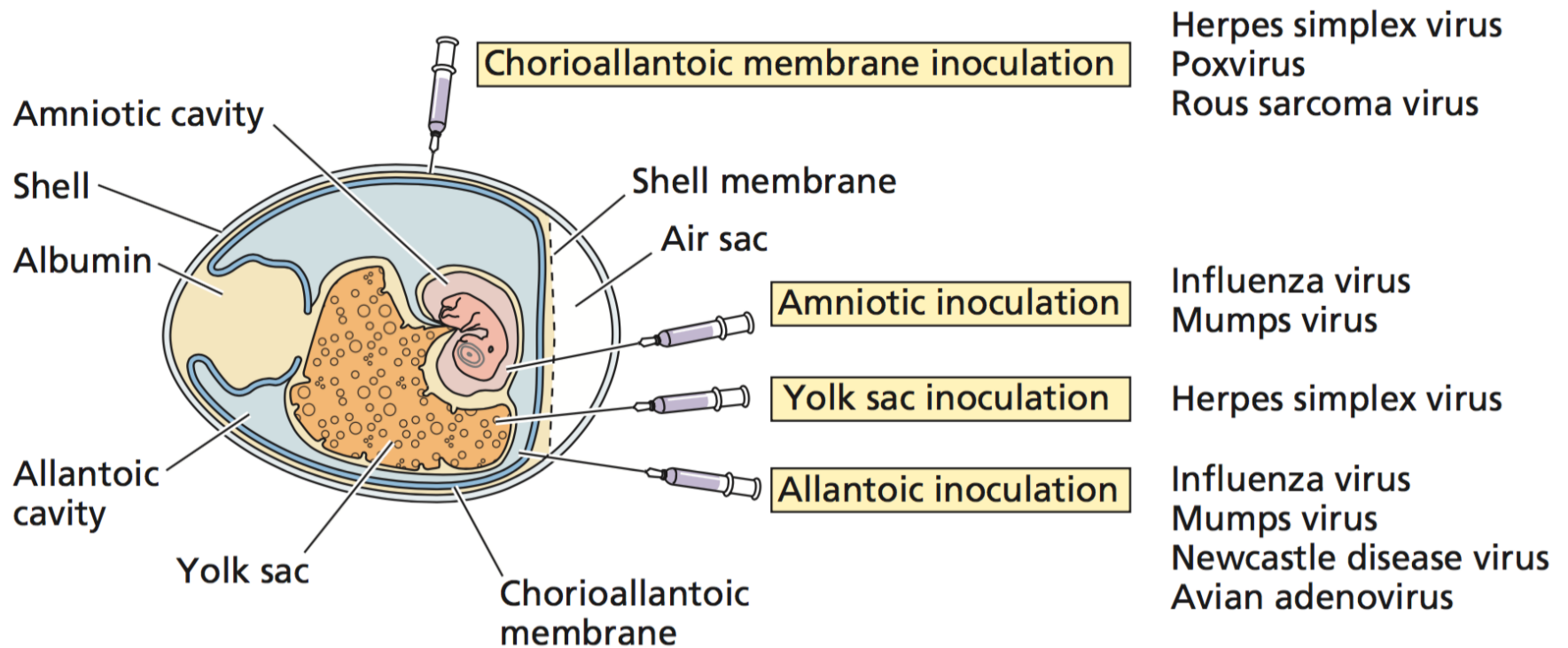
- A **susceptible** cell has a functional receptor for a given virus - *the cell may or may not be able to support viral replication*
- A **resistant** cell has no receptor - *it may or may not be competent to support viral replication*
- A **permissive** cell has the capacity to replicate virus - *it may or may not be susceptible*
- A **susceptible AND permissive** cell is the only cell that can take up a virus particle and replicate it

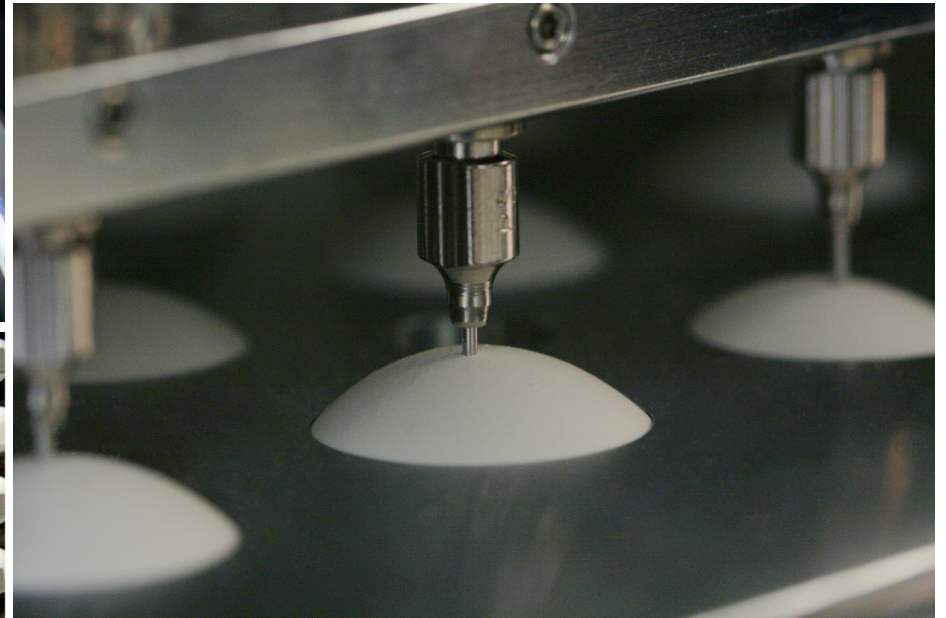




- Animal viruses at first could not be routinely propagated in cultured cells
- Most viruses were grown in laboratory animals







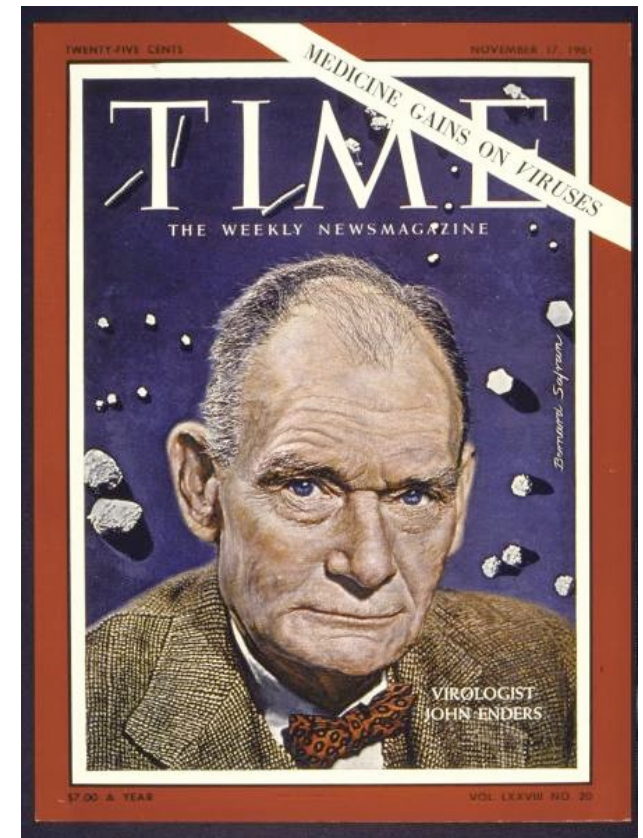
[www.news.sanofi.us](http://www.news.sanofi.us)

[www.vaccinews.net](http://www.vaccinews.net)

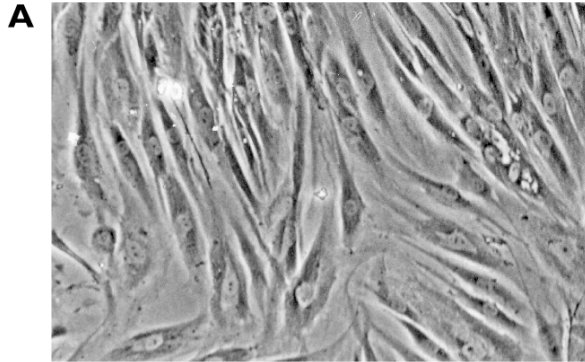


## Studying the infectious cycle in cells

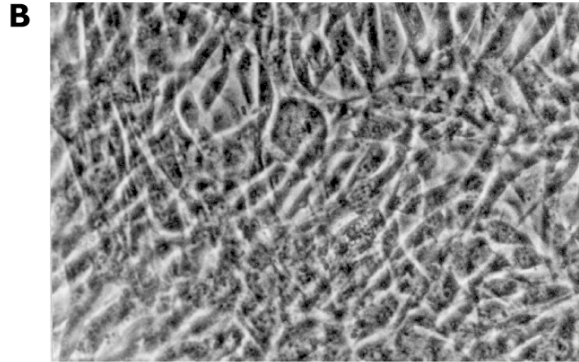
- Not possible before 1949 (animal viruses)
- *Enders, Weller, Robbins* propagate poliovirus in human cell culture - primary cultures of embryonic tissues
- Nobel prize, 1954



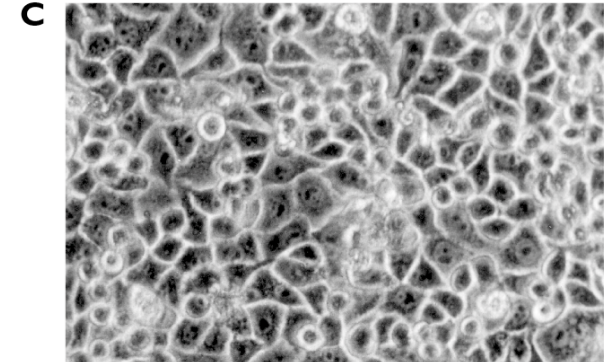
## Virus cultivation



Primary human  
foreskin fibroblasts



Mouse fibroblast  
cell line (3T3)



Human epithelial  
cell line (HeLa)

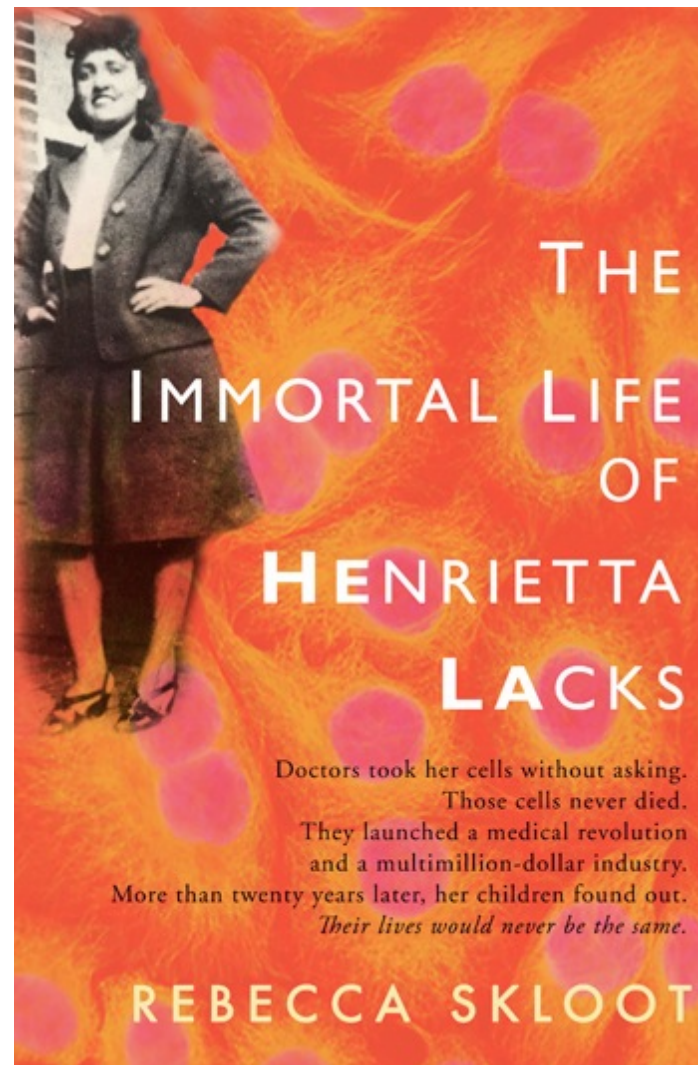
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continuous cell lines

Diploid cell strains (e.g. WI-38, human embryonic lung)



