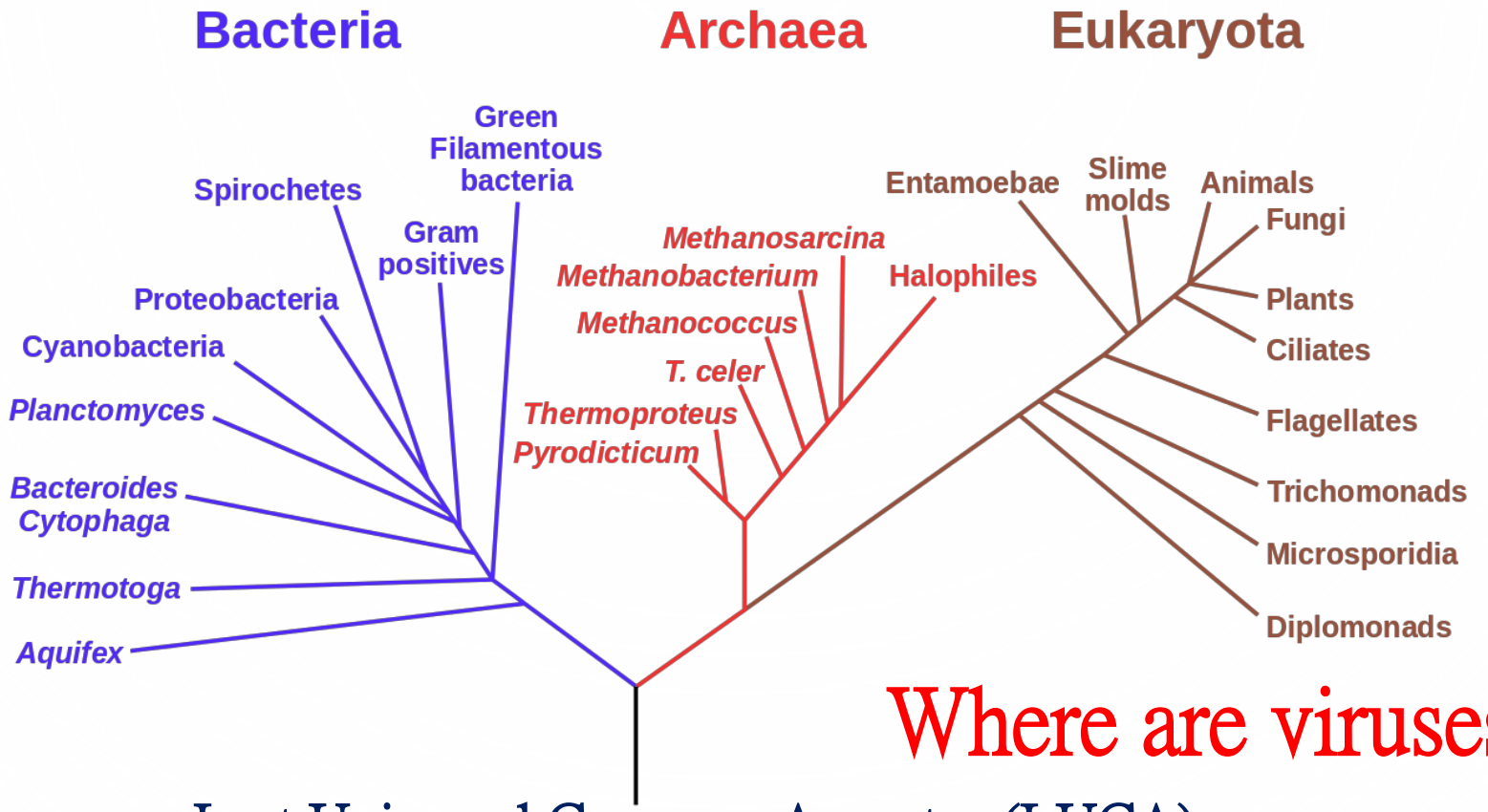
# VIRUS & LAST UNIVERSAL COMMON ANCESTOR

JOINT GRADUATE SEMINAR 2015
M.PHIL. STUDENT: CHEUNG KA WING, KELTON
SUPERVISOR: DR. MARTIN CHAN
15TH DEC 2015
DEPARTMENT OF MICROBIOLOGY
FACULTY OF MEDICINE
THE CHINESE UNIVERSITY OF HONG KONG

# OUTLINE

- Introduction of hypotheses of origin of virus
  - Evidence(s) support individual hypothesis
- New concept of virus origin
  - Evolutionary lineages

# TREE OF LIFE

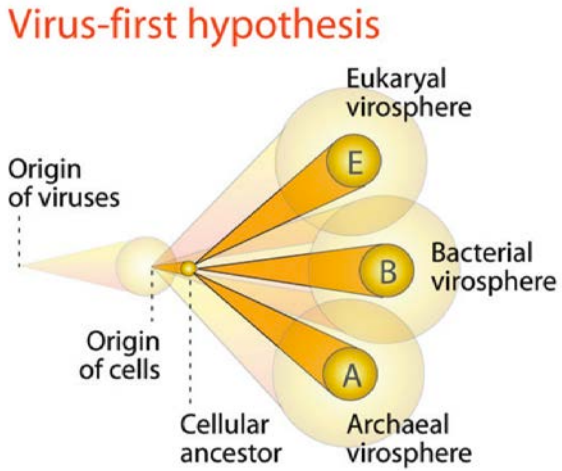



Where are viruses?

