A Bayesian Assessment of the Origins of COVID-19 Using Spatiotemporal & Zoonotic Data

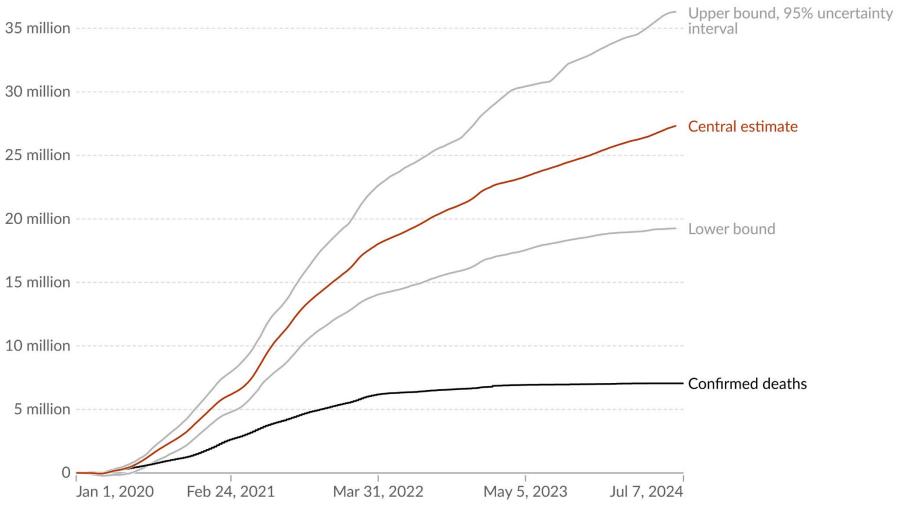
> Andrew Levin Dartmouth College

#### July 2024

Note: This presentation solely reflects the views of the author and should not be interpreted as reflecting the views of any other person or institution.

#### Estimated cumulative excess deaths during COVID-19, World

For countries that have not reported all-cause mortality data for a given week, an estimate is shown, with uncertainty interval. If reported data is available, that value only is shown. For comparison, cumulative confirmed COVID-19 deaths are shown.



Data source: The Economist (2023); WHO COVID-19 Dashboard

OurWorldInData.org/coronavirus | CC BY



Source: BBC (Jan. 2020)



Source: Yahoo News (2020)

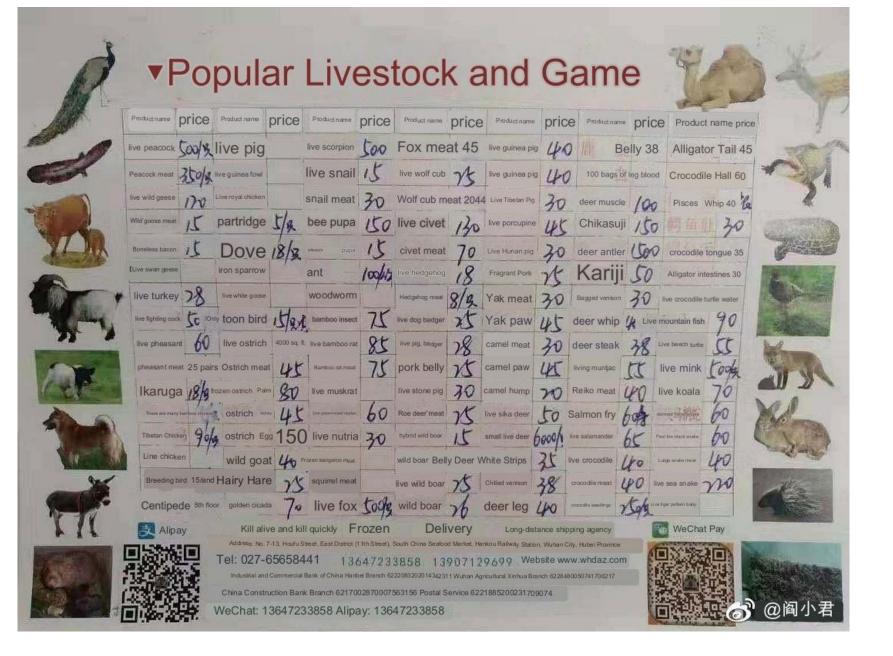




#### Source: WHO via online seminar by Dr. Marion Koopmans (June 2021)

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Source: JustTheNews (Jan. 2020)