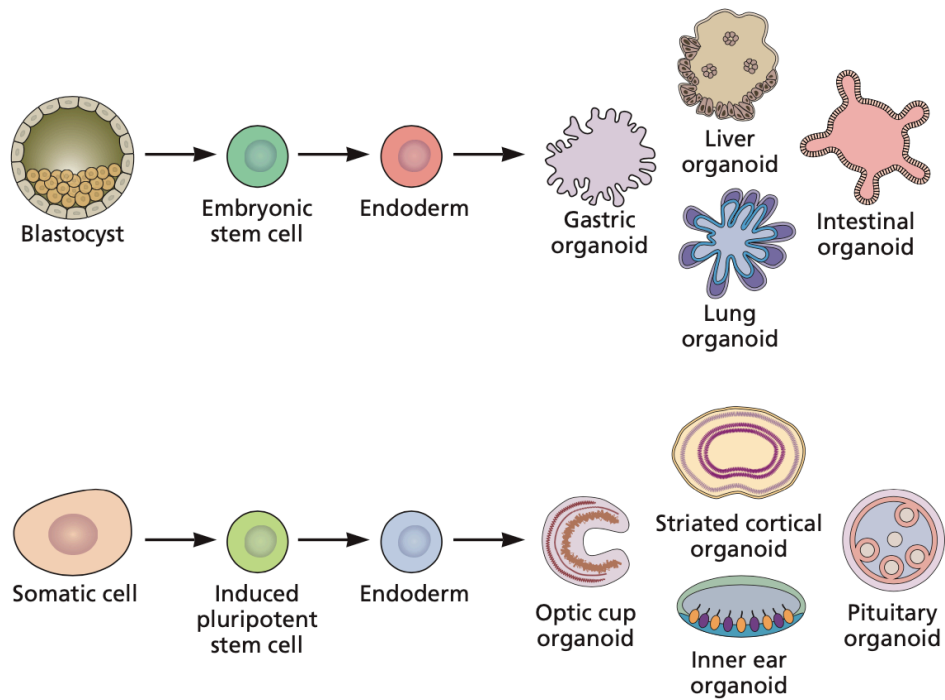






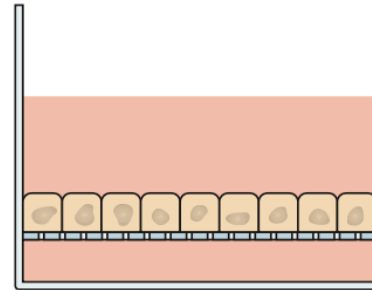
# Amazing advances in cell culture

## Organoid cultures

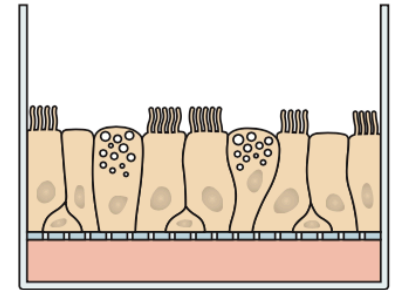


## Air-liquid interface cultures

**A**



**B**

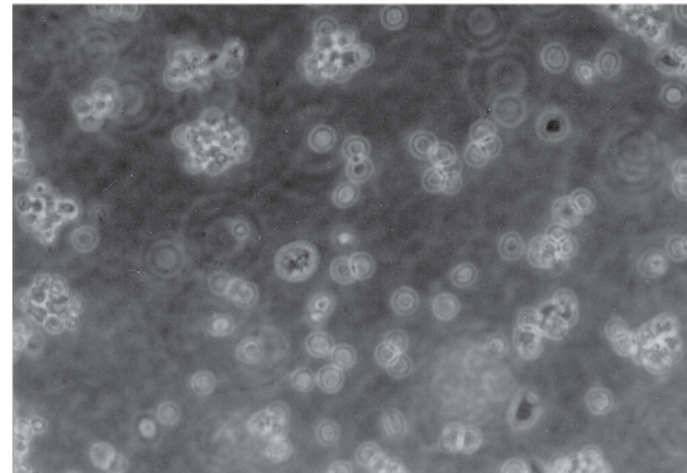
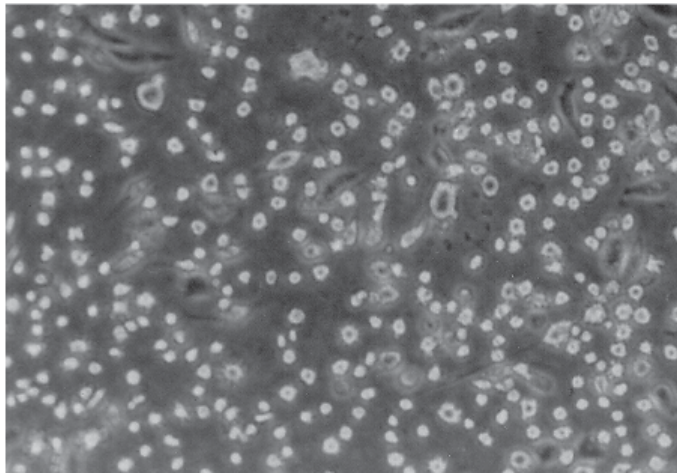
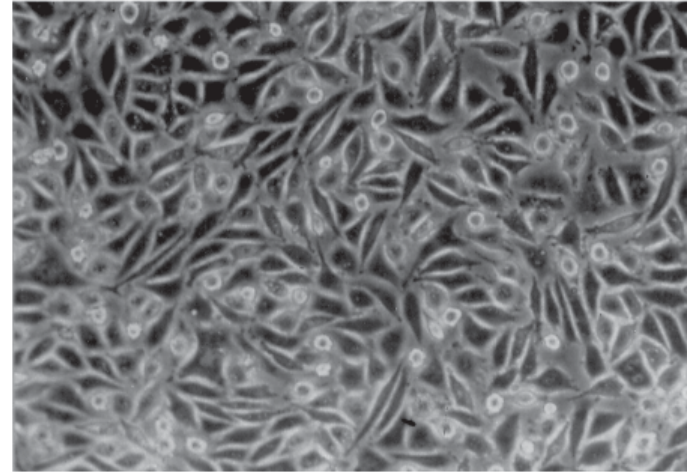
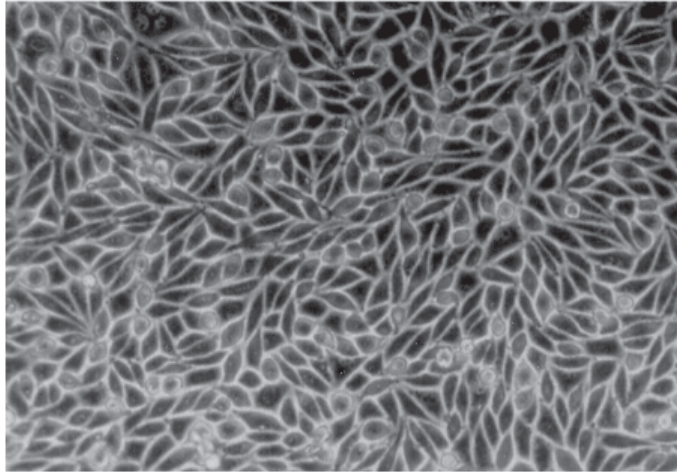


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**[b.socrative.com/login/student](https://b.socrative.com/login/student)  
room number: virus**

A \_\_\_\_\_ and \_\_\_\_\_ cell is the only cell that can take up a virus particle and replicate it (fill in the blanks)

- A. Naive and resistant
- B. Primary and permissive
- C. Susceptible and permissive
- D. Susceptible and naive
- E. Continuous and immortal



*Cytopathic effect (CPE)*

## Article

# A pneumonia outbreak associated with a new coronavirus of probable bat origin

<https://doi.org/10.1038/s41586-020-2012-7>

Received: 20 January 2020

Accepted: 29 January 2020

Published online: 3 February 2020

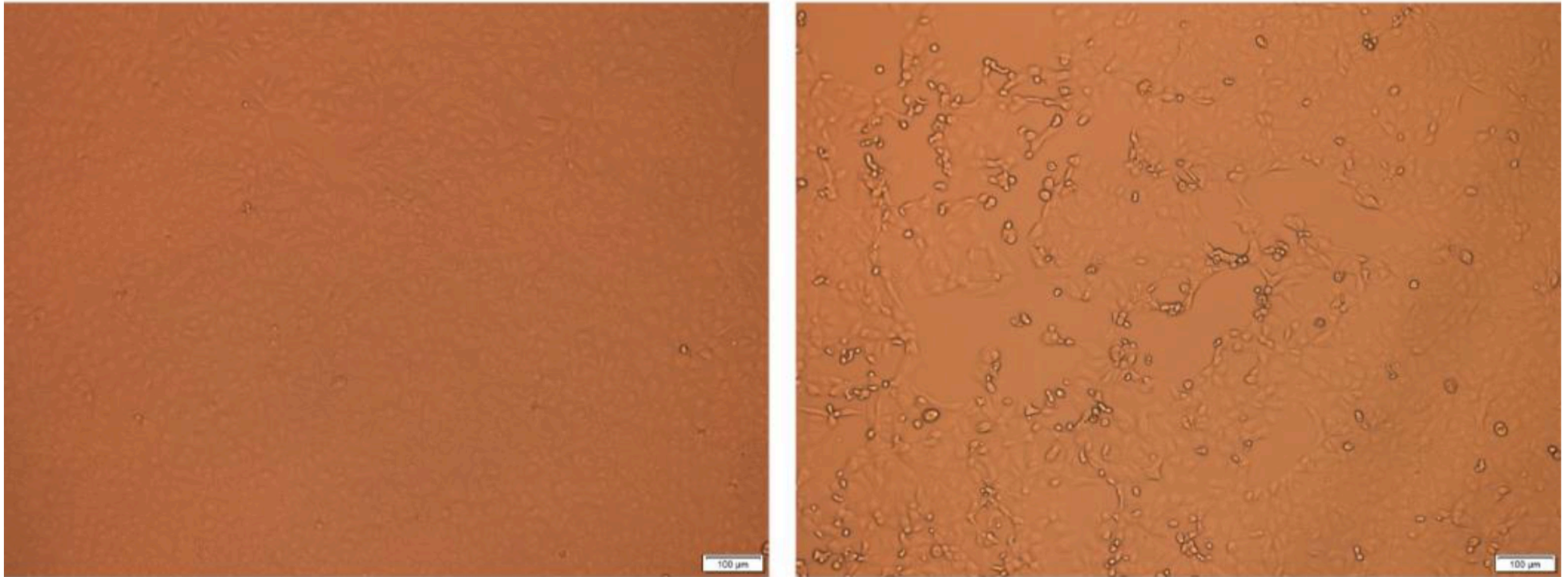
Open access

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Peng Zhou<sup>1,5</sup>, Xing-Lou Yang<sup>1,5</sup>, Xian-Guang Wang<sup>2,5</sup>, Ben Hu<sup>1</sup>, Lei Zhang<sup>1</sup>, Wei Zhang<sup>1</sup>, Hao-Rui Si<sup>1,3</sup>, Yan Zhu<sup>1</sup>, Bei Li<sup>1</sup>, Chao-Lin Huang<sup>2</sup>, Hui-Dong Chen<sup>2</sup>, Jing Chen<sup>1,3</sup>, Yun Luo<sup>1,3</sup>, Hua Guo<sup>1,3</sup>, Ren-Di Jiang<sup>1,3</sup>, Mei-Qin Liu<sup>1,3</sup>, Ying Chen<sup>1,3</sup>, Xu-Rui Shen<sup>1,3</sup>, Xi Wang<sup>1,3</sup>, Xiao-Shuang Zheng<sup>1,3</sup>, Kai Zhao<sup>1,3</sup>, Quan-Jiao Chen<sup>1</sup>, Fei Deng<sup>1</sup>, Lin-Lin Liu<sup>4</sup>, Bing Yan<sup>1</sup>, Fa-Xian Zhan<sup>4</sup>, Yan-Yi Wang<sup>1</sup>, Geng-Fu Xiao<sup>1</sup> & Zheng-Li Shi<sup>1✉</sup>

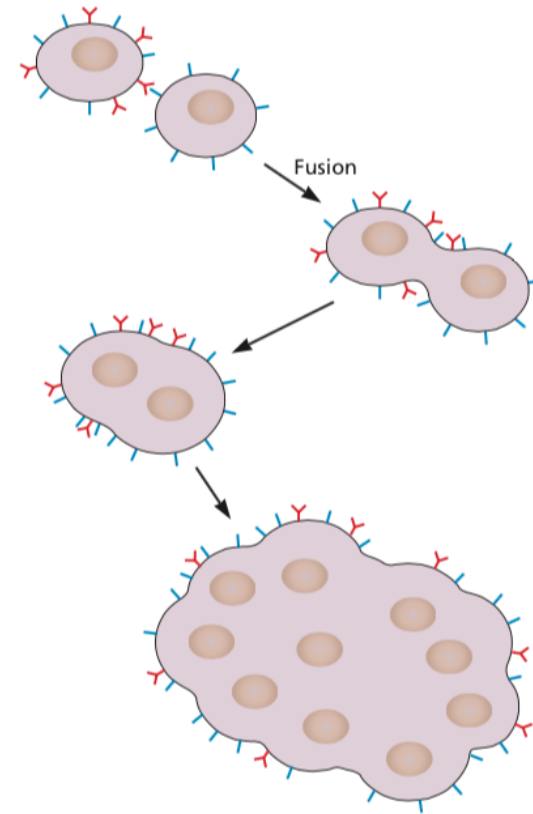
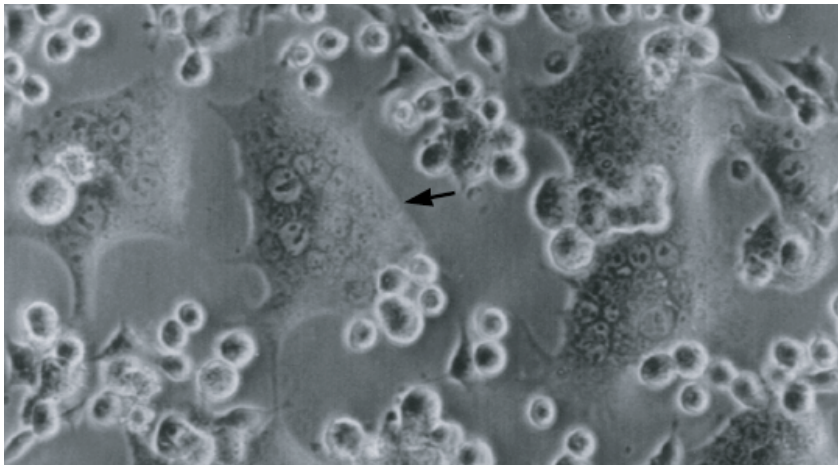
Since the outbreak of severe acute respiratory syndrome (SARS) 18 years ago, a large number of SARS-related coronaviruses (SARSr-CoVs) have been discovered in their natural reservoir host, bats<sup>1–4</sup>. Previous studies have shown that some bat SARSr-CoVs have the potential to infect humans<sup>5–7</sup>. **Here we report the identification and characterization of a new coronavirus (2019-nCoV), which caused an epidemic of acute respiratory syndrome in humans in Wuhan, China.** The epidemic, which started on 12 December 2019, had caused 2,794 laboratory-confirmed infections including 80 deaths by 26 January 2020. Full-length genome sequences were obtained from five patients at an early stage of the outbreak. The sequences are almost identical and share 79.6% sequence identity to SARS-CoV. Furthermore, we show that 2019-nCoV is 96% identical at the whole-genome level to a bat coronavirus. Pairwise protein sequence analysis of seven conserved non-structural proteins domains show that this virus belongs to the species of *SARSr-CoV*. In addition, 2019-nCoV virus isolated from the bronchoalveolar lavage fluid of a critically ill patient could be neutralized by sera from several patients. Notably, we confirmed that 2019-nCoV uses the same cell entry receptor—angiotensin converting enzyme II (ACE2)—as SARS-CoV.