Adopted from Wikipedia

# CURRENT HYPOTHESIS OF ORIGIN OF VIRUS

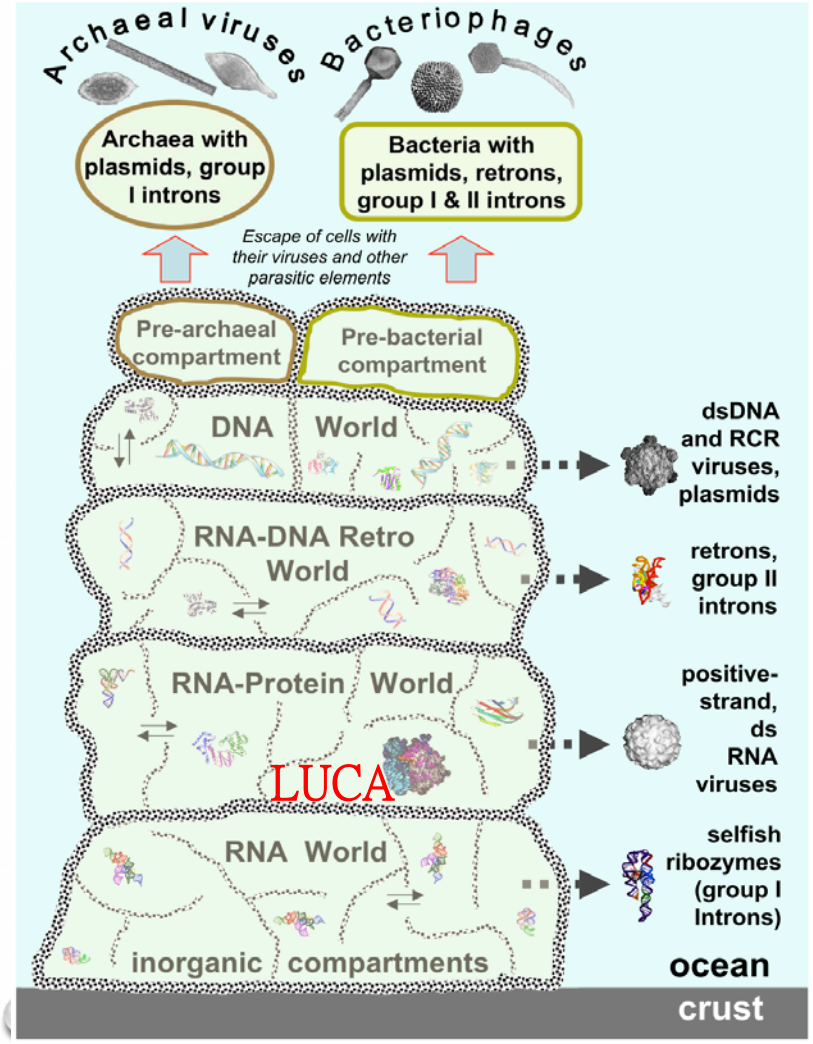
- 3 hypotheses
    1. Virus-first hypothesis




Nasir A, Kim KM, Caetano-Anollés G. Viral evolution: Primordial cellular origins and late adaptation to parasitism. Mob Genet Elements. 2012 Sep 1;2(5):247-252

# VIRUS-FIRST HYPOTHESIS

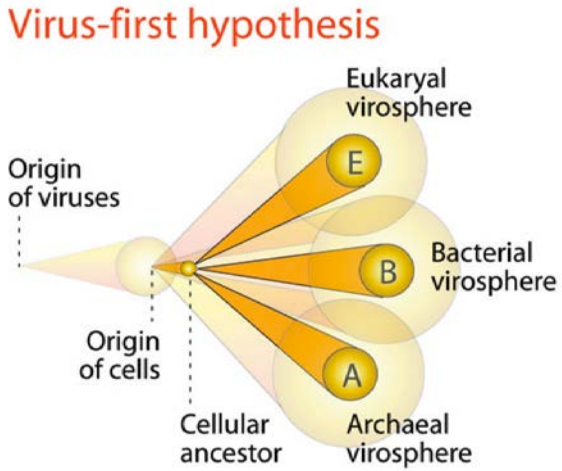
- Primordial genetic pool with compartments
- Transition to ensembles of replication enzymes and translation and nucleic acid synthesis
- Follow evolution of genetic system: RNA→RNA-protein→mixed RNA/DNA→DNA