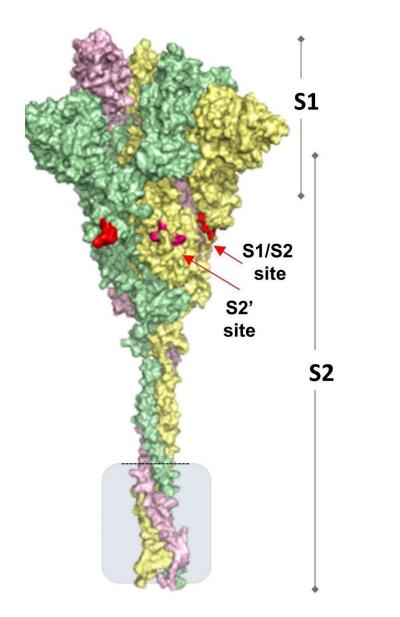


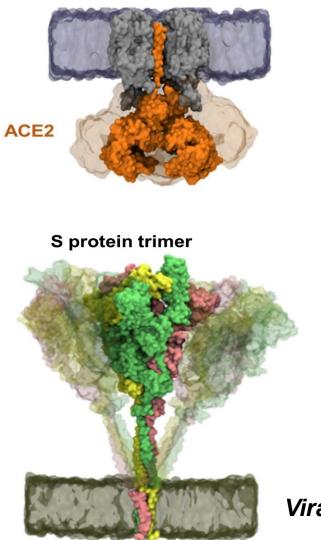


Source: Dr. Edward Holmes (2014)



#### Source: Kaarina Kauhala (2022)



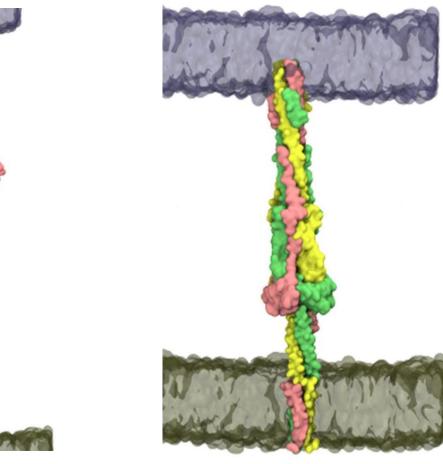


Host Cell

Viral Membrane

Source: Raghuvamsi et al. (2021)

#### **Host Membrane**



**Viral Membra** 

Source: Raghuvamsi et al. (2021)

**S1** 

**S2** 

## **Comparing Genomes of Three Species**

<u>Genetic Sequence</u>	<u># Nucleotides</u>	<u>Relative Scale</u>	<u>Relative Size</u>
Homo sapiens	3,000,000,000	Earth to Moon	400,000 km
E. Coli bacteria	4,600,000	San Francisco to Los Angeles	560 km
<i>Sars-Cov-2</i> virus	29,900	Lincoln Memorial to U.S. Capitol	4 km
Spike gene	3,822	Hoover Tower to Green Library	500 m
<i>Furin cleavage</i> site	4	PC keyboard	0.5 m



The 2020 Nobel Prize for Chemistry was awarded to Jennifer Doudna and Emmanuelle Charpentier for the CRISPR/Cas9 gene editing method developed in 2012.

#### Wuhan Institute of Virology



#### Source: New York Times (2021)

## **Two Competing Hypotheses**

• Hypothesis A: The pandemic was triggered by an accidental lab leak of a bat-related coronavirus.

• Hypothesis Z: The pandemic was triggered by a zoonotic spillover from a wild animal that was an intermediate host for a bat-related coronavirus.