123 We then successfully isolated the virus (named nCoV-2019  
124 BetaCoV/Wuhan/WIV04/2019), in Vero and Huh7 cells using BALF sample from  
125 ICU-06 patient. Clear cytopathogenic effects were observed in cells after three days  
126 incubation (Extended Data Figure 5a and 5b). The identity of the strain WIV04 was





# Formation of syncytia



# Examples of cytopathic effects

Cytopathic effect(s)	Virus(es)
<b>Morphological alterations</b>	
Nuclear shrinking (pyknosis), proliferation of membrane	Picornaviruses
Proliferation of nuclear membrane	Alphaviruses, herpesviruses
Vacuoles in cytoplasm	Polyomaviruses, papillomaviruses
Syncytium formation (cell fusion)	Paramyxoviruses, coronaviruses
Margination and breaking of chromosomes	Herpesviruses
Rounding up and detachment of cultured cells	Herpesviruses, rhabdoviruses, adenoviruses, picornaviruses
<b>Inclusion bodies</b>	
Virions in nucleus	Adenoviruses
Virions in cytoplasm (Negri bodies)	Rabies virus
“Factories” in cytoplasm (Guarnieri bodies)	Poxviruses
Clumps of ribosomes in virions	Arenaviruses
Clumps of chromatin in nucleus	Herpesviruses

# How many viruses in a sample?

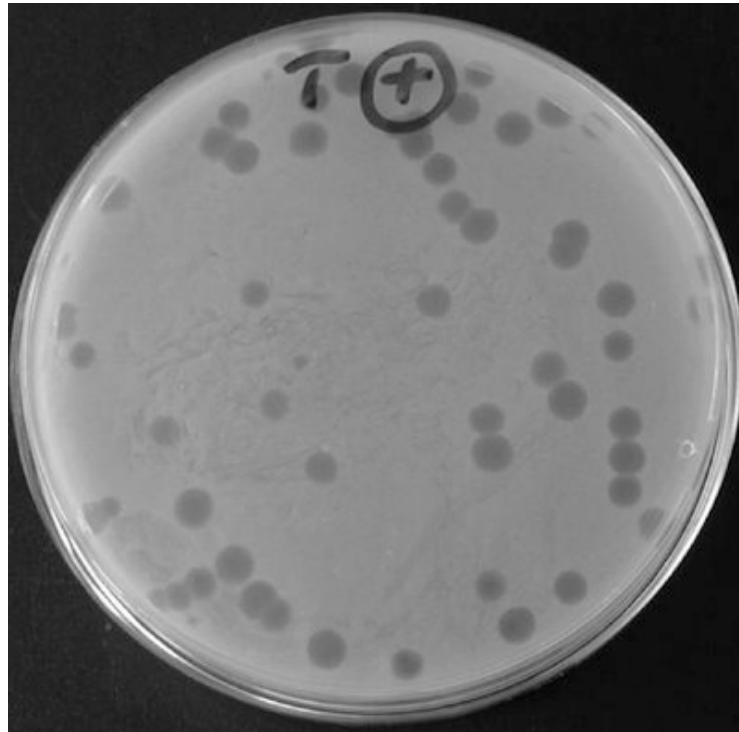
- Infectivity
- Physical: virus particles and their components

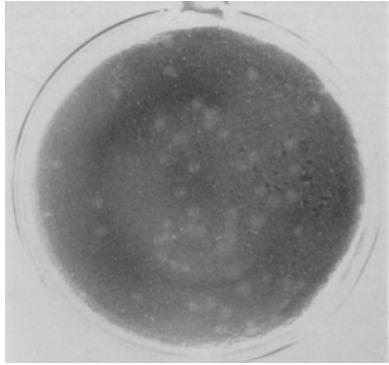




# Plaque assay

*1930s: used to study multiplication of bacteriophages*





## Plaque assay



*1952, Renato Dulbecco developed plaque assay for animal viruses*

*Nobel Prize, 1975*

*PRODUCTION OF PLAQUES IN MONOLAYER TISSUE CULTURES BY SINGLE PARTICLES OF AN ANIMAL VIRUS*

BY RENATO DULBECCO

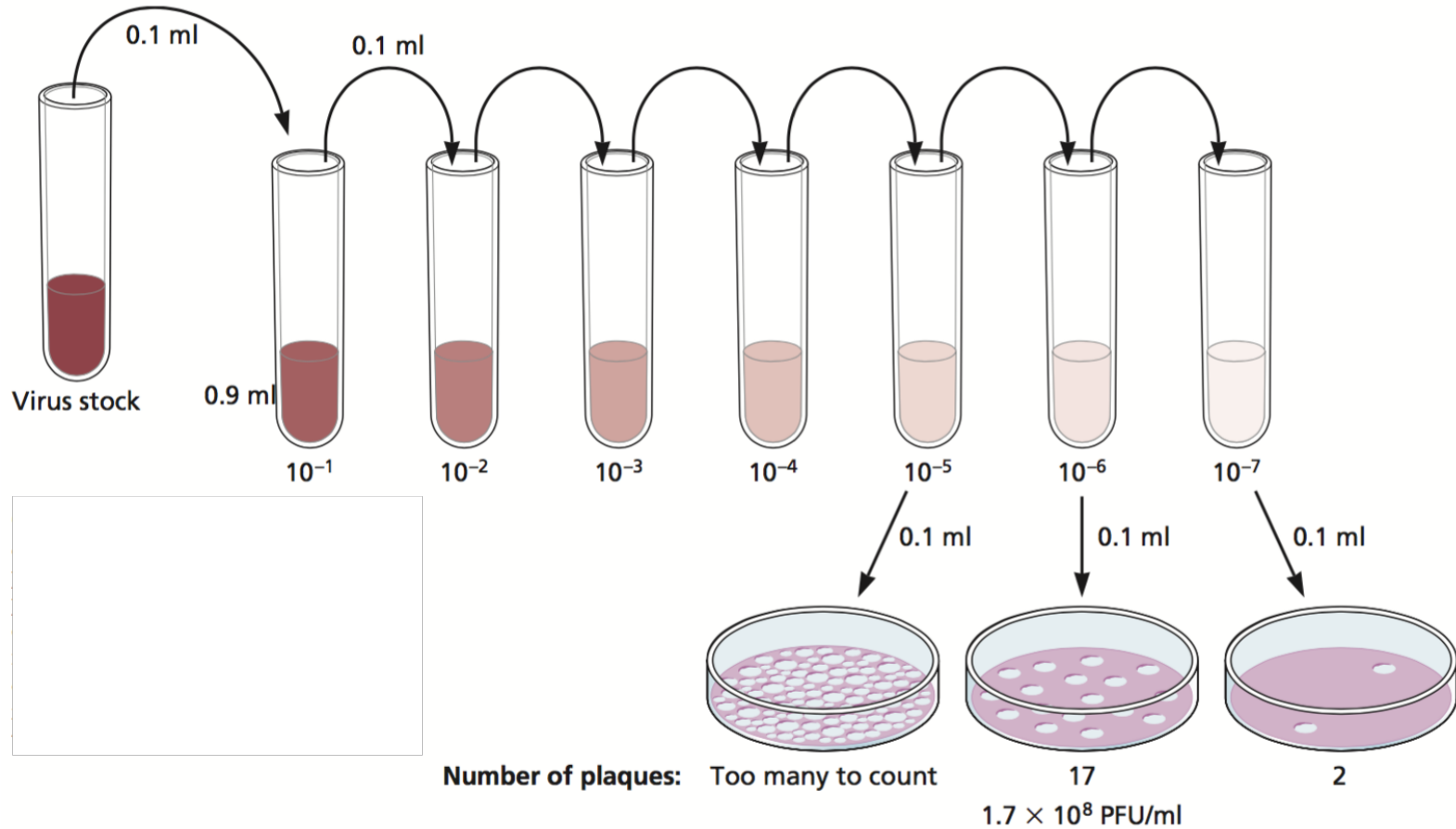
CALIFORNIA INSTITUTE OF TECHNOLOGY, PASADENA, CALIFORNIA

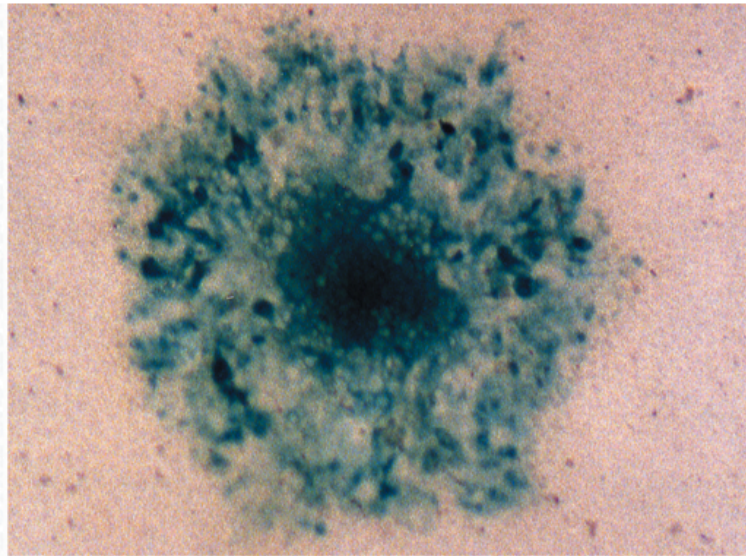
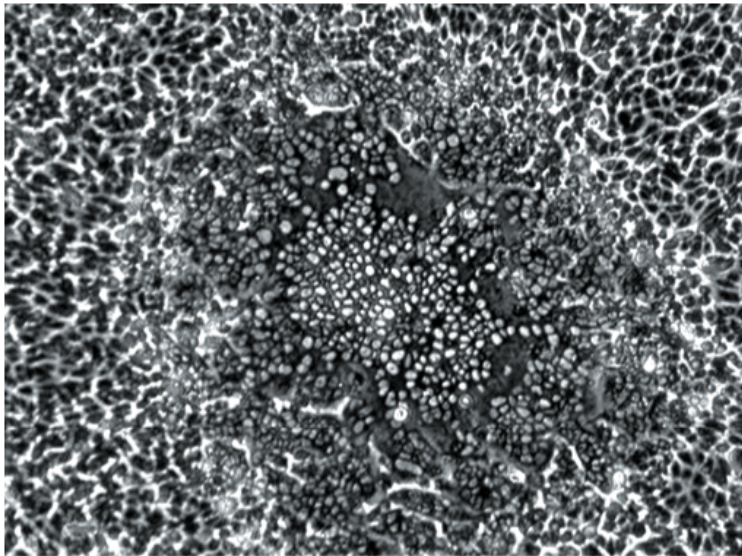
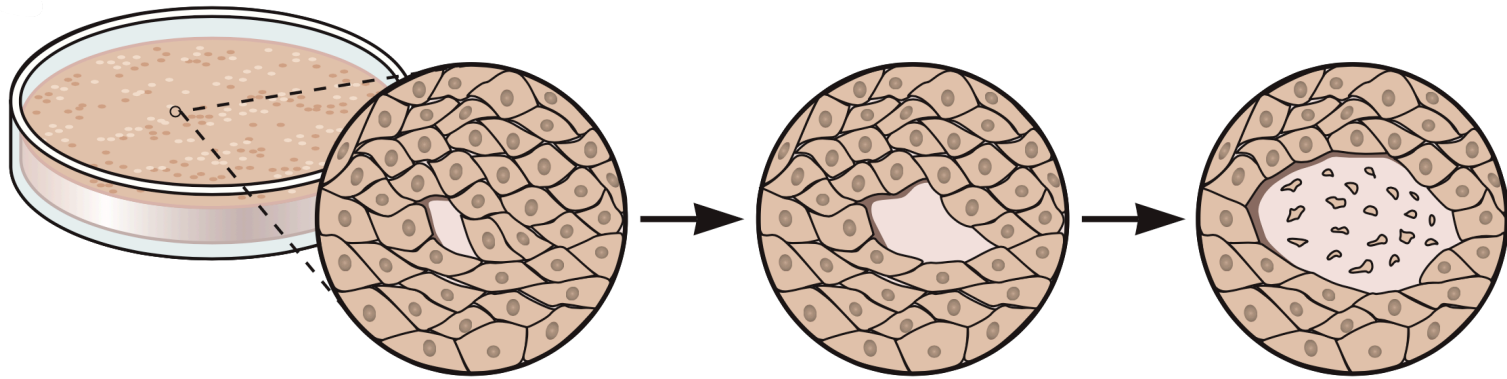
Read before the Academy, April 29, 1952

Research on the growth characteristics and genetic properties of animal viruses has stood greatly in need of improved quantitative techniques, such as those used in the related field of bacteriophage studies.

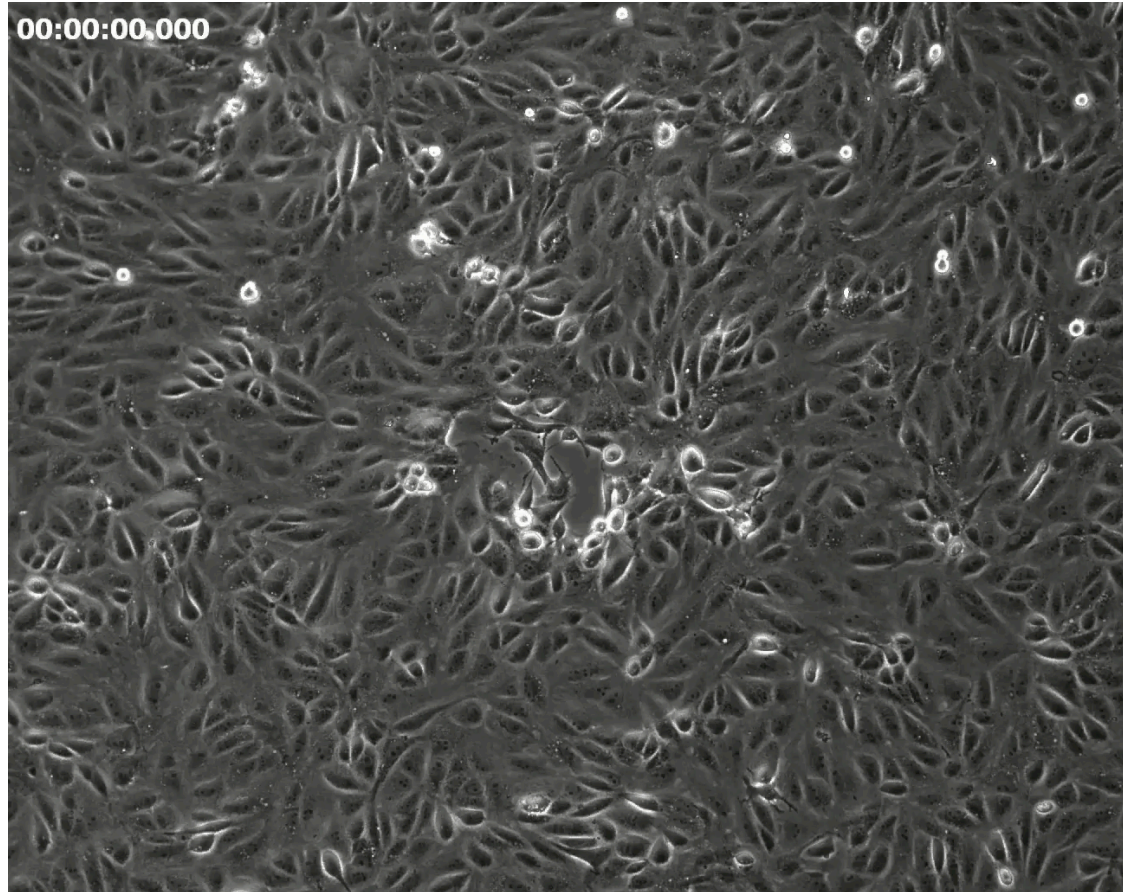
The requirements for a quantitative virus technique are as follows: (1) The use of a uniform type of host cell; (2) an accurate assay technique; (3) the isolation of the progeny of a single virus particle; and (4) the separate isolation of each of the virus particles produced by a single infected