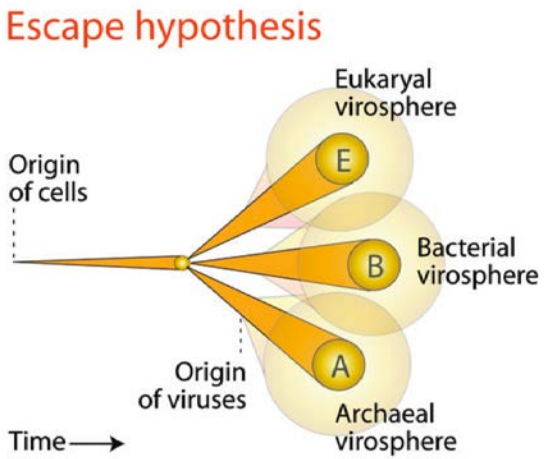



Koonin EV, Senkevich TG, Dolja VV. The ancient Virus World and evolution of cells. Biol Direct. 2006 Sep 19;1:29

# CURRENT HYPOTHESES OF ORIGIN OF VIRUS

- 3 hypotheses
  1. Virus-first hypothesis
  2. Escape hypothesis (progressive hypothesis)

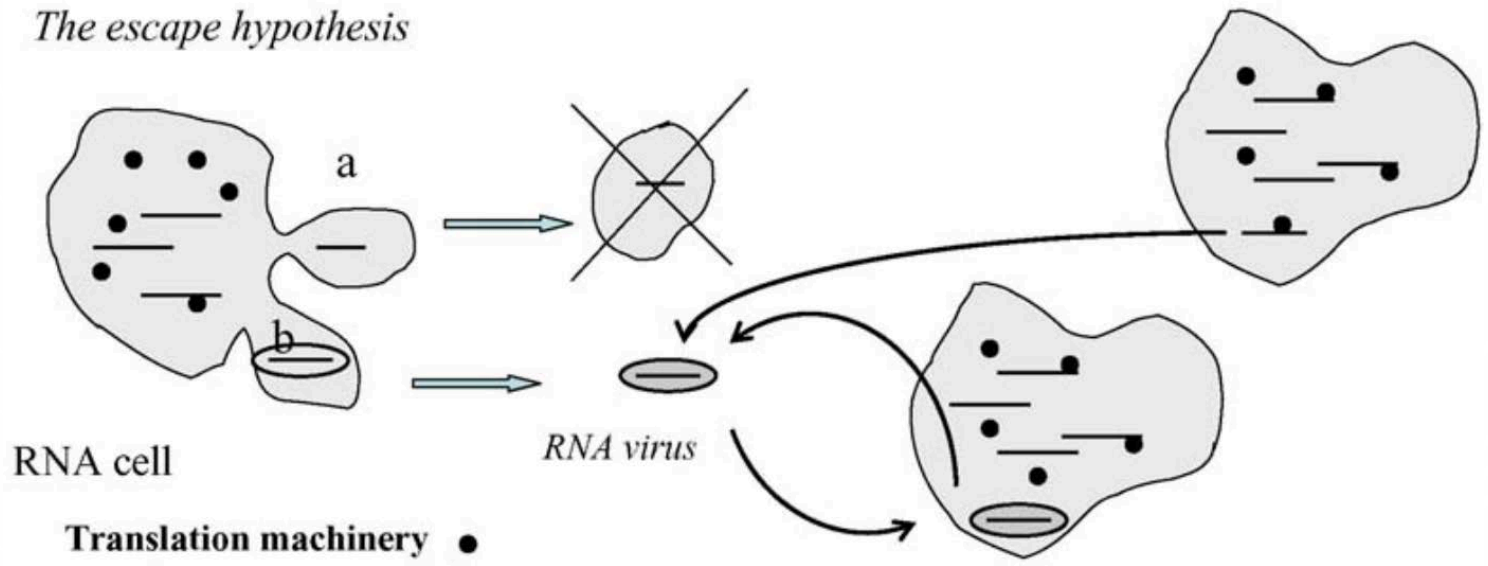



Nasir A, Kim KM, Caetano-Anollés G. Viral evolution: Primordial cellular origins and late adaptation to parasitism. Mob Genet Elements. 2012 Sep 1;2(5):247-252

