



浙江大学
生命演化研究中心

Host phylogeny shapes viral transmission networks in an island ecosystem



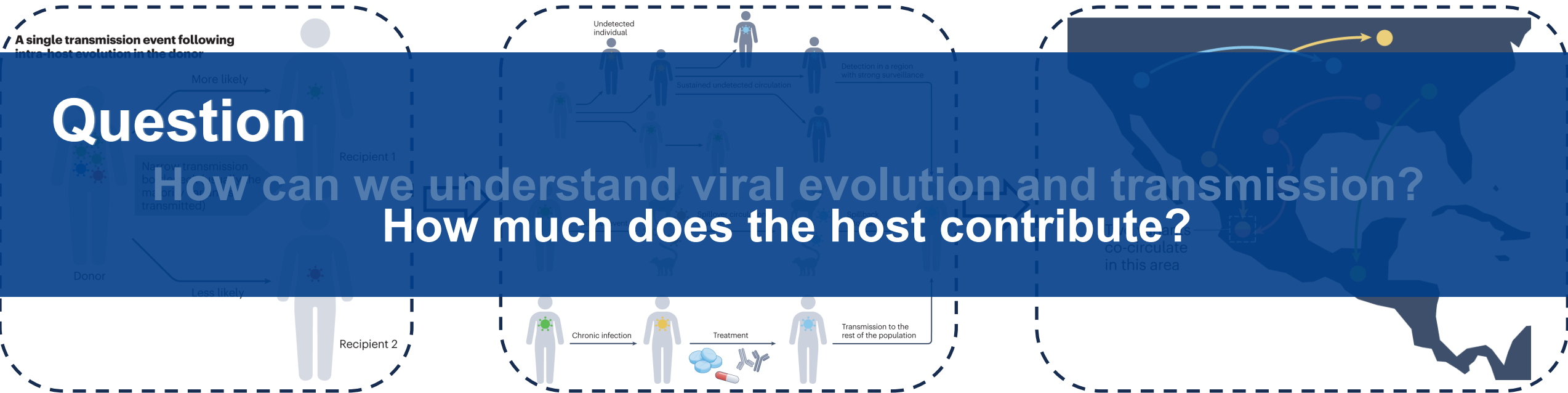
Wenjing Wei

2026.05.22

Viruses Do Not Evolve in Isolation

SARS-CoV-2

- The most familiar example about viral evolution: **COVID-19**



- SARS-CoV-2 did not evolve into Omicron in isolation
- It evolved while moving through different people, populations, and transmission networks.

Omicron



About the Author

Edward Charles Holmes

- Fellow of Australia's National Health and Medical Research Council (NHMRC)
- Professor at the University of Sydney
- Honorary visiting professor at Fudan University

- Viral Phylogeny
- Cross-species transmission of viruses

Edward Charles Holmes. 1962 ~

2020

There is no evidence that SARS-CoV-2, the virus that causes COVID-19 in humans, originated in a laboratory in Wuhan, China.