# Plaque assay











Virology Live 2021 • Vincent Racaniello

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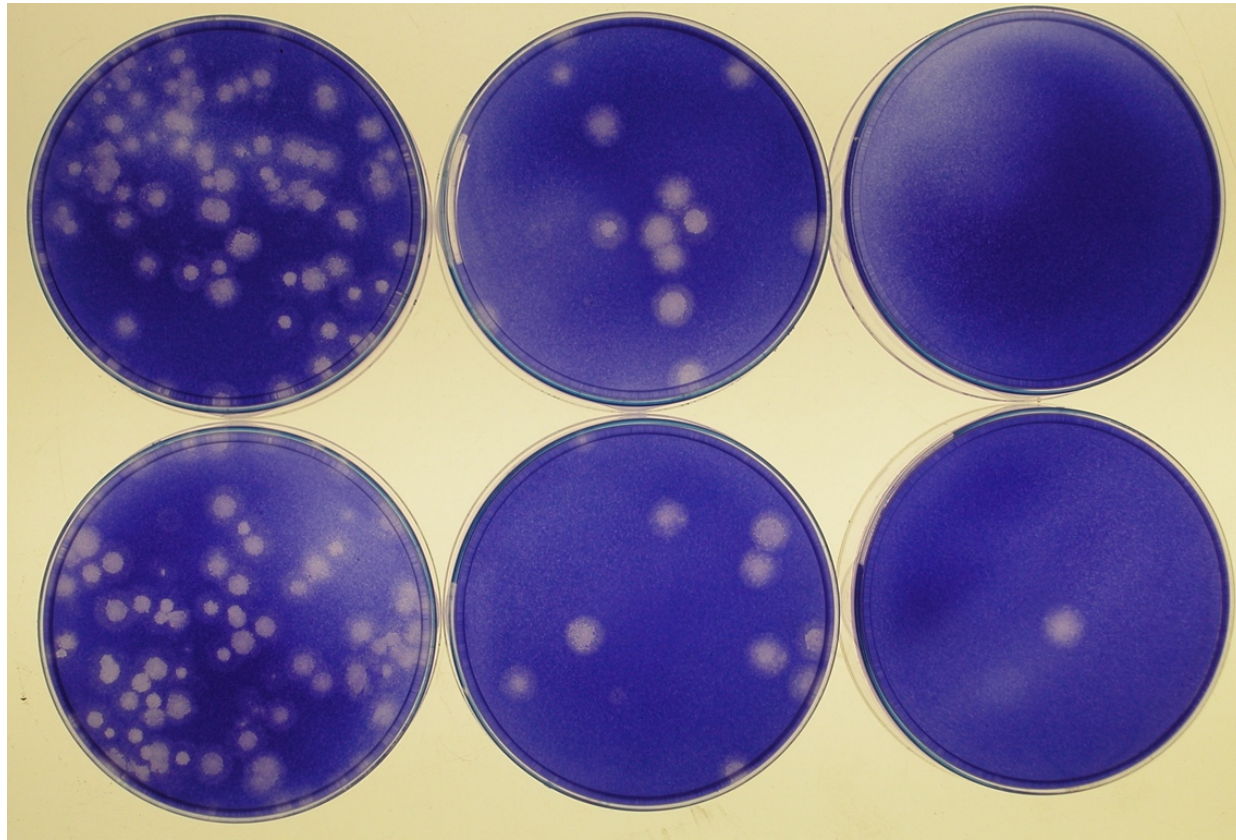
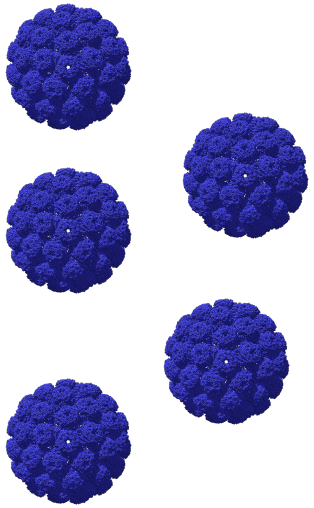
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room number: virus**

When doing a plaque assay, what is the purpose of adding a semi-solid agar overlay on the monolayer of infected cells?

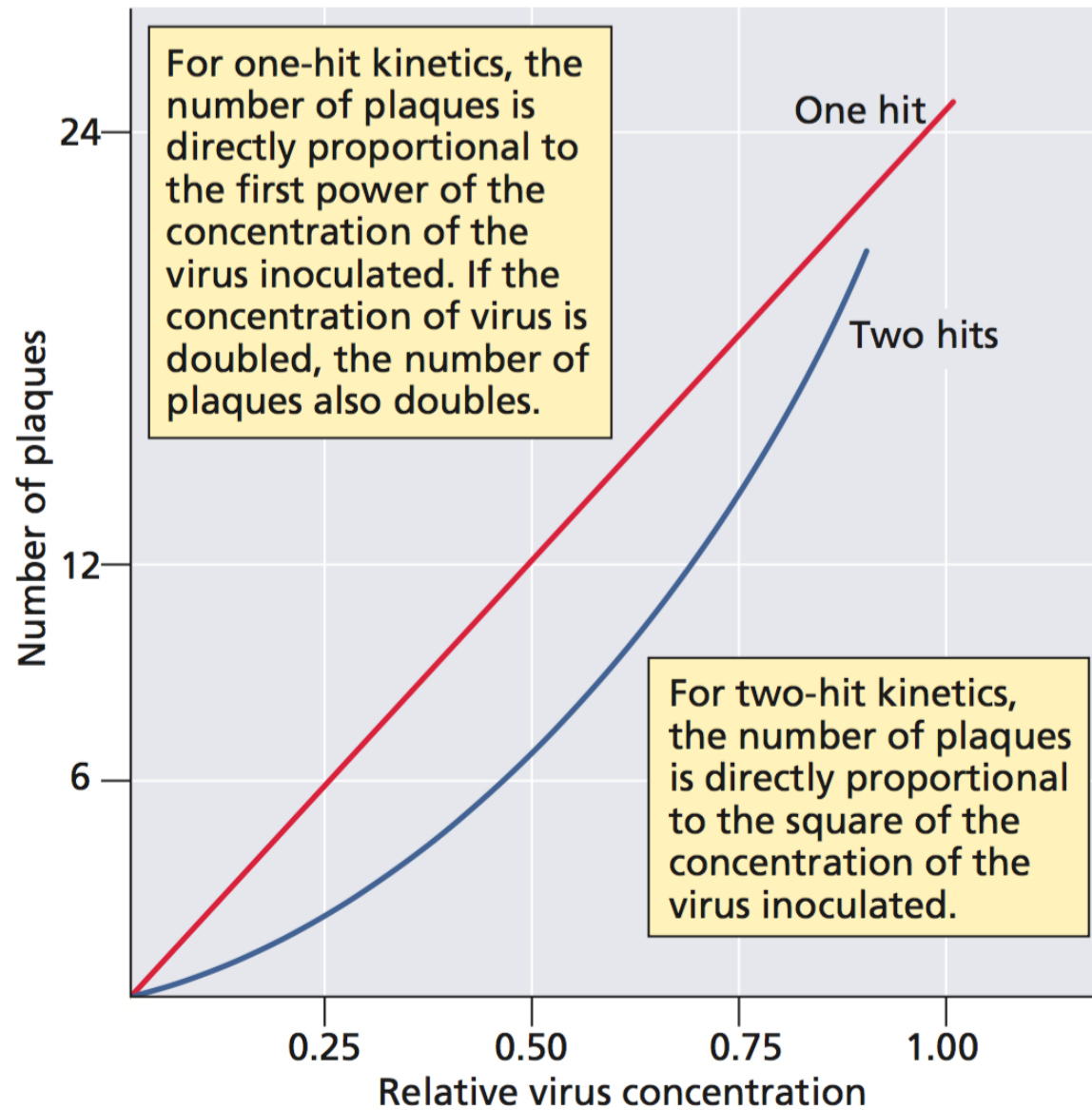
- A. To stabilize progeny virus particles
- B. To ensure that cells remain susceptible and permissive
- C. To act as a pH indicator
- D. To keep cells adherent to the plate during incubation
- E. To restrict viral diffusion after lysis of infected cells



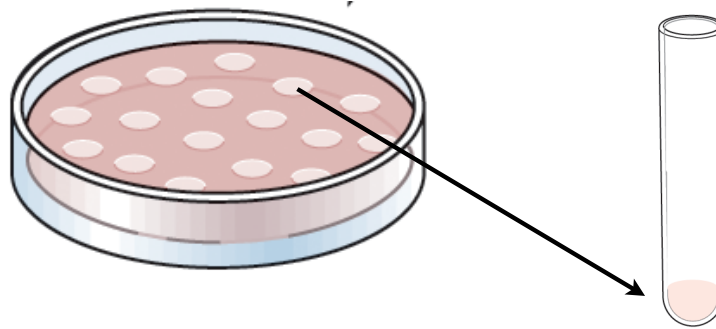
# How many viruses are needed to form a plaque?





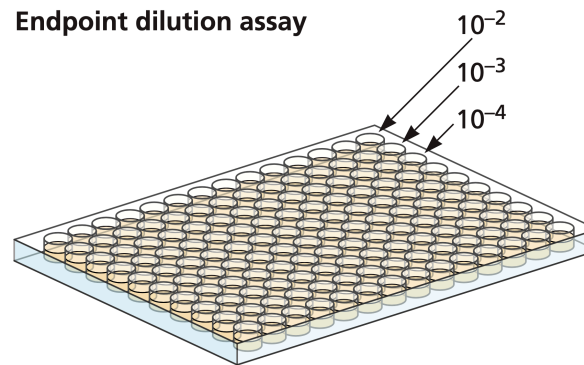


# Plaque purification



A method for producing virus stocks  
Usually done 3 times

# For viruses that do not form plaques: Endpoint dilution assay



TCID<sub>50</sub>

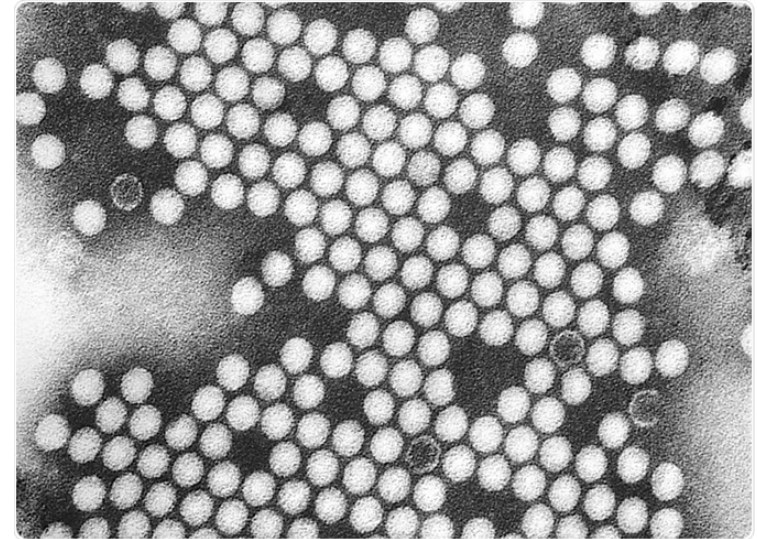
Virus dilution		Cytopathic effect									
10 <sup>-2</sup>		+	+	+	+	+	+	+	+	+	+
10 <sup>-3</sup>		+	+	+	+	+	+	+	+	+	+
10 <sup>-4</sup>		+	+	—	+	+	+	+	+	+	+
10 <sup>-5</sup>	➔	—	+	+	—	+	—	—	+	—	+
10 <sup>-6</sup>		—	—	—	—	—	—	+	—	—	—
10 <sup>-7</sup>		—	—	—	—	—	—	—	—	—	—

# Not all virus particles are infectious!

Virus	Particle/PFU ratio	# of <i>physical</i> particles # of <i>infectious</i> particles
<i>Papillomaviridae</i>		
Papillomavirus	10,000	
<i>Picornaviridae</i>		
Poliovirus	30–1,000	
<i>Herpesviridae</i>		
Herpes simplex virus	50–200	
<i>Polyomaviridae</i>		
Polyomavirus	38–50	
Simian virus 40	100–200	
<i>Adenoviridae</i>	20–100	
<i>Poxviridae</i>	1–100	
<i>Orthomyxoviridae</i>		
Influenza virus	20–50	
<i>Reoviridae</i>		
Reovirus	10	
<i>Alphaviridae</i>		
Semliki Forest virus	1–2	

## Particle-to-PFU ratio

- # of *physical* particles ÷ # of *infectious* particles
- A single particle *can* initiate infection
- Not all viruses are successful
  - Damaged particles
  - Mutations
  - Complexity of infectious cycle
- Complicates study



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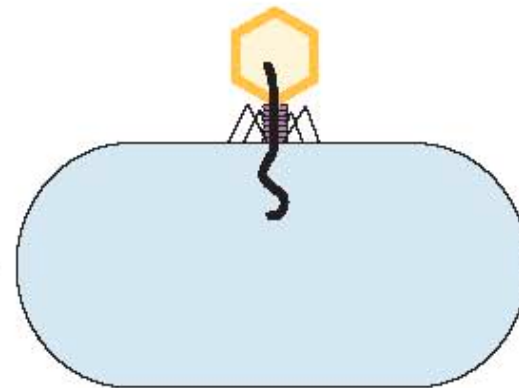
In the 'particle to pfu ratio', 'particle' can best be described as:

- A. One of the proteins which makes up the virus
- B. A virus which may or may not be infectious
- C. A virus which is infectious
- D. A virus which is not infectious
- E. Elementary or composite

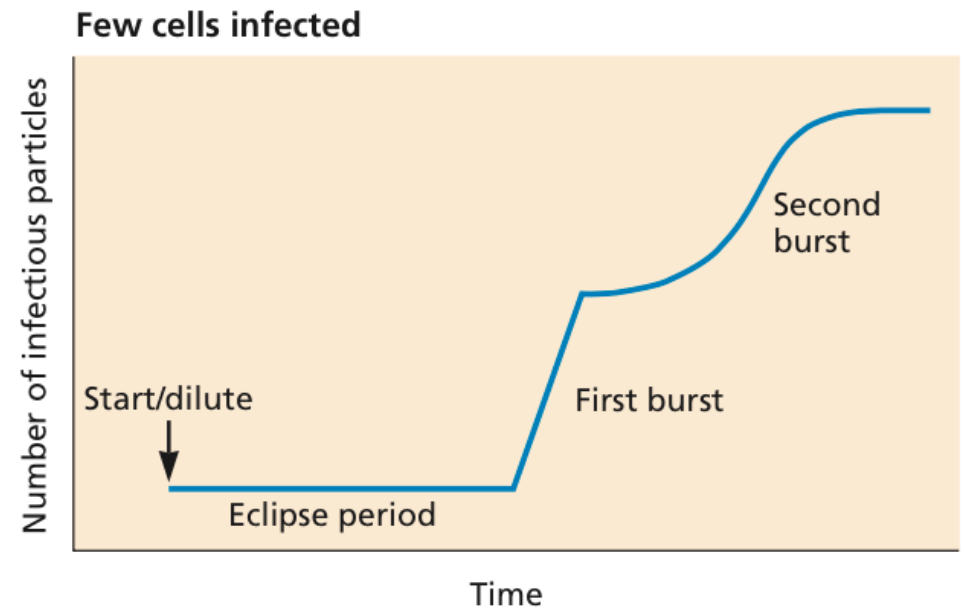
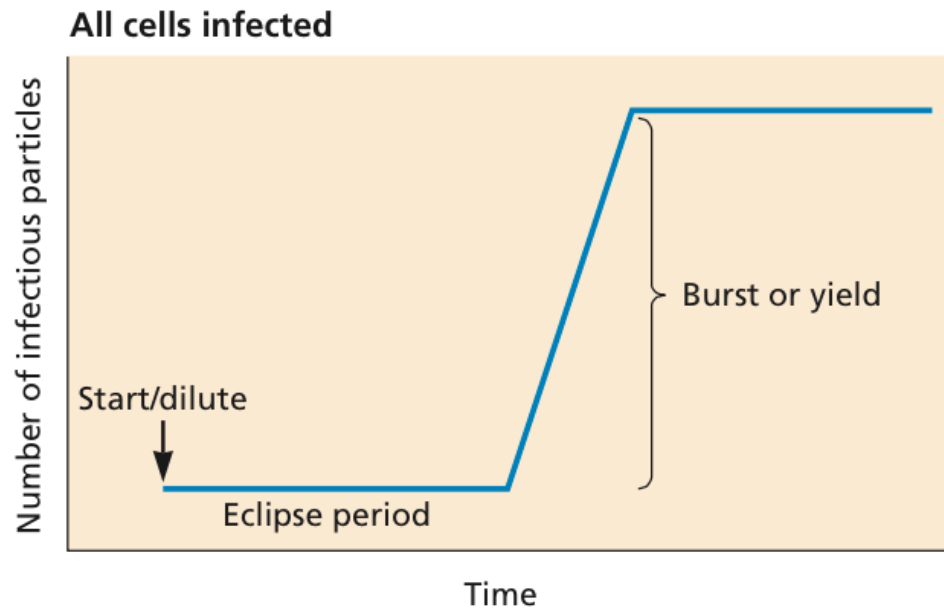
# **One-step growth cycle:**