# ESCAPE HYPOTHESIS

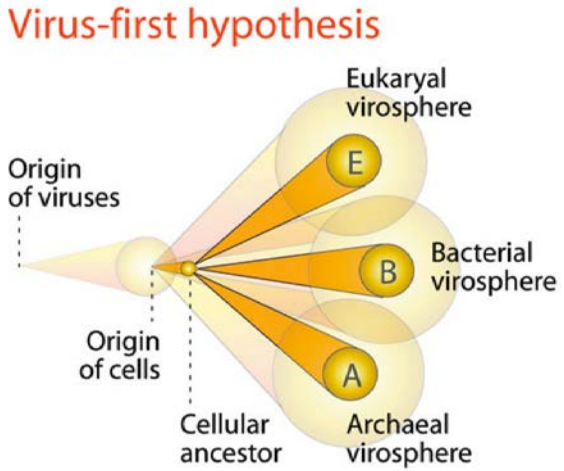
- Unequal cell division
- Minicell with RNA and protein coat but without ribosome
- Gain ability to be transferred

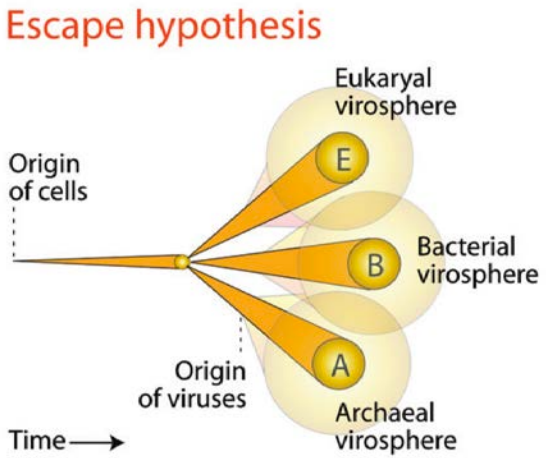


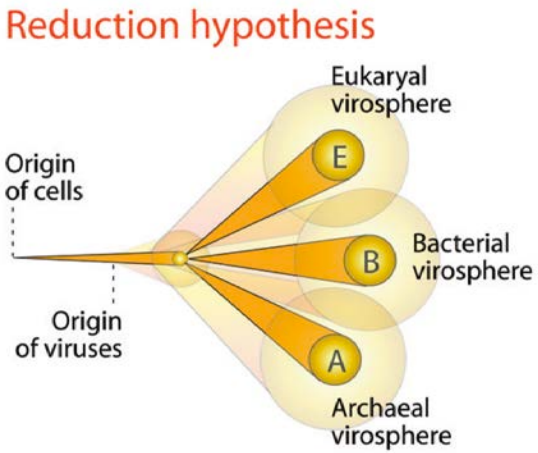

Forterre P. The origin of viruses and their possible roles in major evolutionary transitions. Virus Res. 2006 Apr;117(1):5-16

# CURRENT HYPOTHESIS OF ORIGIN OF VIRUS

- 3 hypotheses
  1. Virus-first hypothesis
  2. Escape hypothesis (progressive hypothesis)
  3. Reduction hypothesis (regressive hypothesis)