The Proximal Origin of SARS-CoV-2

Nature Medicine

Transmission Dynamics of Emerging Viruses Across Species and Populations

E. Ramirez¹, L. Chen², M. Patel¹, A. Nguyen², and J. K. Lee¹

¹Department of Virology, Global Health Institute, University of Brookdale

²Center for Infectious Disease Modeling, Eastview University

³Wildlife Health Program, National Institute of Ecology

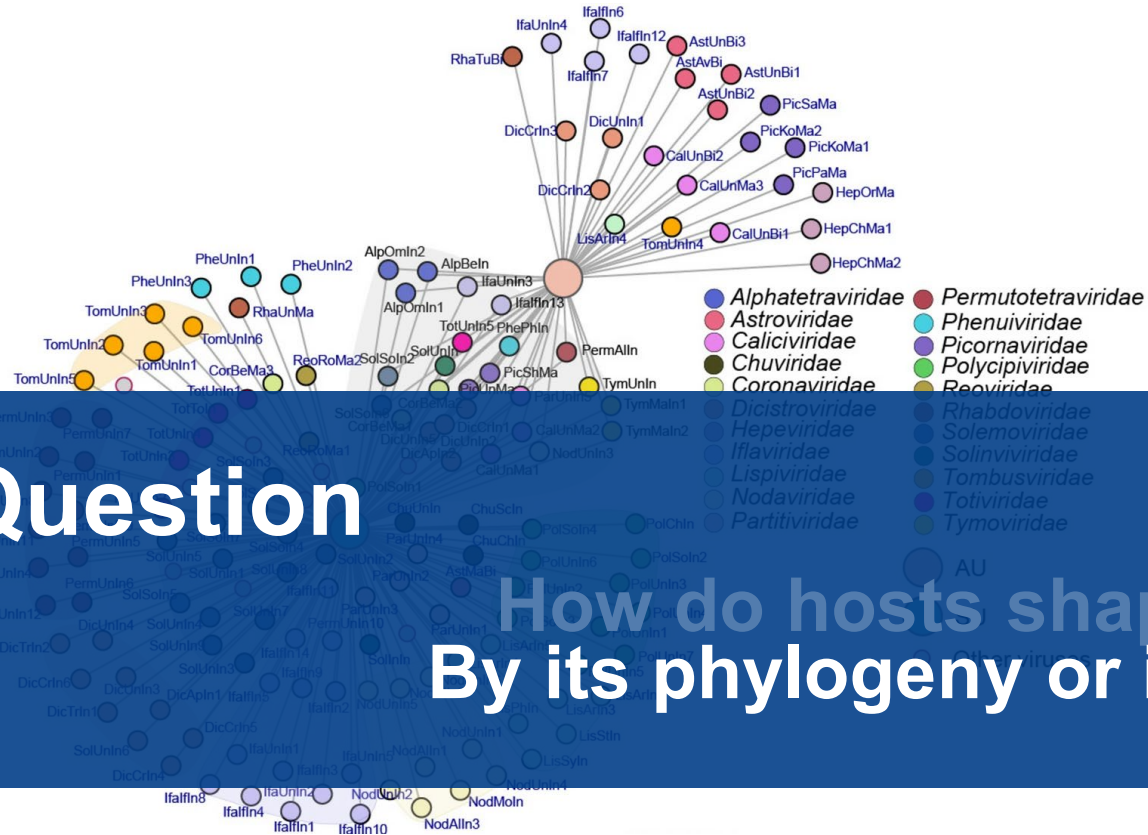
2.2 Transmission Modeling

We developed a stochastic, multi-host SEIR model with host-specific transmission rates (β), cross-species transmission (β_{ij}), and environmental persistence (ϵ). Parameters were estimated using Bayesian inference.

2.3 Statistical Analysis

We estimated the basic reproduction number (R_0) for each host and assessed risk factors for spillover using multivariable regression. Uncertainty was quantified using 95% credible intervals (CrI).

Background



Question

How do hosts shape viral evolution? By its phylogeny or its feeding ecology?