## **A method to study virus reproduction in cells**

- Ellis & Delbruck, 1939, studies on *E. coli* bacteriophages
- Adsorb
- Dilute culture
- Sample
- Assay

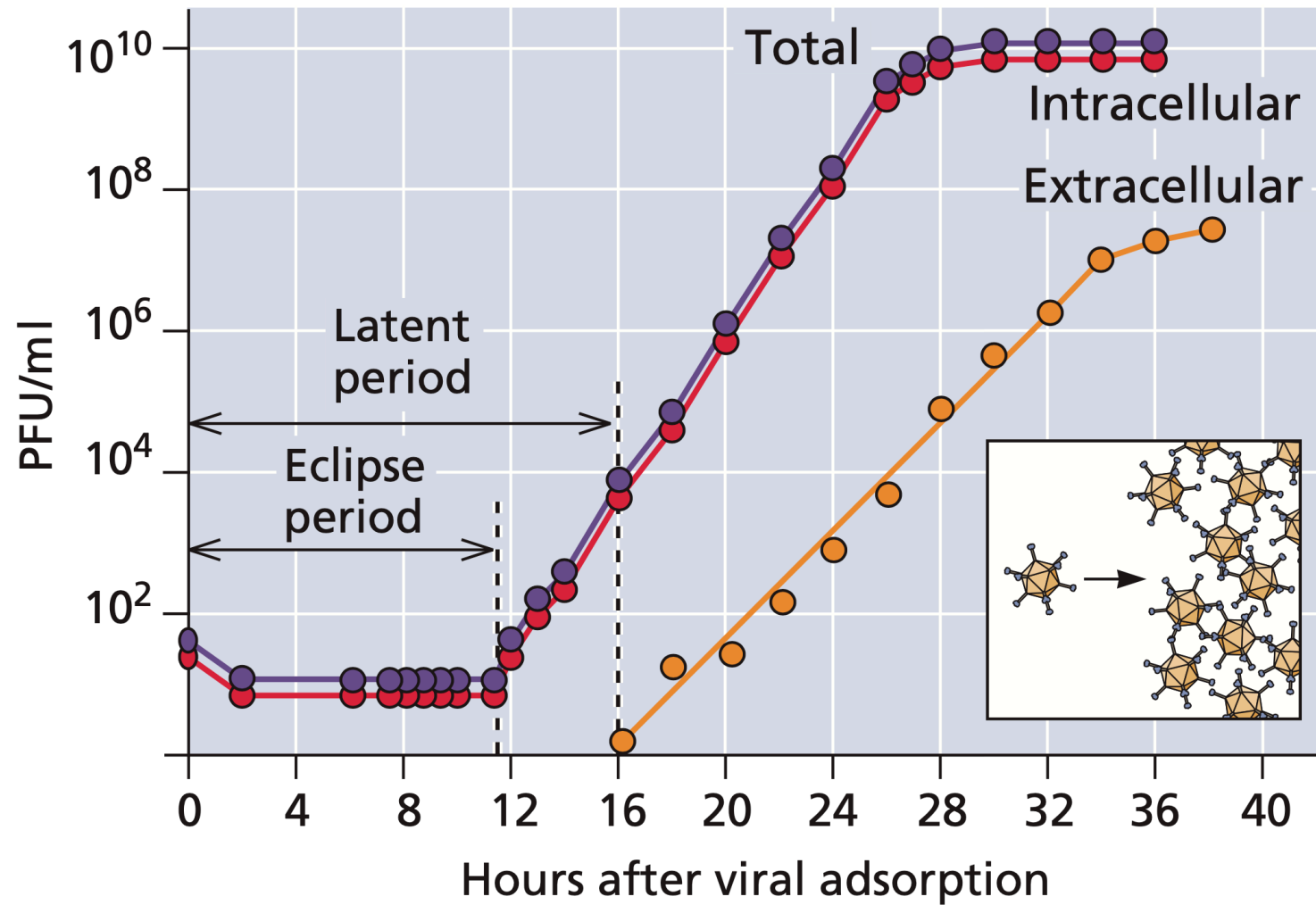


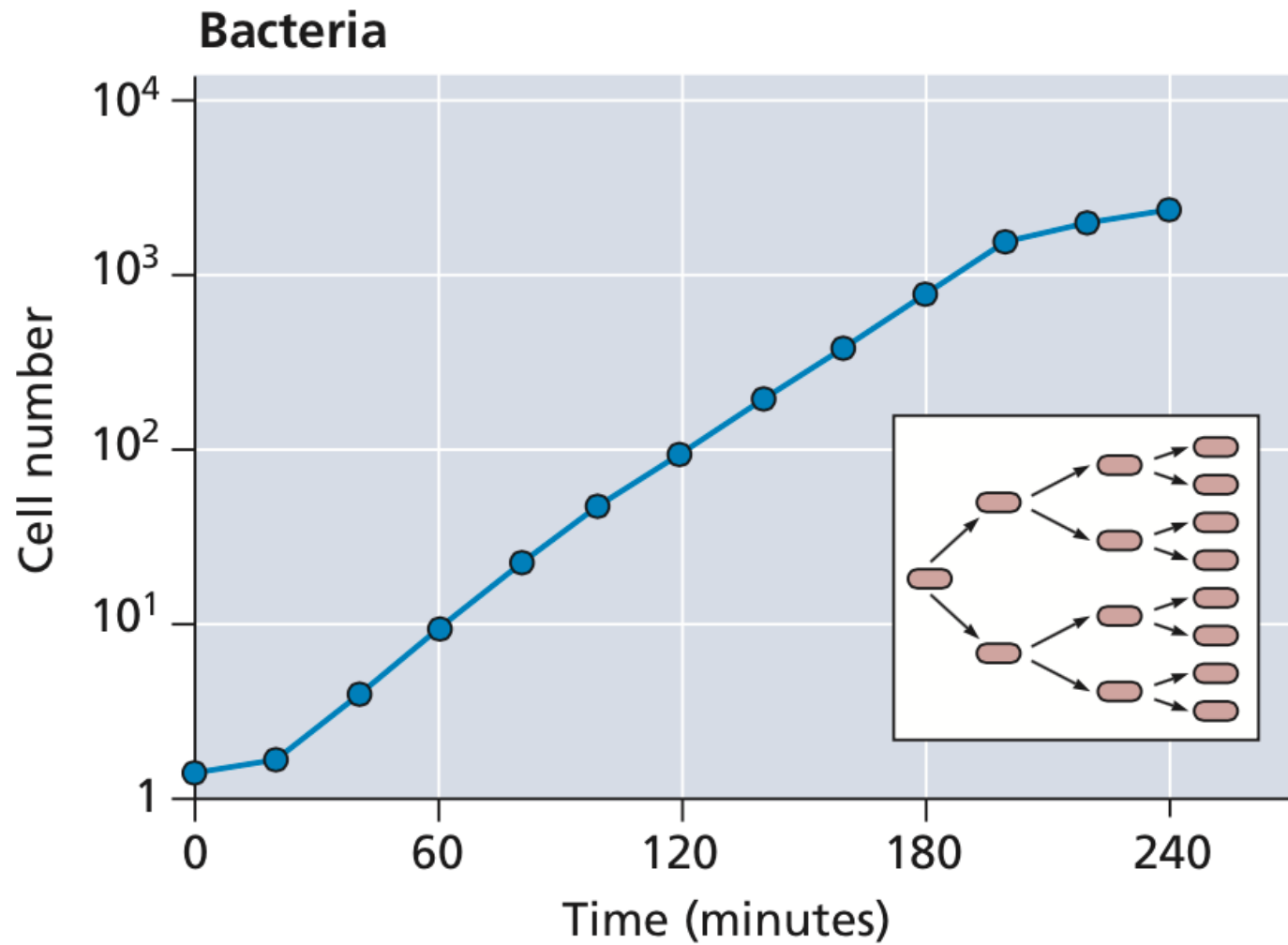
# Single and multi-step growth cycles





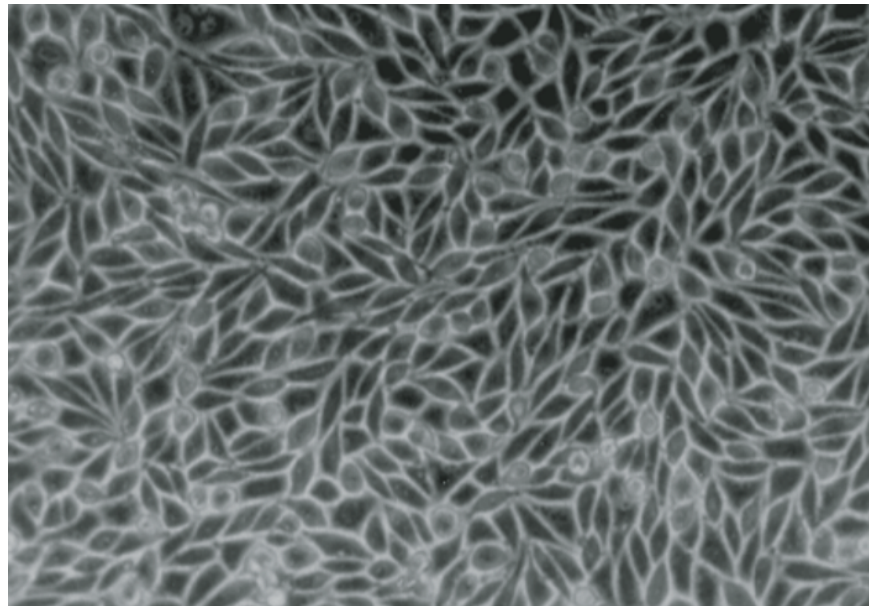
## Adenovirus type 5





## **Synchronous infection - key to one-step growth cycle**

*To achieve this, we need to infect all the cells - but how do we know?*



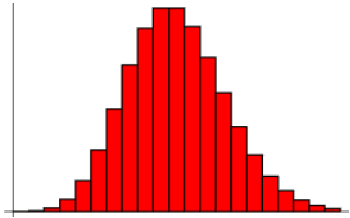
## Multiplicity of infection (MOI)

- Number of infectious particles ADDED per cell
- Amount of virus (PFU)  $\div$  # of cells
- Not the number of infectious particles each cell *receives*
- Add  $10^7$  virus particles to  $10^6$  cells - MOI of 10 - each cell does NOT receive 10 virus particles

# MOI

- Infection depends on the random collision of virus particles and cells
- When susceptible cells are mixed with virus, some cells are uninfected, some receive one, two, three or more particles
- The distribution of virus particles per cell is best described by the *Poisson distribution*





$$P(k) = e^{-m} m^k / k!$$

$P(k)$ : fraction of cells infected by  $k$  virus particles

$m$ : multiplicity of infection (moi)

uninfected cells:  $P(0) = e^{-m}$

cells receiving 1 particle:  $P(1) = m e^{-m}$

cells multiply infected:  $P(>1) = 1 - e^{-m}(m+1)$

[obtained by subtracting from 1 {the sum of all probabilities for any value of  $k$ }  
the probabilities  $P(0)$  and  $P(1)$ ]



Examples:

If  $10^6$  cells are infected at **moi of 10**:

45 cells are uninfected

450 cells receive 1 particle

the rest receive >1 particle

If  $10^6$  cells are infected at **moi of 1**:

37% of the cells are uninfected

37% of the cells receive 1 particle

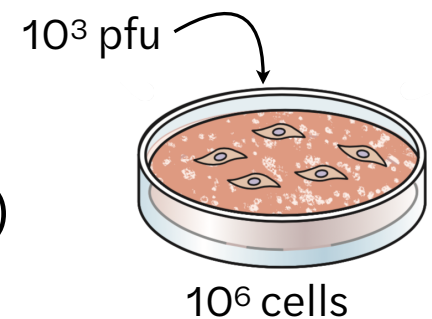
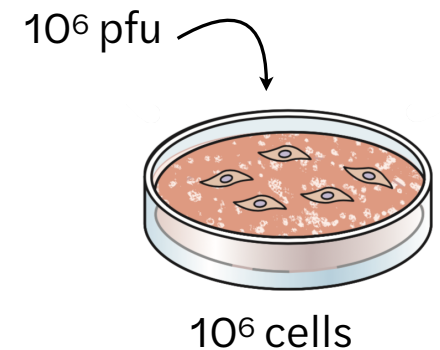
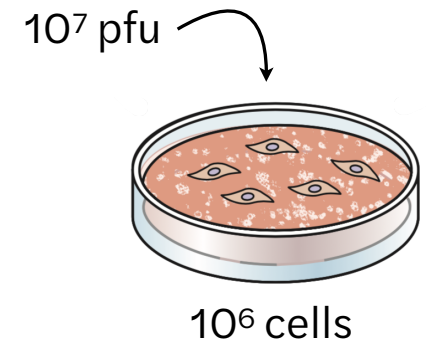
26% receive >1 particle

If  $10^6$  cells are infected at **moi of .001**:

99.9% of the cells are uninfected

00.099% of the cells receive 1 particle (990)

00.0001% receive >1 particle



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room number: virus**

If cells are infected at an  $\text{MOI}=10$  in a one-step growth cycle experiment, in the growth curve you will likely see...