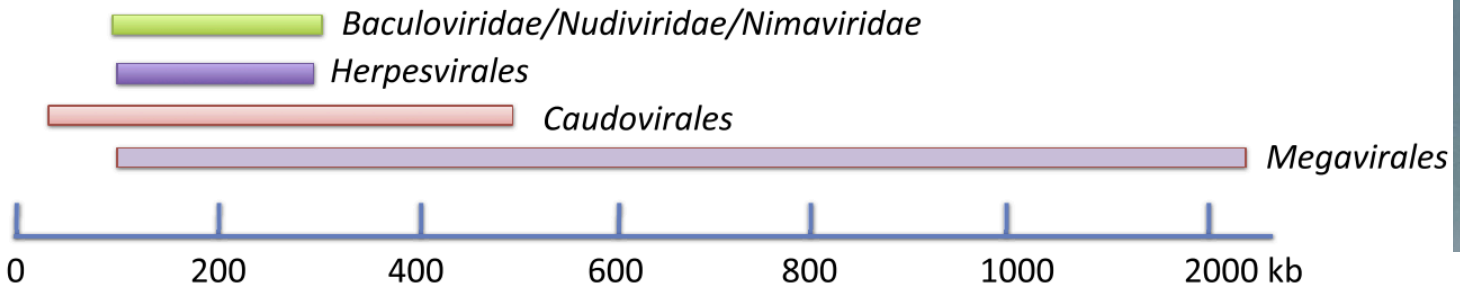



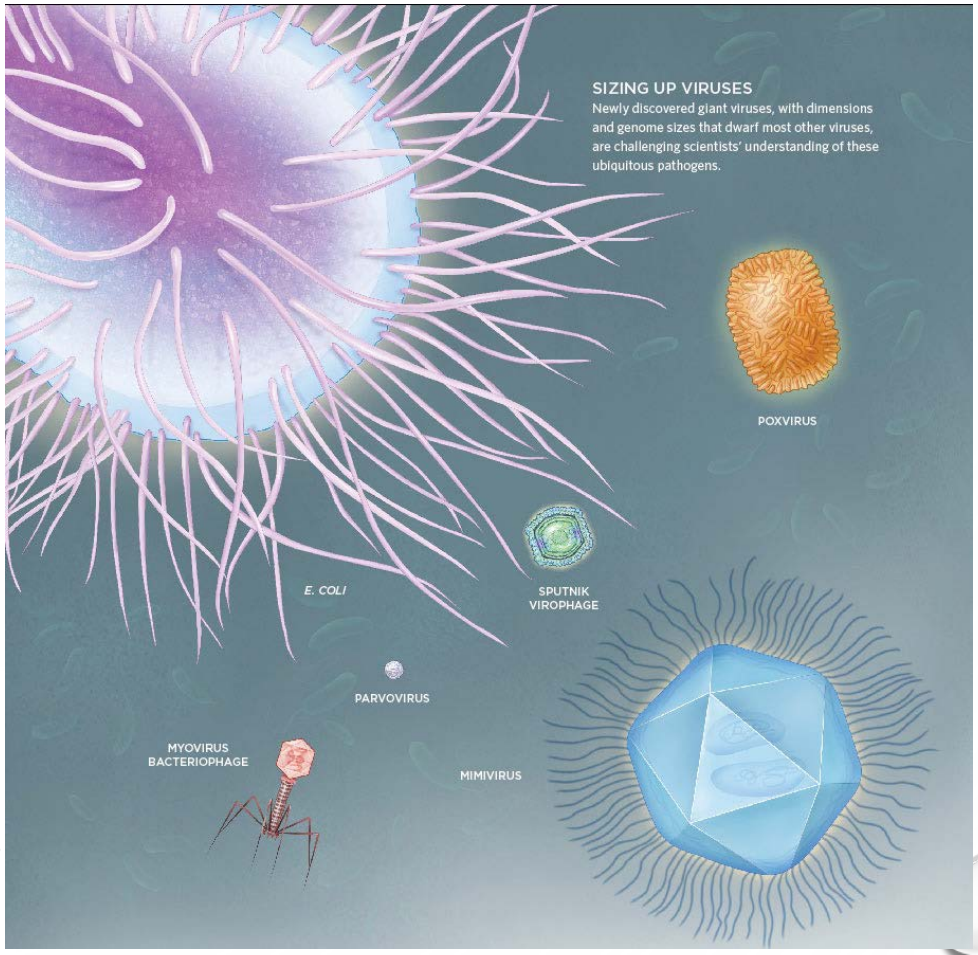




Nasir A, Kim KM, Caetano-Anollés G. Viral evolution: Primordial cellular origins and late adaptation to parasitism. Mob Genet Elements. 2012 Sep 1;2(5):247-252

# REDUCTION HYPOTHESIS

- Discovery of order *Megavirales*,
  - Previously called nucleocytoplasmic large DNA viruses (NCLDV)
- Virion size: 400-800nm
- Gene number: up to 3 thousand
  - Orthologs of DNA repair, protein folding and protein translation genes