Zhenglanyi Huang et al., 2024

Wan Ting He et al., 2022



Fiordland National Park



➤ Only about 11 square kilometers in size





18 Bird species



1 Skink



21 Arthropod



6 Plant taxa

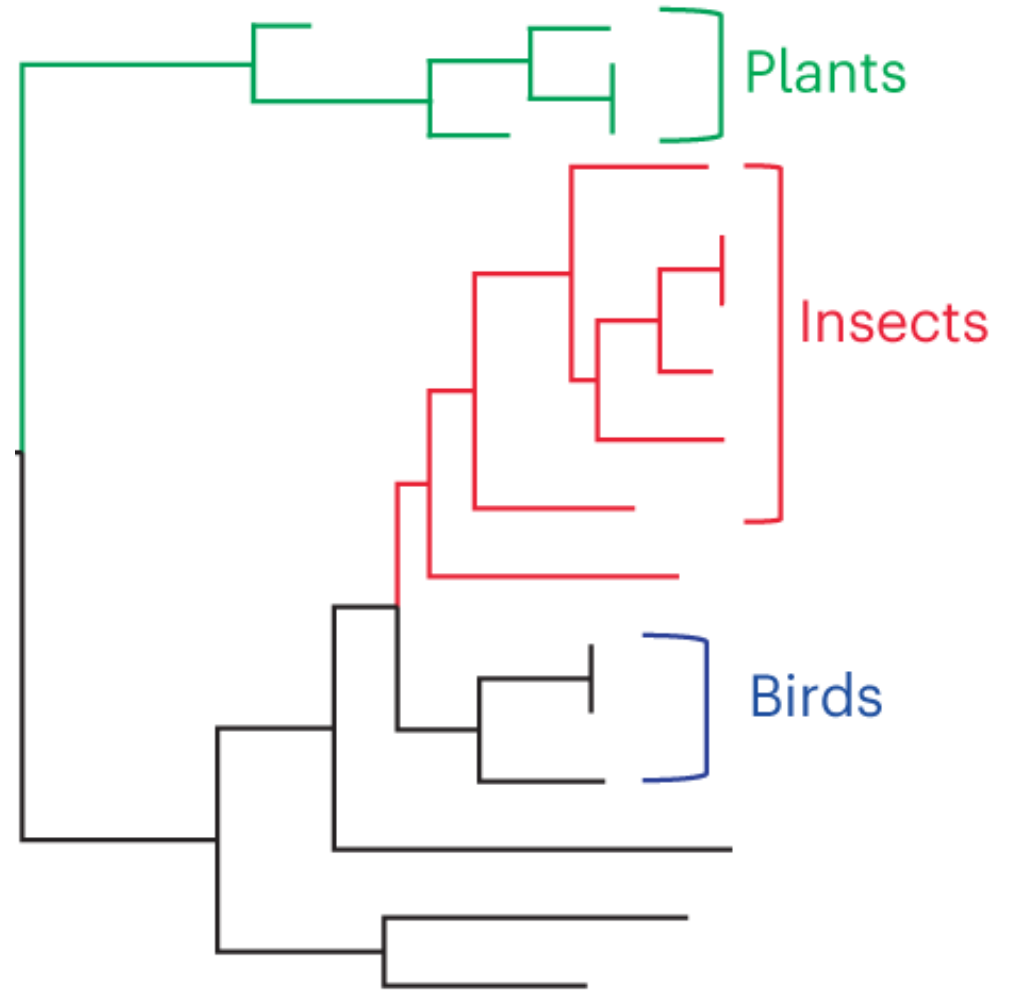
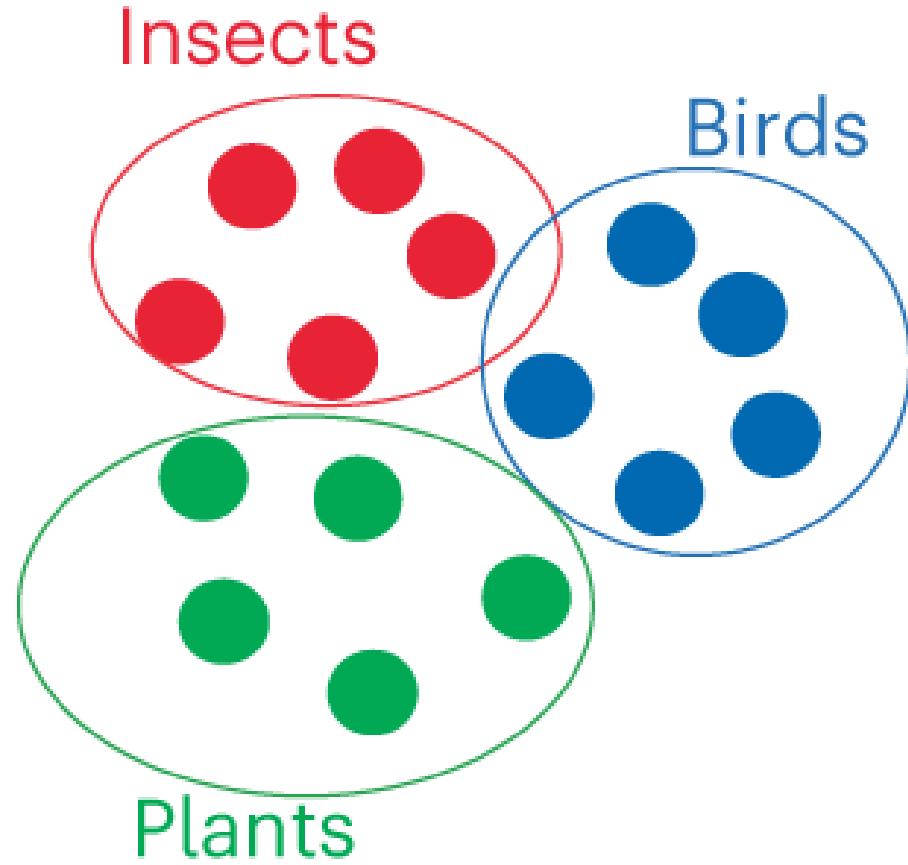