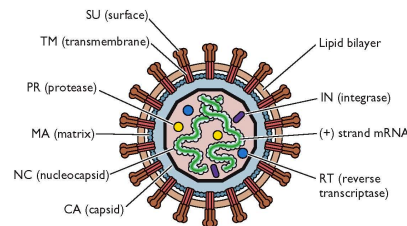
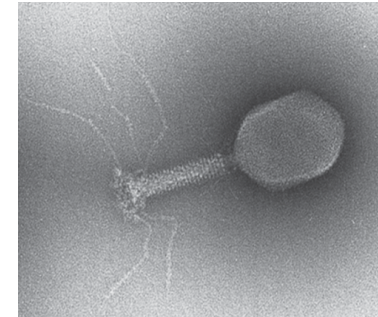
- A. Multiple bursts of virus release
- B. Multiple eclipse periods
- C. A single burst of virus release
- D. No burst of virus release
- E. Asynchronous infection

# Physical measurements of virus particles

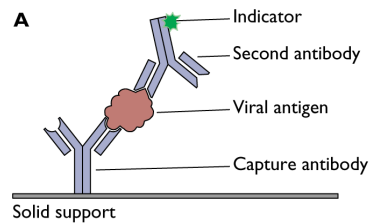


- Hemagglutination

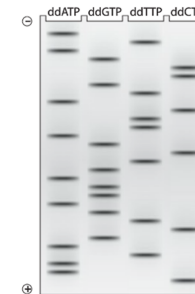
- Electron microscopy



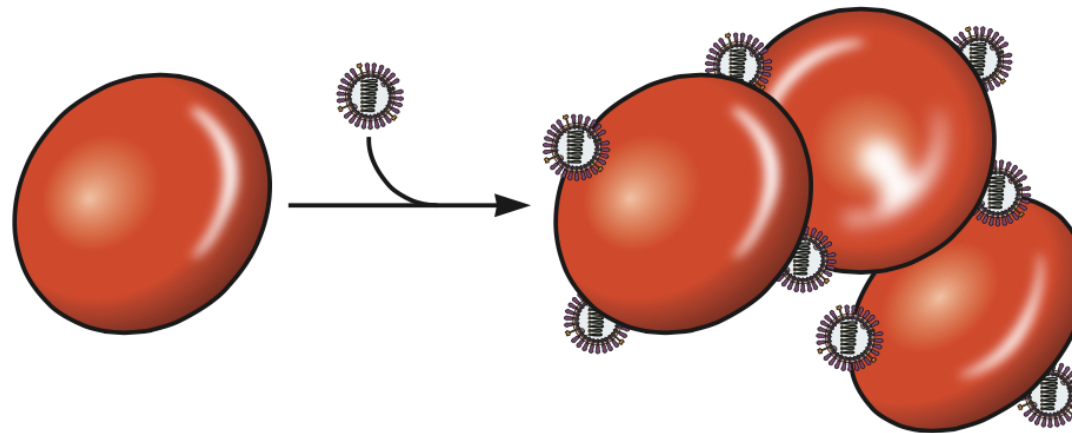
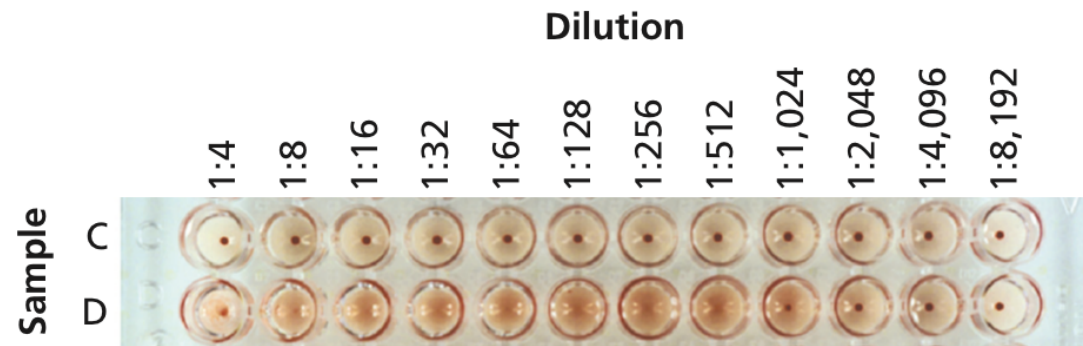
- Viral enzymes



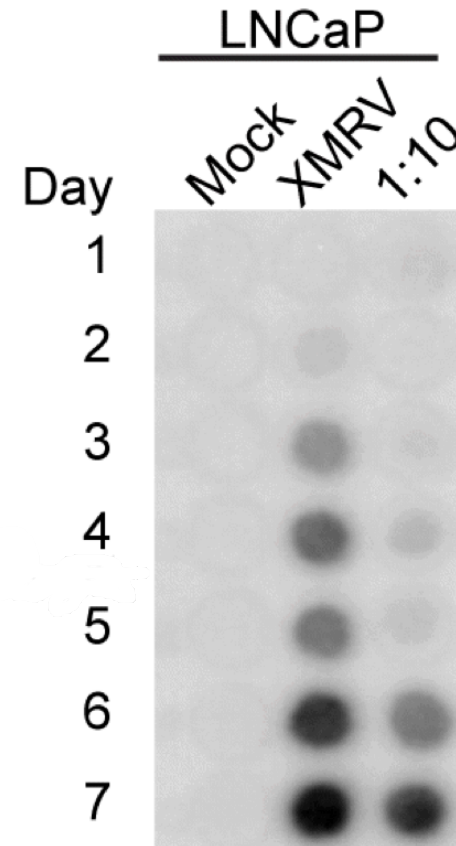
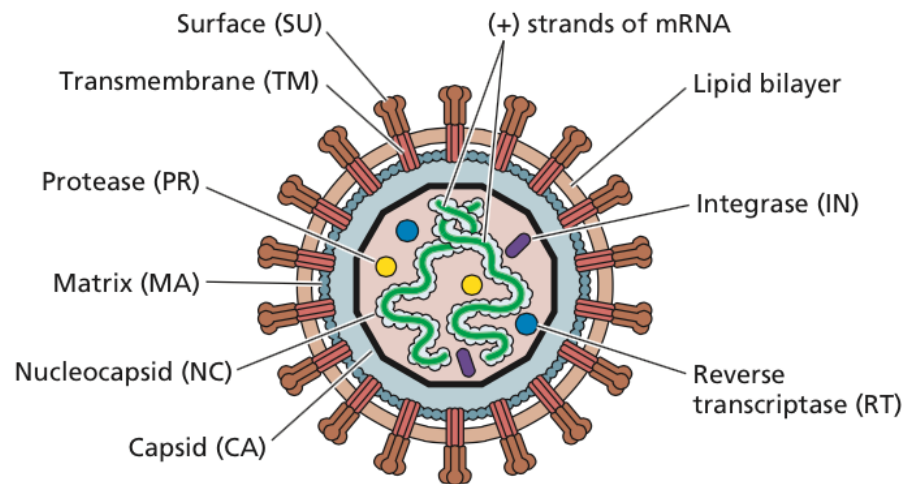
- Serology



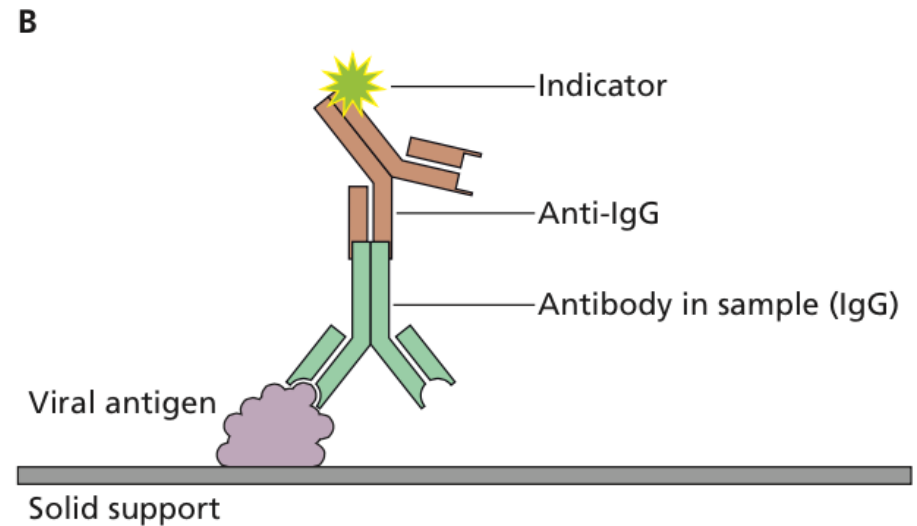
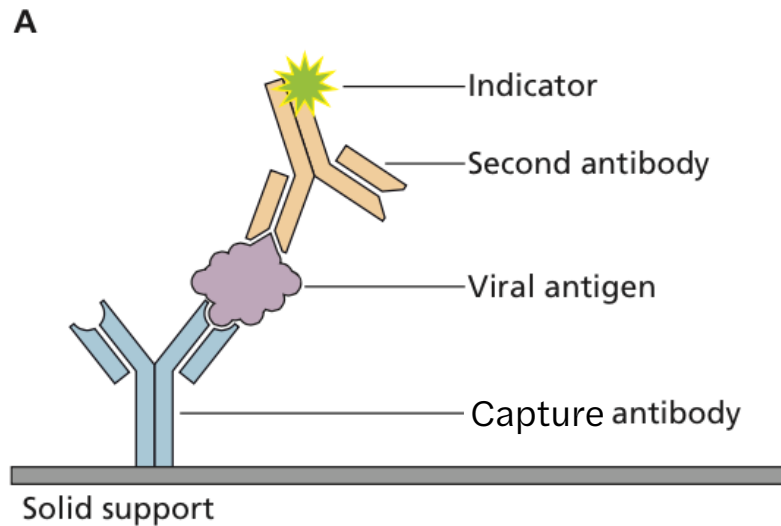
# Hemagglutination



# Measurement of viral enzyme activity

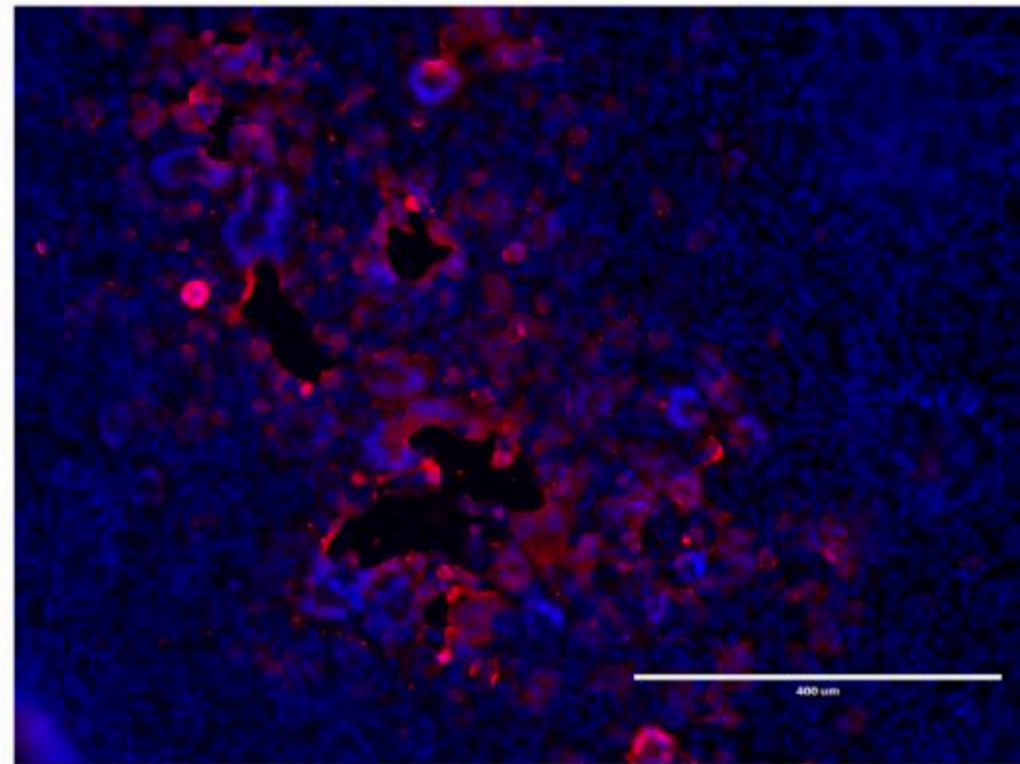
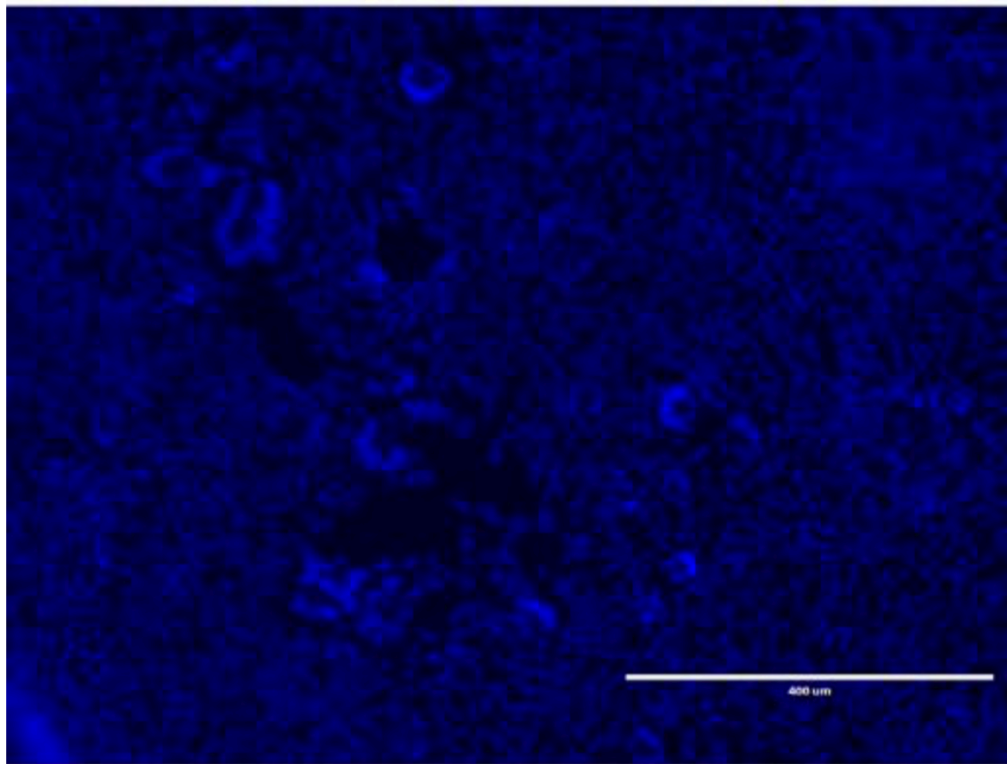