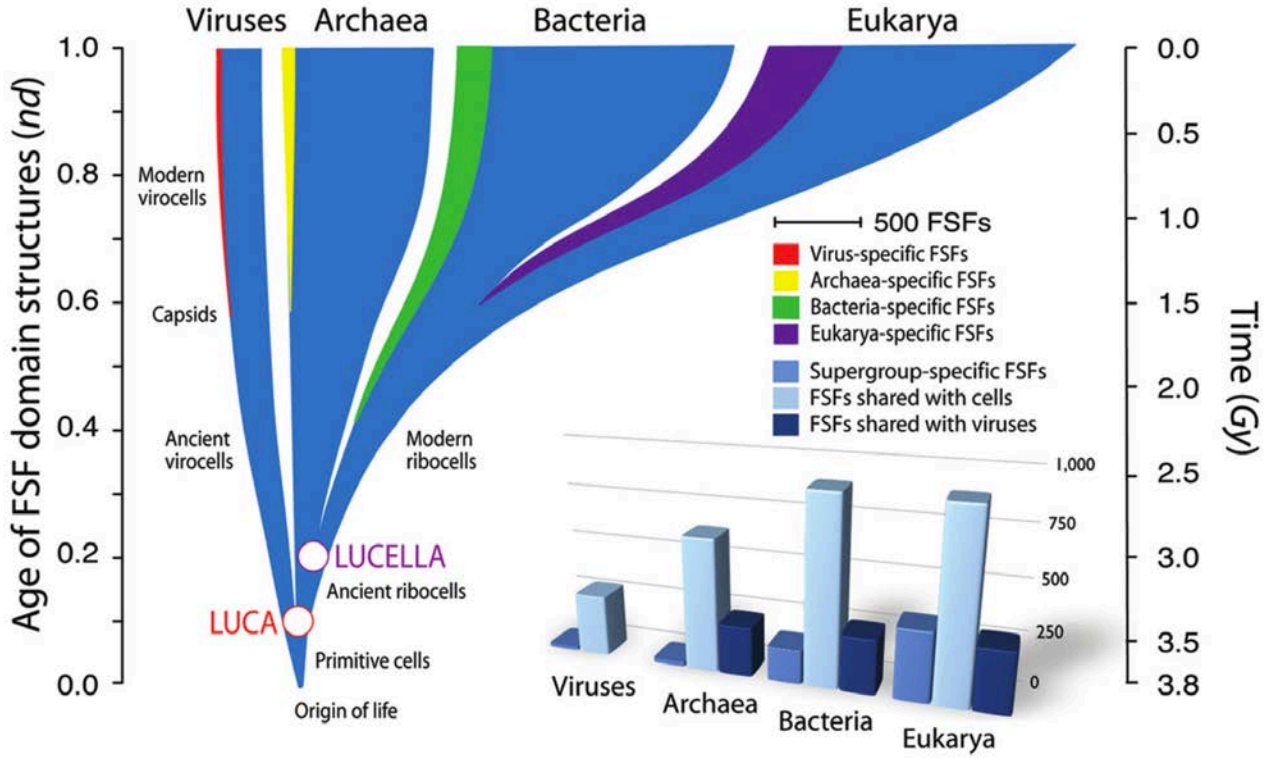




Adopted from The Scientist March 1,2014

Forterre P, Krupovic M, Prangishvili D. Cellular domains and viral lineages. Trends Microbiol. 2014 Oct;22(10):554-8

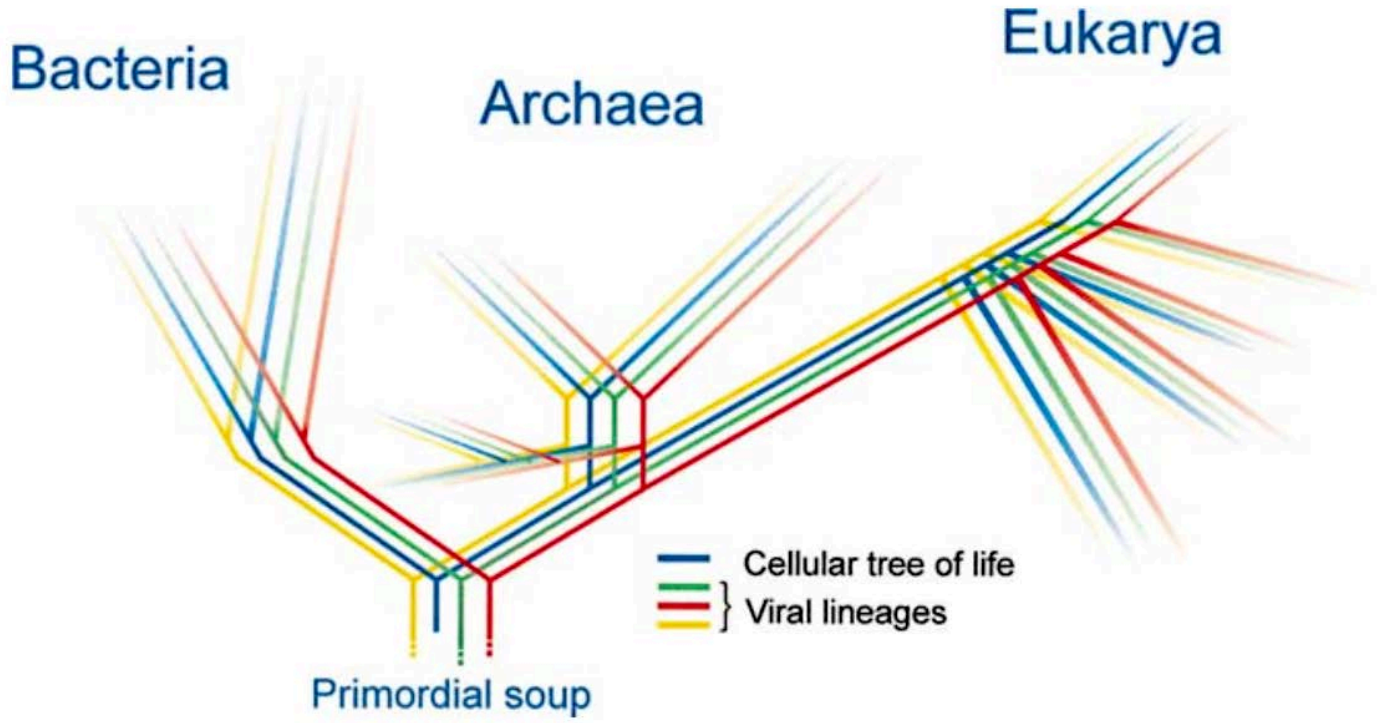
# WHEN DID VIRUS APPEAR?