2 Annelids



1 Flatworm

Expectation before analysis

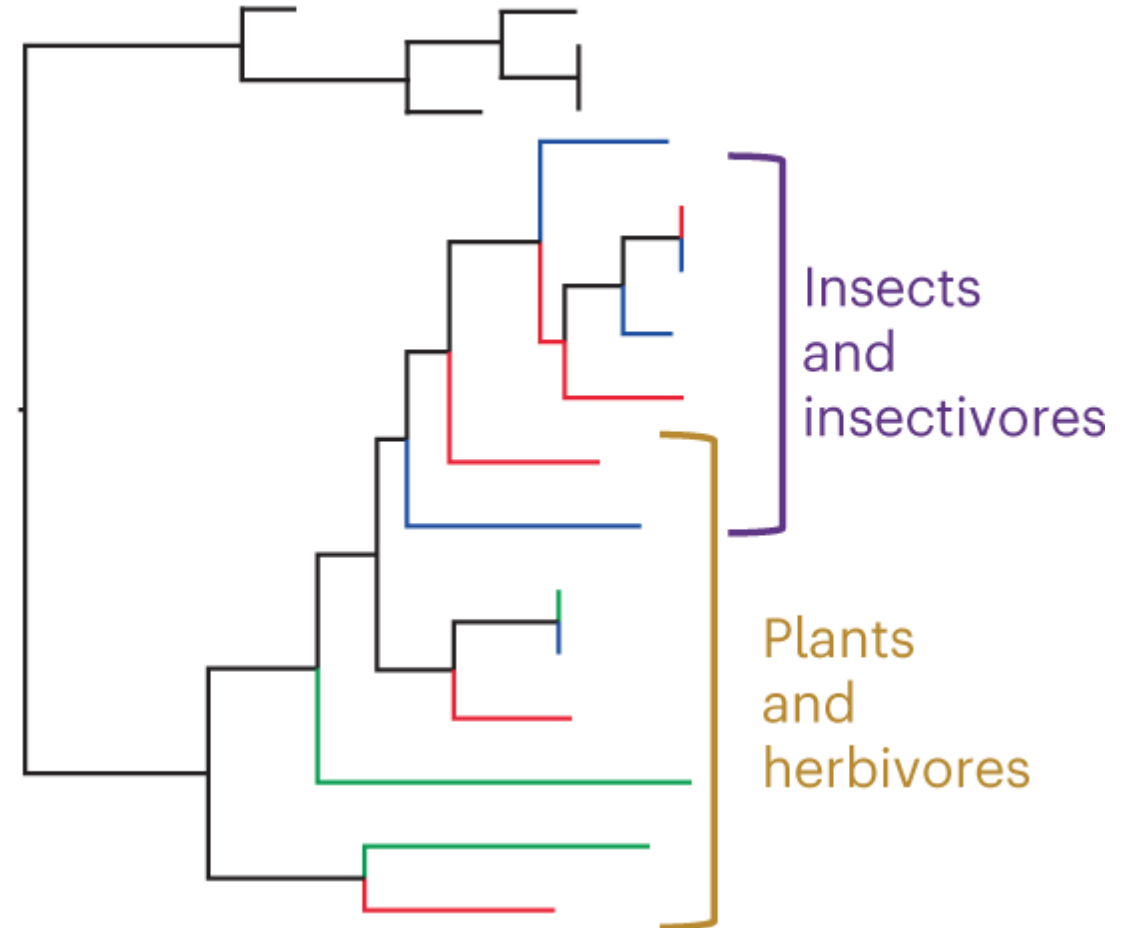
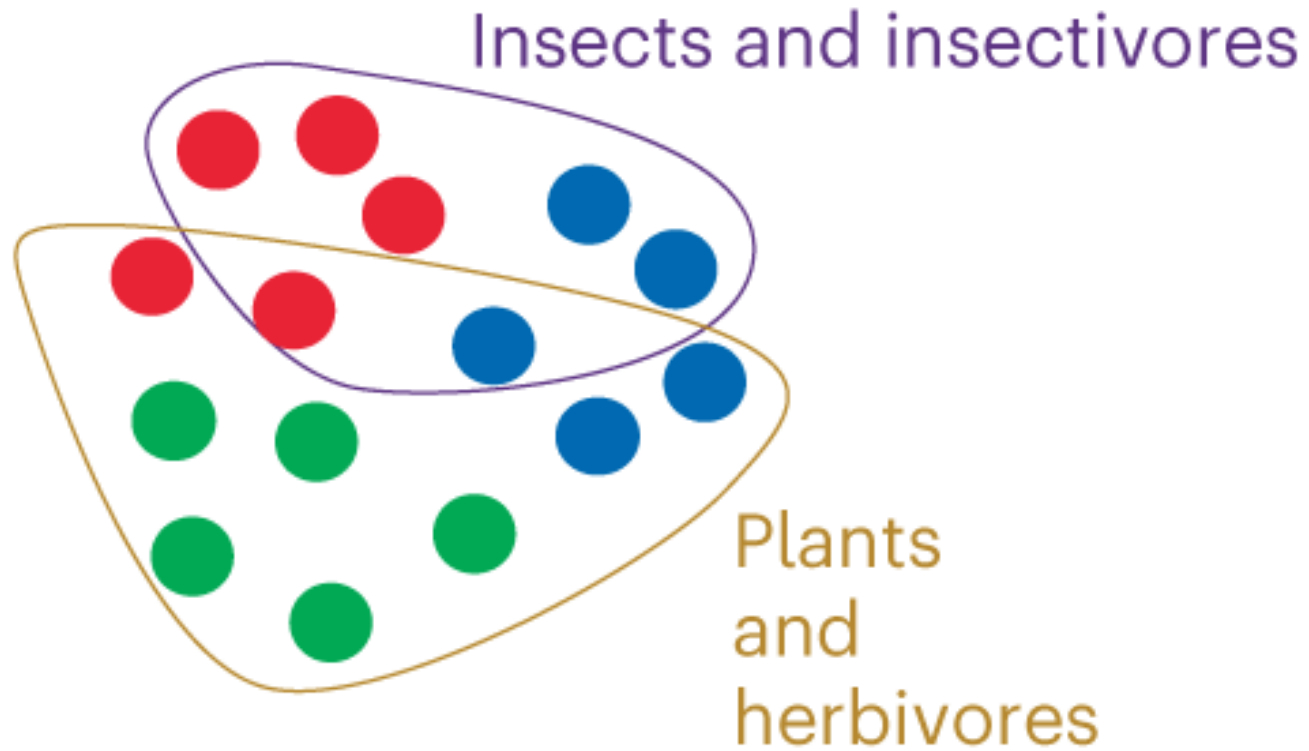