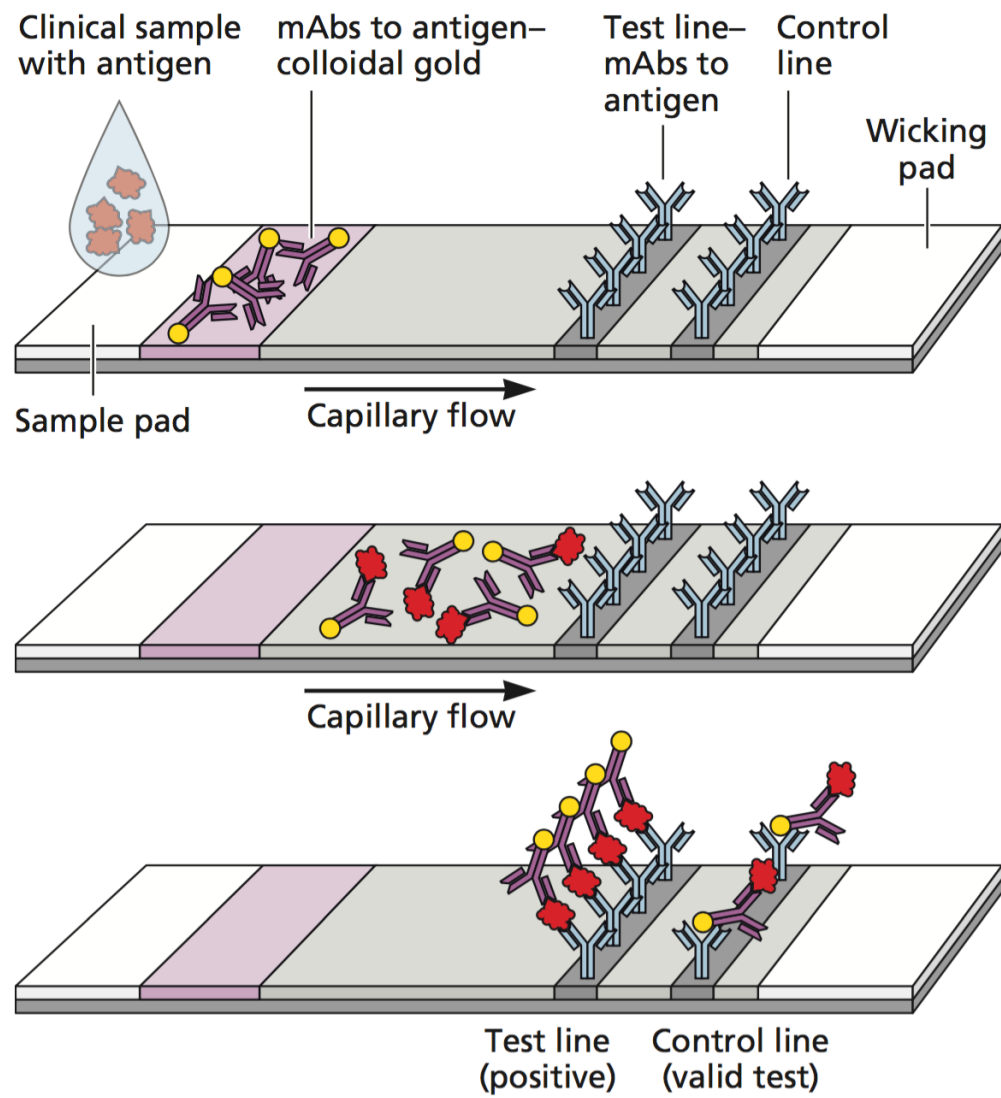
# Enzyme-linked immunosorbent assay (ELISA): detecting viral antigens or antibodies



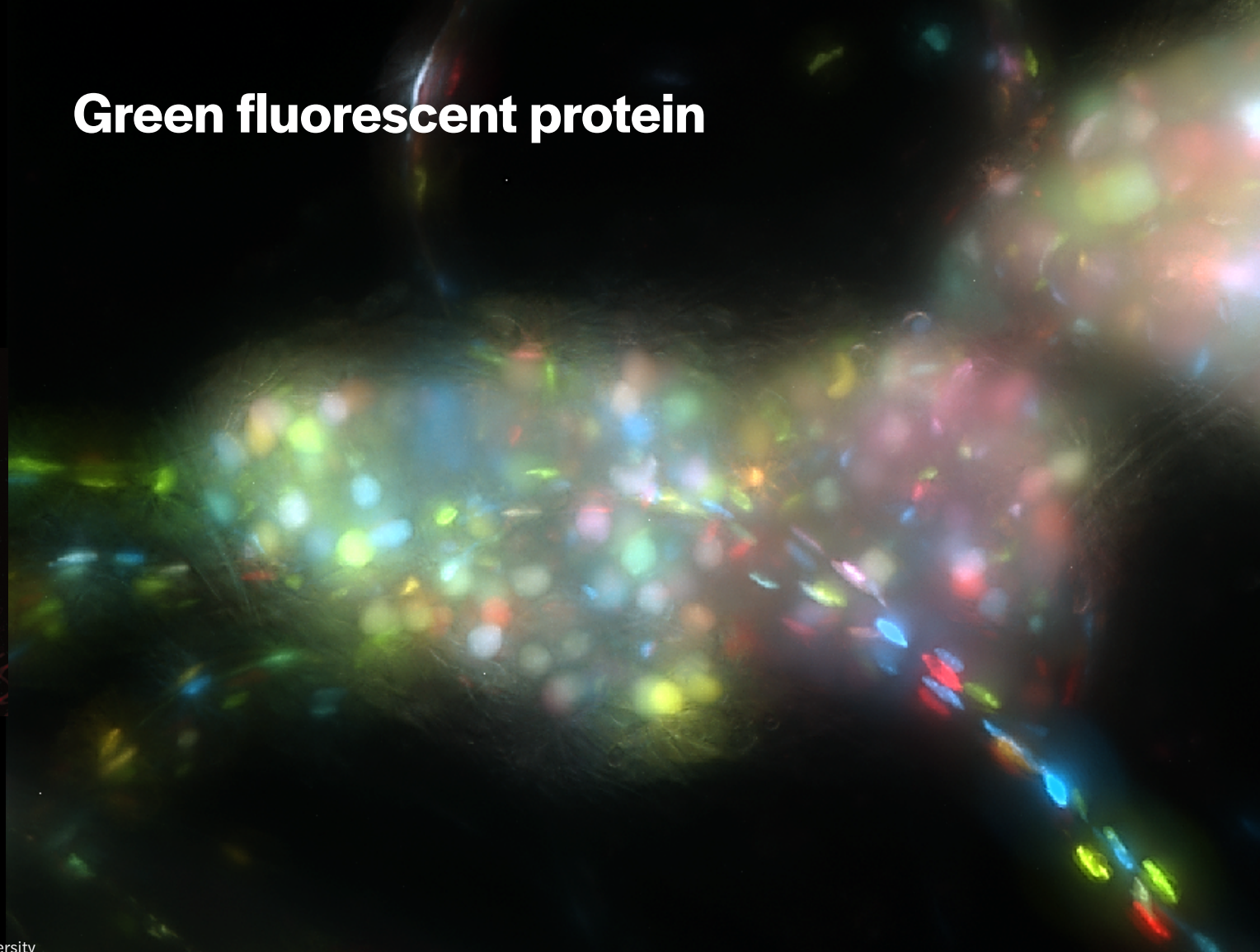
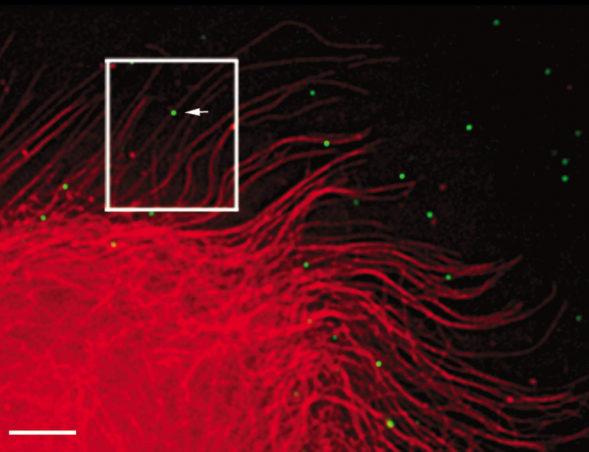
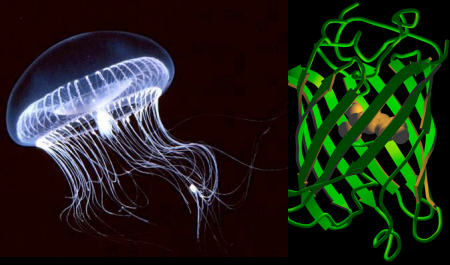


126 incubation (Extended Data Figure 5a and 5b). The identity of the strain WIV04 was  
127 verified in Vero E6 cells by immunofluorescence microscopy using cross-reactive  
128 viral NP antibody (Extended Data Figure 5c and 5d), and by metagenomic sequencing,





# Green fluorescent protein



# Deep, high-throughput sequencing

- Metagenomics
- Identification of new viruses in a sample
- Identification of new pathogens
- Human genome: 10 yr/\$3B vs 1 day/\$1000

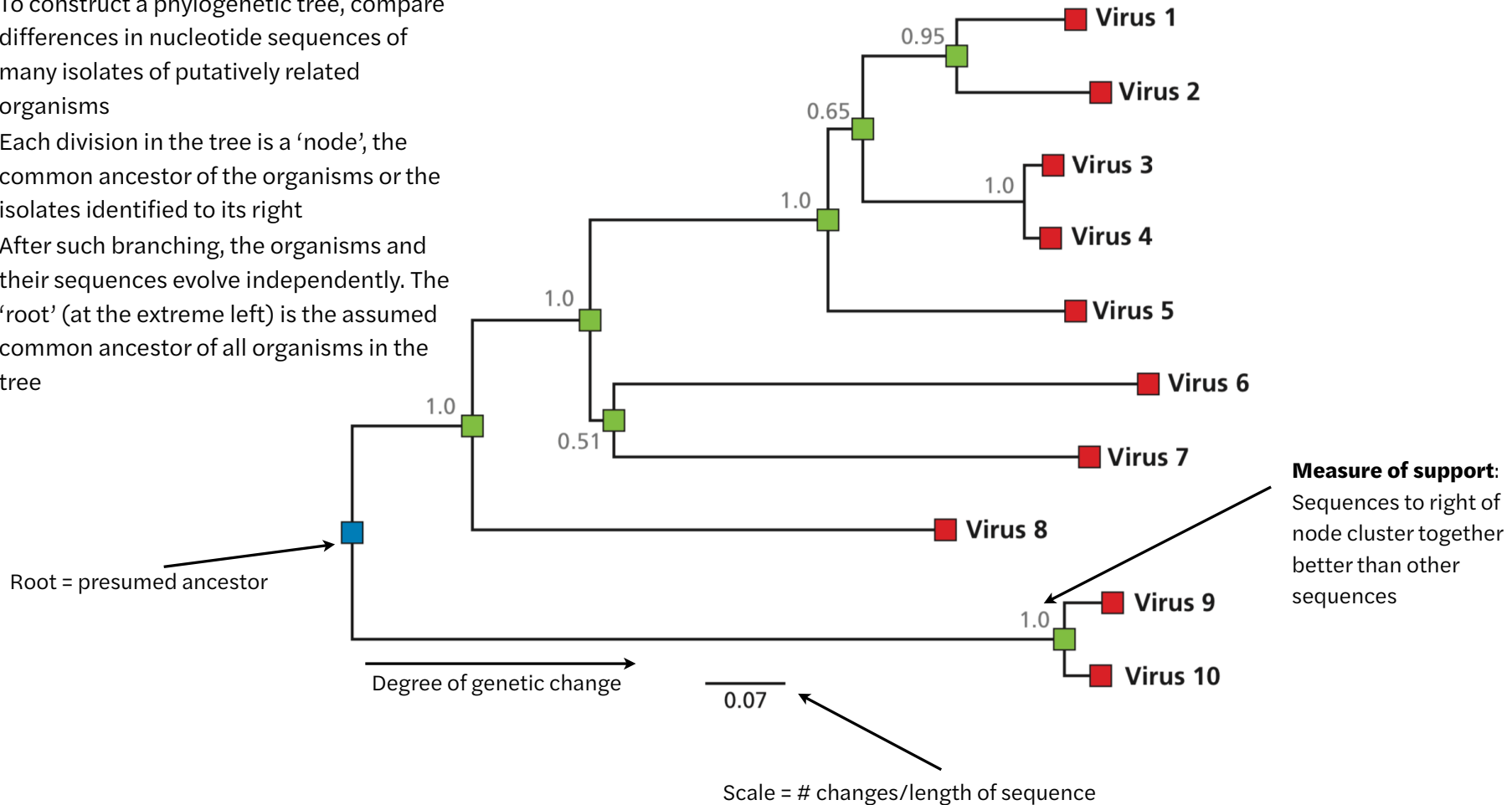


*(this is not DHTS)*



# Phylogenetic trees

- Phylogenetic trees measure the genetic distance between organisms, and identify the nearest relatives
- To construct a phylogenetic tree, compare differences in nucleotide sequences of many isolates of putatively related organisms
- Each division in the tree is a 'node', the common ancestor of the organisms or the isolates identified to its right
- After such branching, the organisms and their sequences evolve independently. The 'root' (at the extreme left) is the assumed common ancestor of all organisms in the tree



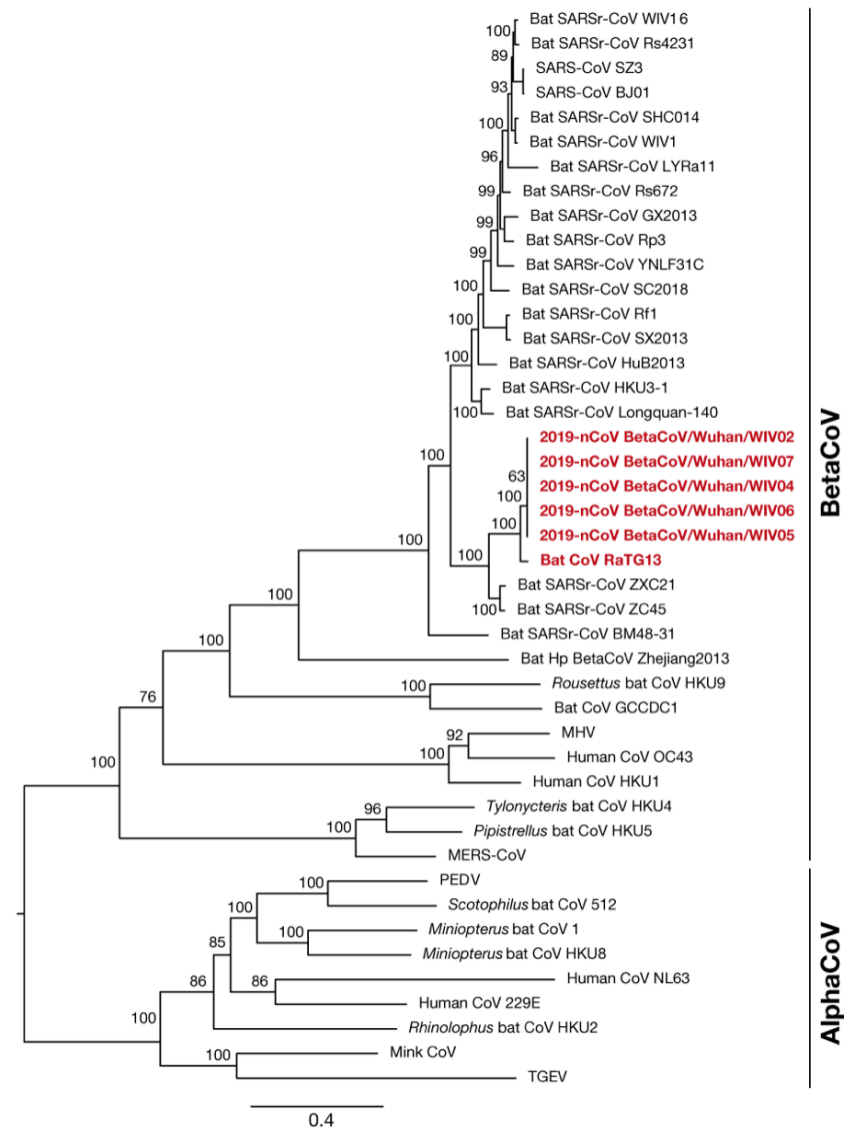
Article | [Open Access](#) | Published: 03 February 2020