- Molecular phylogenetic analysis using protein domain structures
- Fold superfamilies (FSF) & fold families (FF) were assigned
- FSFs common in virus & cells appeared to be ancient
- Virus-specific FSFs (viral capsid protein) appeared late, concurrently with Archaea-specific & Eukarya-specific FSFs




Nasir A, Kim KM, Caetano-Anollés G. Viral evolution: Primordial cellular origins and late adaptation to parasitism. Mob Genet Elements. 2012 Sep 1;2(5):247-252

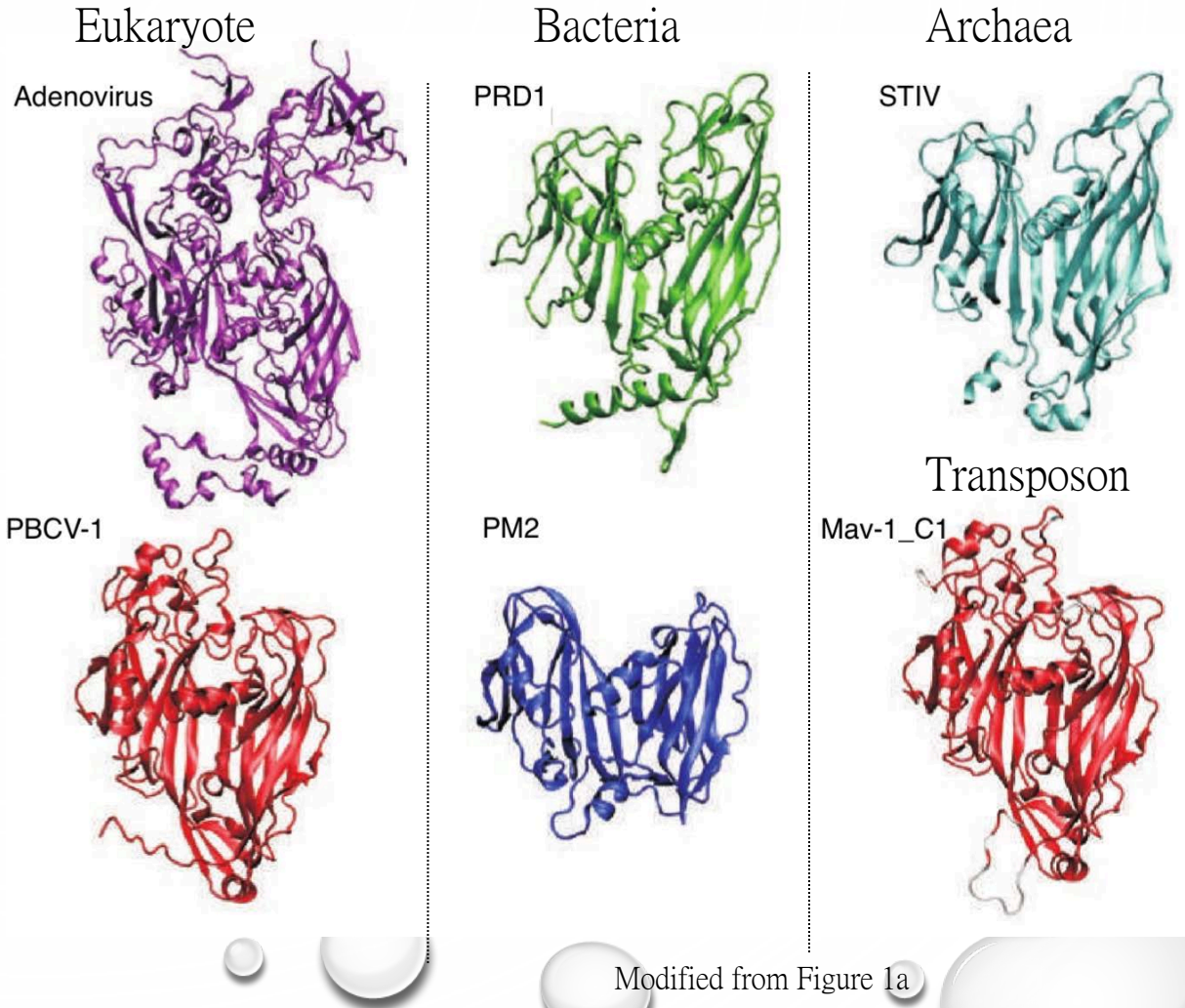
# DO VIRUSES FORM LINEAGES ACROSS DIFFERENT DOMAINS OF LIFE?