➤ Viruses would group together based on the host's phylum

➤ The viral phylogeny matches the host phylogeny

● **The idealized situation**

Expectation before analysis



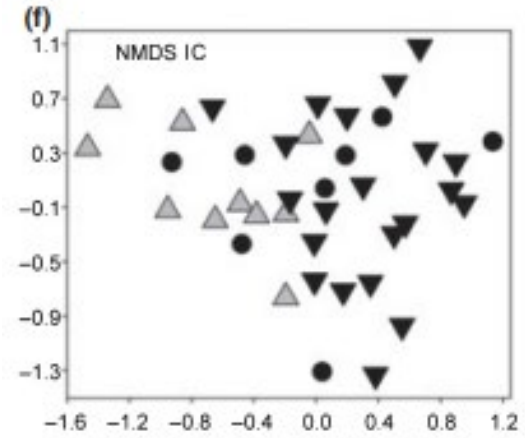
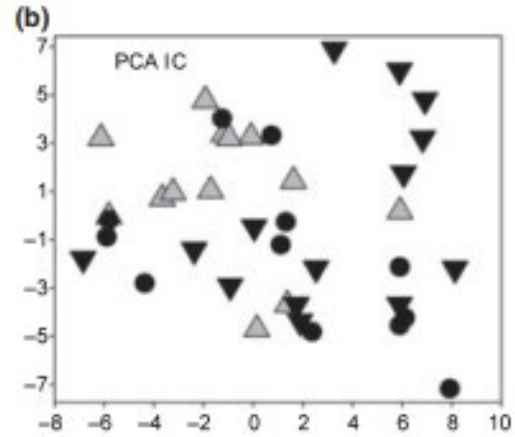
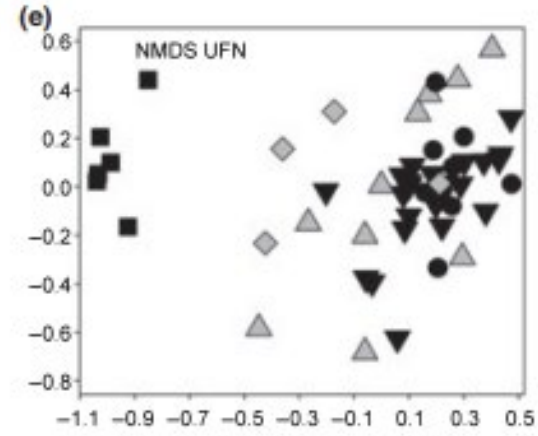
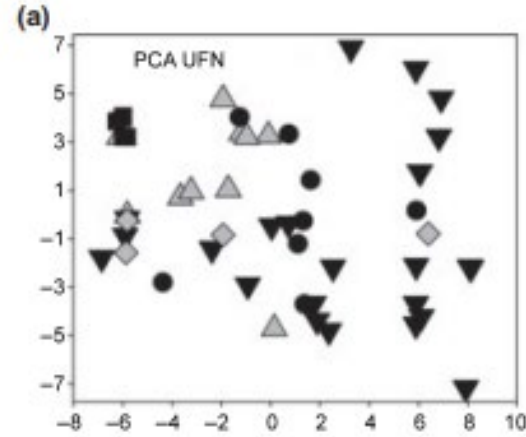
➤ Viruses might cluster based on major dietary links

➤ Hosts with similar diets may carry similar viruses

● **Predators may share similar viruses with their prey**

Whether different hosts actually carried different viral communities

	H1	H2	H3
V1			
V2			
V3			



NMDS 1



Key difference:

- NMDS more care about distance
- PCA more care about contribution

Host–virome bipartite network analysis

The algorithm looked for groups of nodes highly connected internally and weekly connected with rest

Module 4

- Chordata (13) 
- Arthropoda (3) 

Module 3



- Chordata (6) 
- Arthropoda (1) 



Each Node Represents a Host of a Viral Family

Are these host-virus associations just random?
Do they show a real structure?