# A pneumonia outbreak associated with a new coronavirus of probable bat origin

Peng Zhou, Xing-Lou Yang, [...] Zheng-Li Shi 

*Nature* **579**, 270–273(2020) | [Cite this article](#)

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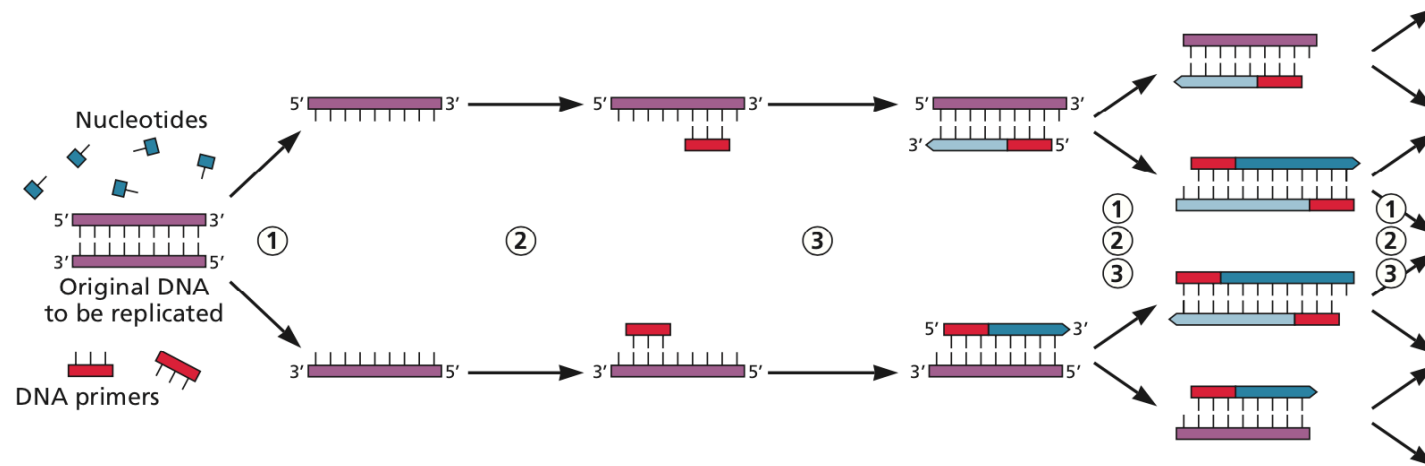




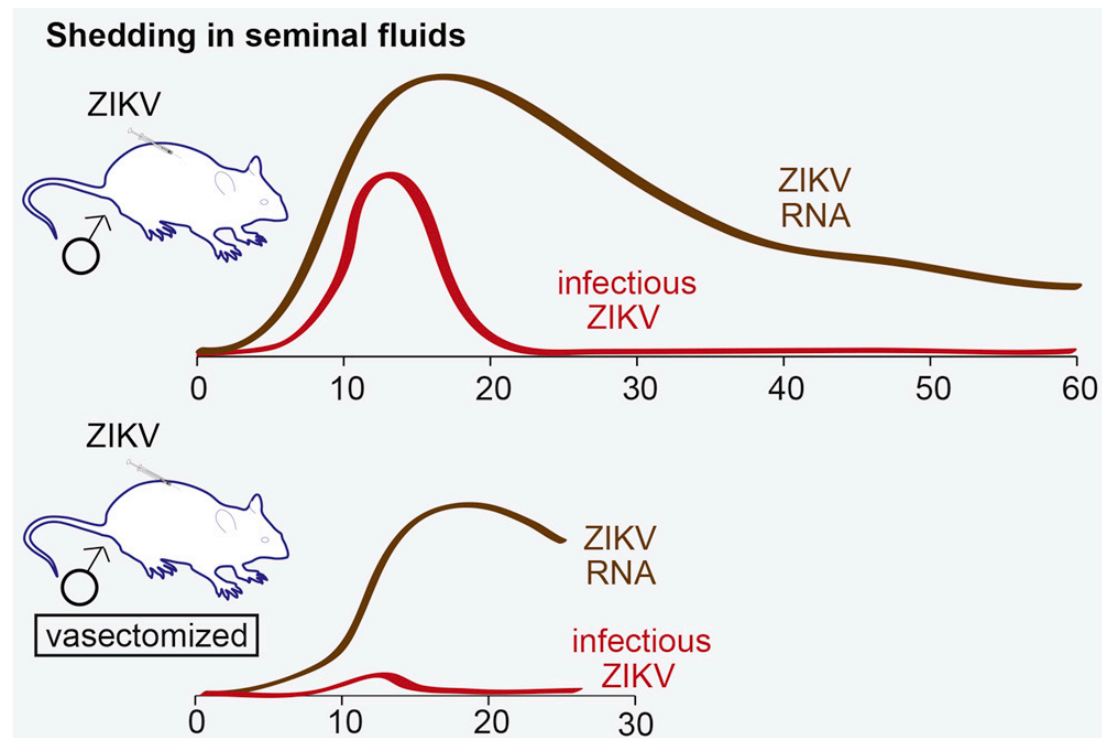
# Polymerase chain reaction (PCR)



- Research
- Industry
- Diagnosis

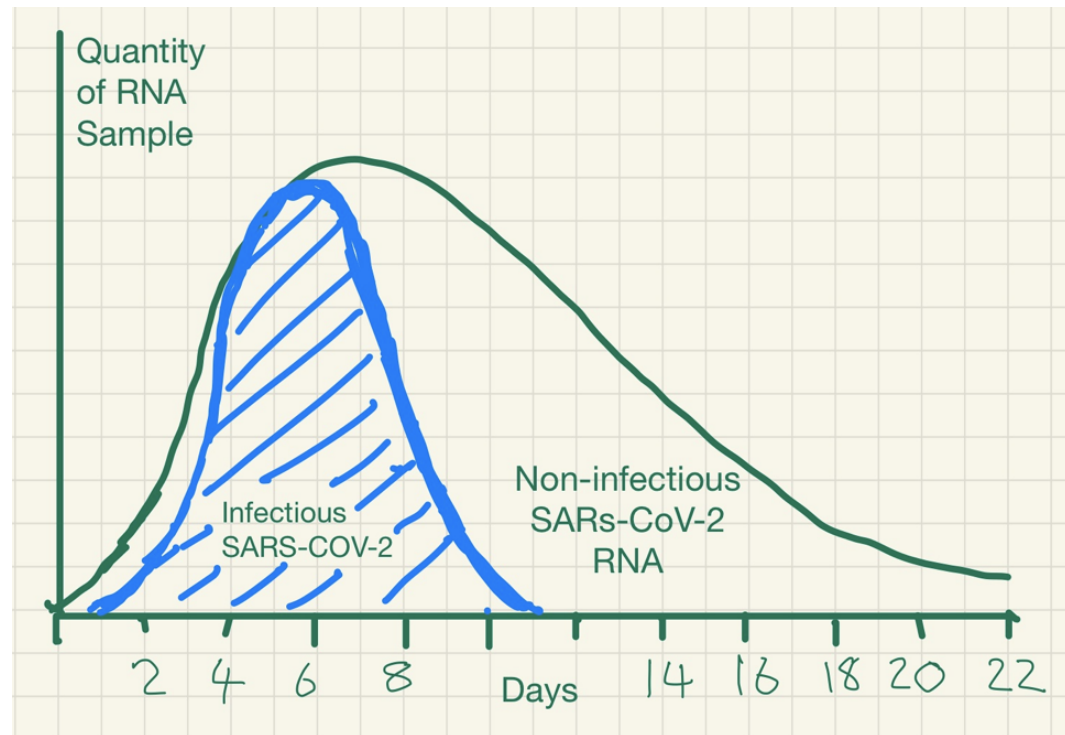


# PCR product is not the same as infectious virus

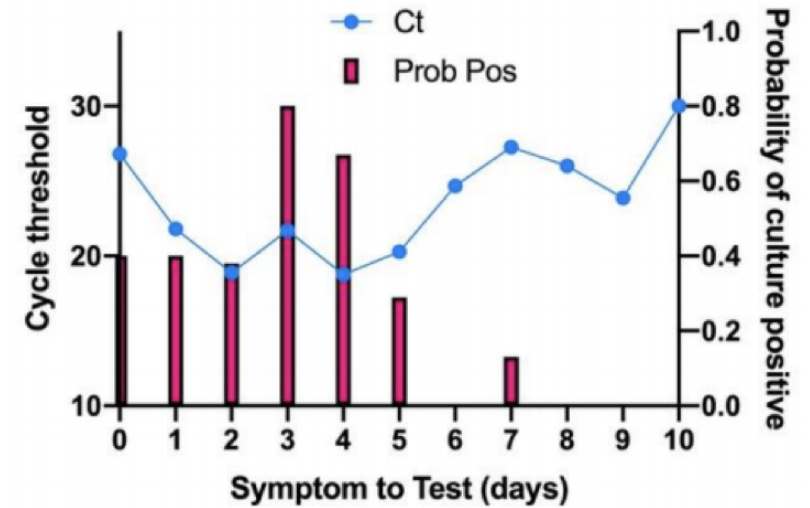
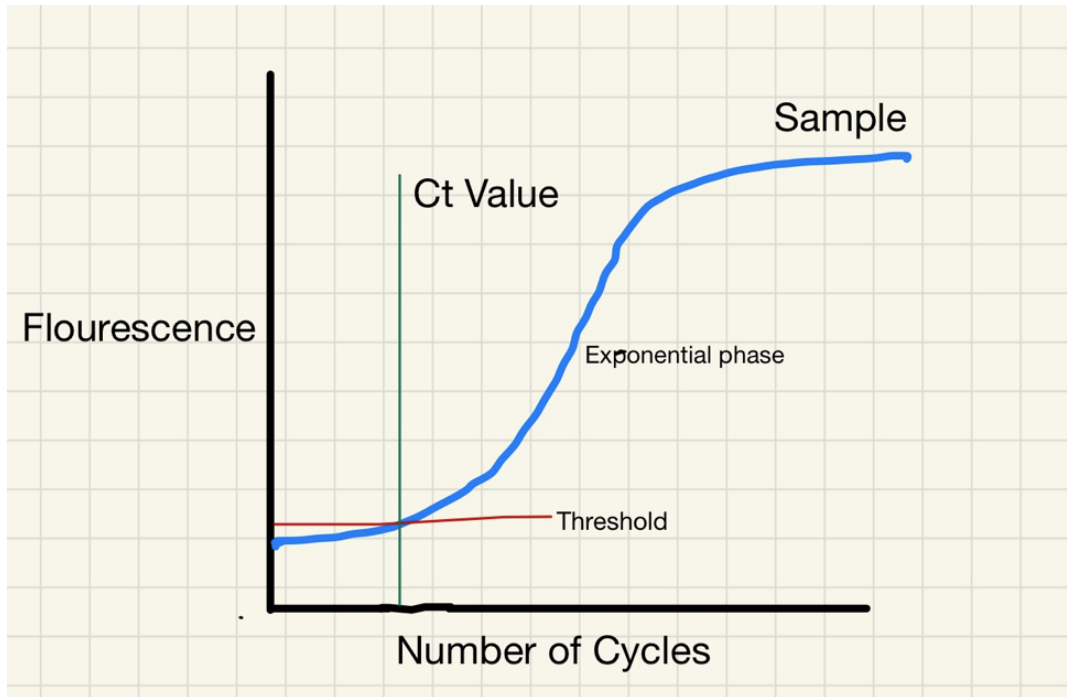


*For many RNA viruses, RNA can be detected long after disappearance of infectious virus*

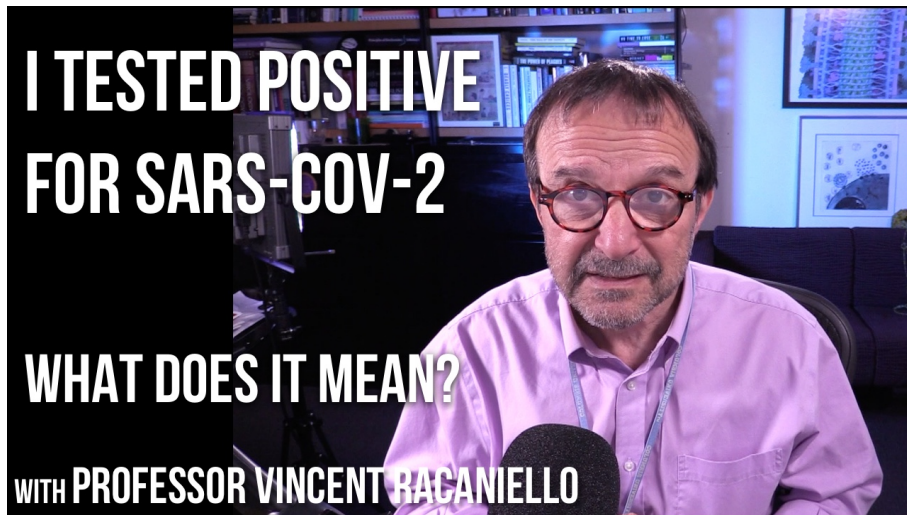
# SARS-CoV-2 RNA and infectivity



# Cycle threshold and SARS-CoV-2



# My experience with Ct and antibody tests



<https://youtu.be/Lk64Zwcj3W8>



<https://youtu.be/HvXCISbrK9Q>





# **VIROLOGY LIVE**

**WITH VINCENT RACANIELLO**

**Next time: Genomes and Genetics**