Bamford DH. Do viruses form lineages across different domains of life? Res Microbiol. 2003 May;154(4):231-6

# DO VIRUSES FORM LINEAGES ACROSS DIFFERENT DOMAINS OF LIFE?

- 3D structure of major capsid protein
- Viruses infect different domains share similar protein folding-double beta-barrel
- High structural resemblance
- Similar genome packaging method and replication mechanism
- PRD1-adenovirus lineage



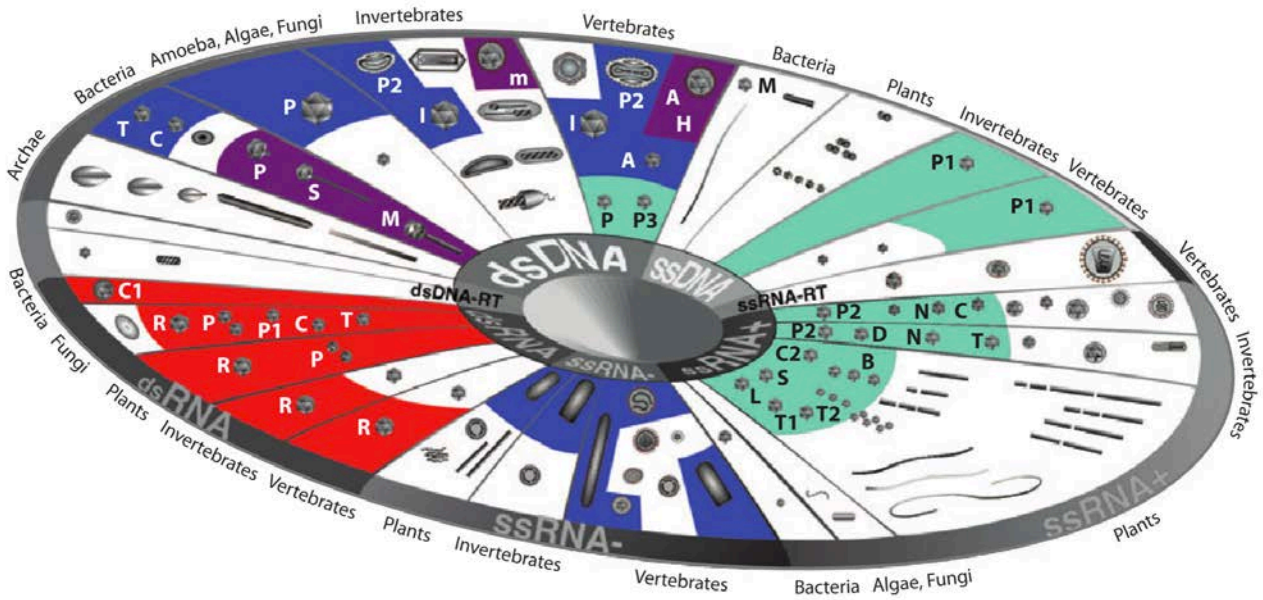

Modified from Figure 1a

Krupovic M, Bamford DH. Virus evolution: how far does the double beta-barrel viral lineage extend? Nat Rev Microbiol. 2008 Dec;6(12):941-8

# MORE VIRAL LINEAGES ALSO EXIST

- Viruses infect different domains share similar protein folding

➢ Origin of viruses with this protein folding predated LUCA diverged into 3 domains




**Lineage: BTV like**
C: *Chrysoviridae*
C1: *Cystoviridae*
P: *Partitiviridae*
P1: *Picobirnaviridae*
R: *Reoviridae*
T: *Totiviridae*

**Lineage: PRD1/Adeno**
A: *Adenoviridae*
C: *Corticoviridae*
I: *Iridoviridae*
P: *Phycodnaviridae*
P2: *Poxviridae*
T: *Tectiviridae*

**Lineage: HK97 like**
M: *Myoviridae*
P: *Podoviridae*
S: *Siphoviridae*
A: *Alloherpesviridae*
H: *Herpesviridae*
m: *Malacoherpesviridae*

**Lineage: Picorna like**
B: *Bromoviridae*
C: *Caliciviridae*
C2: *Comoviridae*
D: *Dicistroviridae*
L: *Luteoviridae*
M: *Microviridae*
N: *Nodaviridae*
P: *Papillomaviridae*
P1: *Parvoviridae*
P2: *Picornaviridae*
P3: *Polyomaviridae*
S: *Sequiviridae*
T: *Tetraviridae*
T1: *Tombusviridae*
T2: *Tymoviridae*

Abrescia NG, Bamford DH, Grimes JM, Stuart DI. Structure unifies the viral universe. Annu Rev Biochem. 2012;81:795-822. doi: 10.1146/annurev-biochem-060910-095130

# SUMMARY & FUTURE PERSPECTIVE

- Emergence of virus before or after LUCA still unknown
- Still a hot debate in field of evolutionary virology
- Digging more viruses by metagenomic analysis from different environments
    - Find out missing links

END

THANK YOU