Module 2

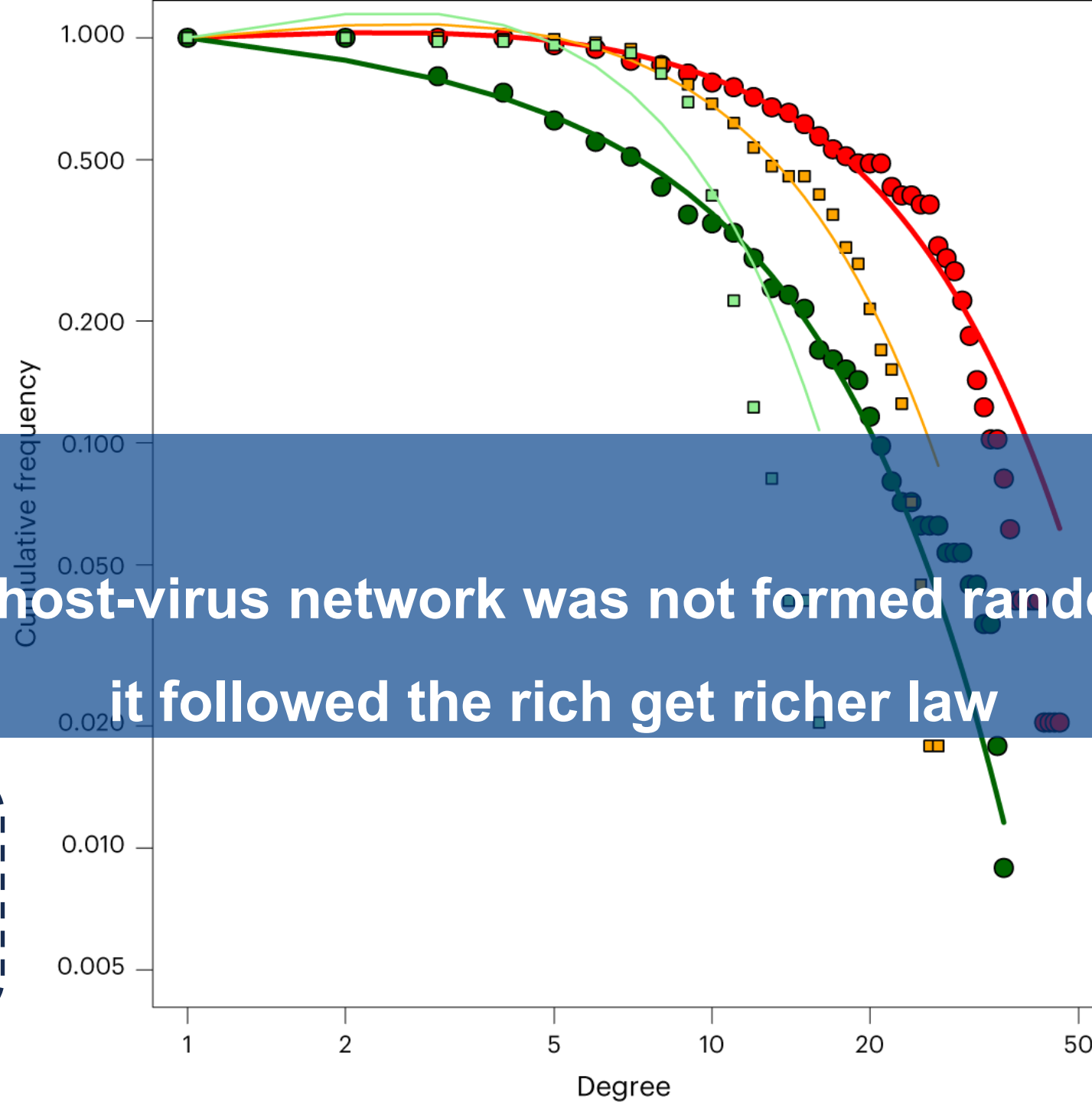
- Streptophyta (6) 
- Arthropoda (2) 

Module 1

- Arthropoda (15) 
- Annelida (2) 
- Platyhelminthes (1) 

Module 1: Arthropods and Diet-Linked Taxa
Module 2: Plants and Plant-Associated Arthropods
Modules 3 & 4: Vertebrates and Diet-Linked Taxa

Analyzed the number of links connected to each node in the network:
Degree Distribution



Cumulative frequency:

- The proportion of nodes with a degree greater than or equal to the x axis

Answer

The host-virus network was not formed randomly,
it followed the rich get richer law

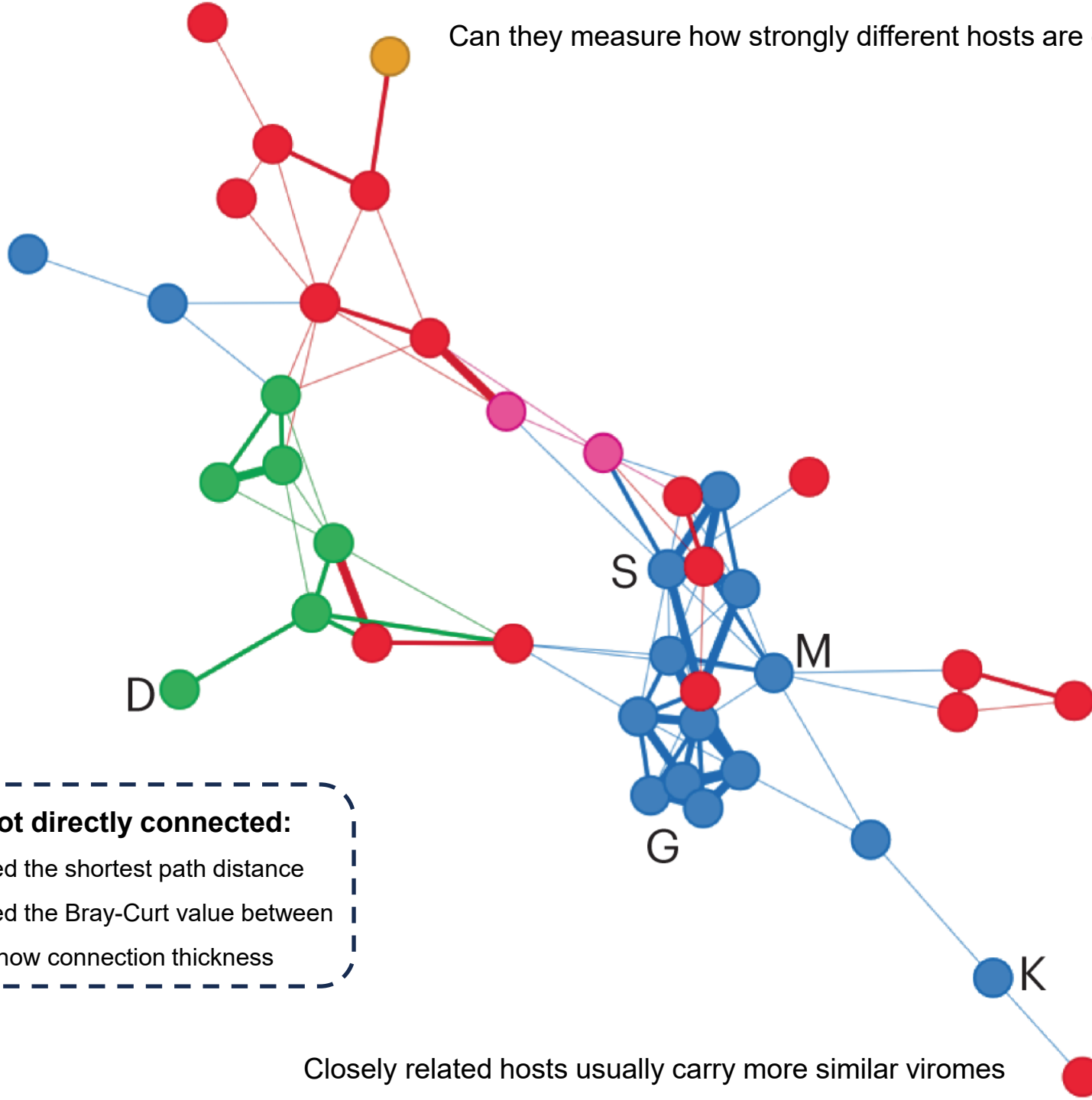
Degree:

- How many other nodes a node is connected to

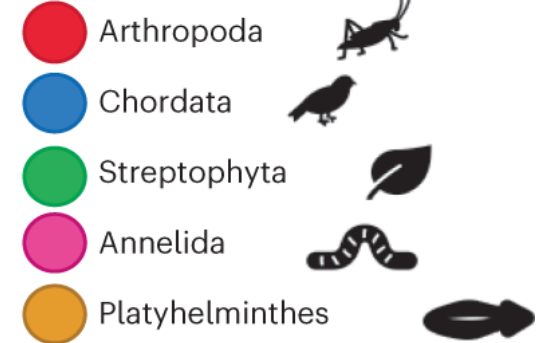
Rich Get Richer:

- Highly connected hosts tend to gain more viral links
- Highly connected viruses tend to reach more hosts

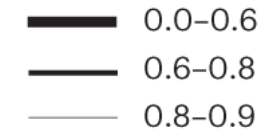
Can they measure how strongly different hosts are connected?



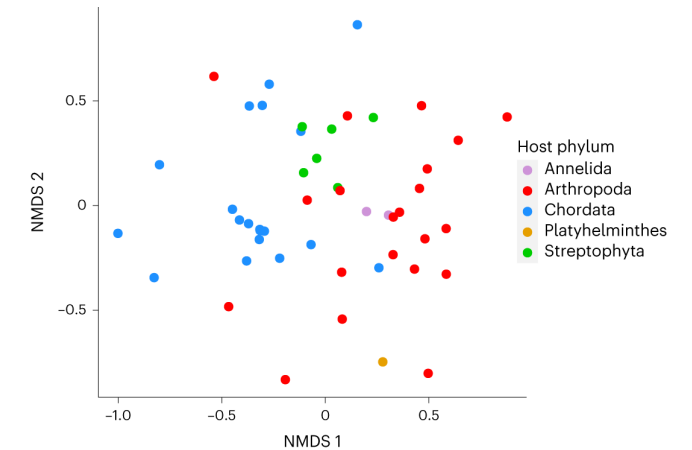
Host phylum



Bray-Curtis dissimilarity



This pattern is similar to the NMDS result



Host are not directly connected:

- They used the shortest path distance
- They used the Bray-Curt value between host to show connection thickness

Closely related hosts usually carry more similar viromes

It looks like hosts phylogeny is the major factor shaping the virome

Module 4

- Chordata (13)
- Arthropoda (3)

Module 3

- Chordata (6)
- Arthropoda (1)

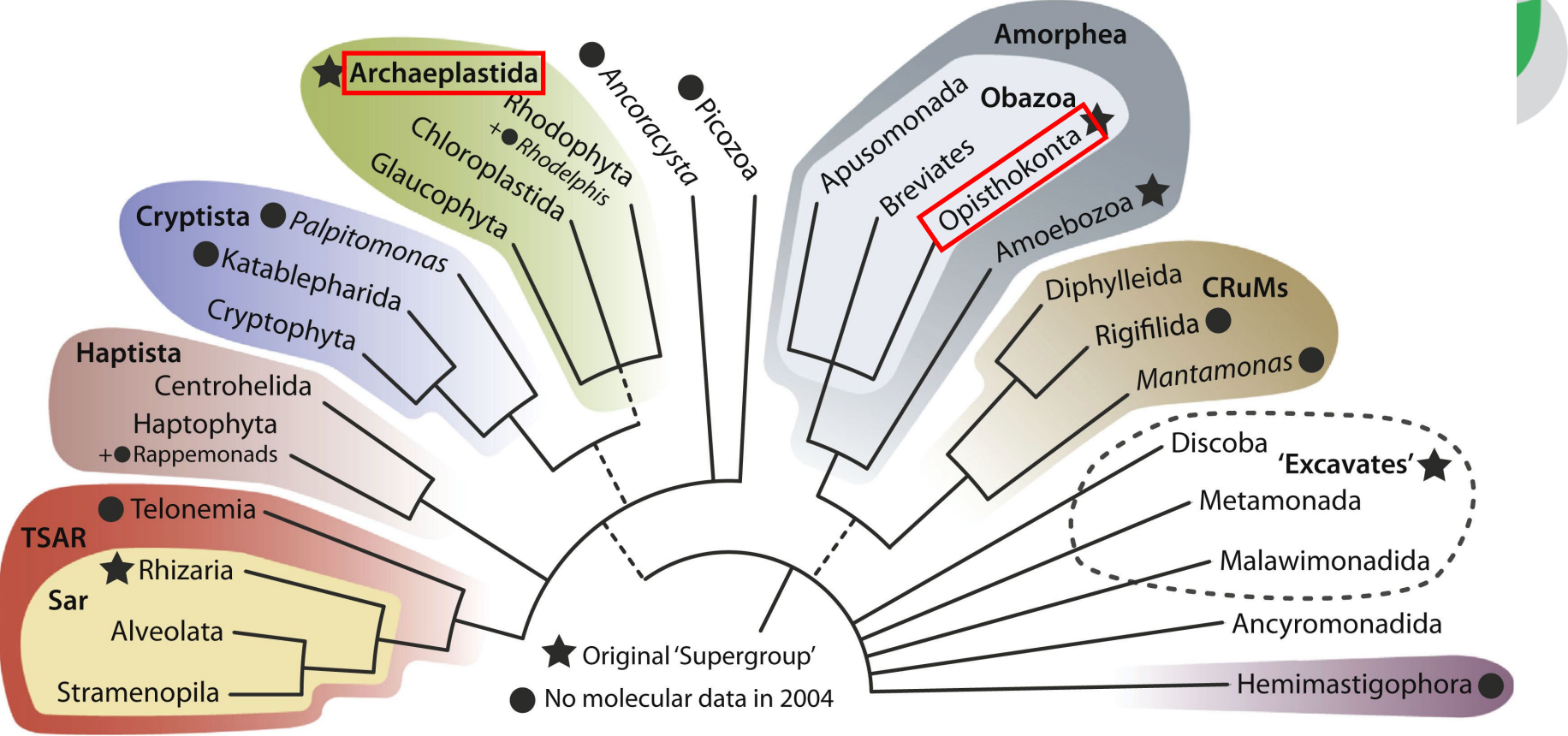


Host phylum

- Streptophyta
- Chordata

Module 1

- Arthropoda (15)
- Annelida (2)
- Platyhelminthes (1)



Badnavirus

Host Ecology

- Host phylogeny
- But feeding ecology
- In Module 2, ... on the viral tree
- This suggests host feeding ecology is also a signal to virus shaping



Summary

Host phylogeny dominates virus transmission networks

- Closely related hosts tend to carry more similar viromes

Host–virus associations are structured, not random

- The host–virome bipartite network shows modularity and a rich-get-richer pattern

Host feeding ecology still leaves signals

- Feeding relationships may also promote virus shaping

Limitation

Virus detection does not equal active infection

- Viruses detected in a host may come from diet, gut contents, or environmental exposure

Network links are potential associations

- Shared viruses or similar viromes suggest possible connections, but do not prove direct virus transmission

Taxonomic resolution is limited

- Many viruses were analyzed at the family level, which may hide species- level transmission patterns.

Thanks for your attention!

Q&A