## **Bayesian Analysis**

#### $POSTERIOR\_ODDS_{AZ} = PRIOR\_ODDS_{AZ} * BF_1 * BF_2 * BF_3 * BF_4$

where  $BF_i = Marginal Likelihood_{Ai} / Marginal Likelihood_{Zi}$ 

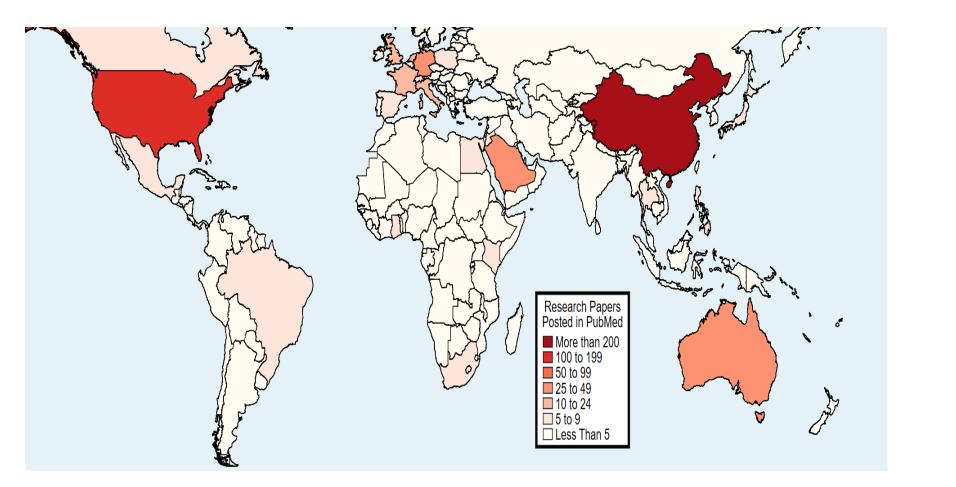
- **Component #1**: The marginal likelihood that the pandemic outbreak would be observed in PRC under each hypothesis.
- Component #2: The marginal likelihood that the pandemic outbreak would be observed in Wuhan, conditional on its occurrence in PRC, under each hypothesis.
- **Component #3**: The marginal likelihood of observing the spatiotemporal pattern of early COVID cases at Huanan Market, conditional on an outbreak in Wuhan, under each hypothesis.
- **Component #4:** The marginal likelihood of observing the pattern of early COVID cases unlinked to Huanan market, conditional on the outbreak occurring in Wuhan, under each hypothesis.

# Why Did the Pandemic Start in PRC?

• Hypothesis A: Assess the global distribution of research on bat-related coronaviruses as well as cross-country differences in biosafety standards.

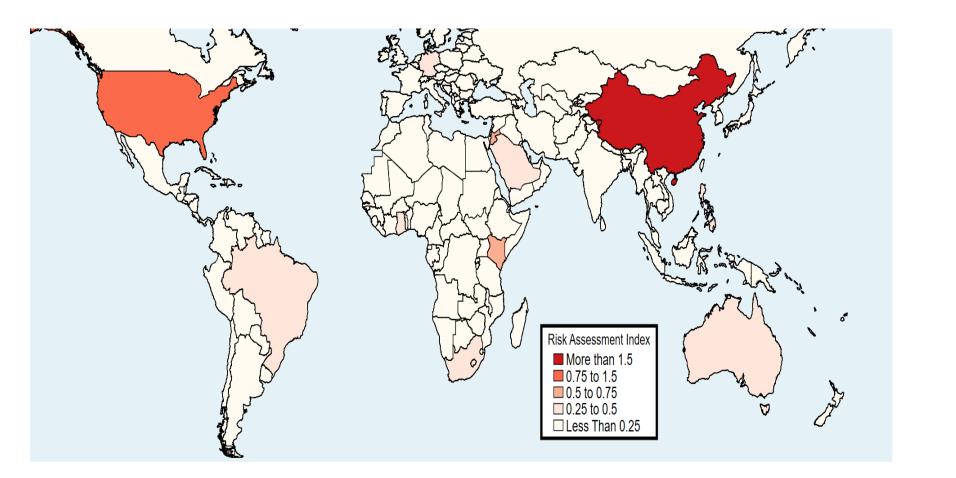
• Hypothesis Z: Assess the global distribution of bat species identified as hosts of betacoronaviruses, particularly MERS-related and SARS-related viruses.

## The Global Distribution of Research on Bat-Related Coronaviruses



Source: Phelps et al. (2019)

## The Global Distribution of Risks of Bat-Related Viral Research



#### Source: Author's calculations

## The Global Distribution of Risks of Bat-Related Viral Research

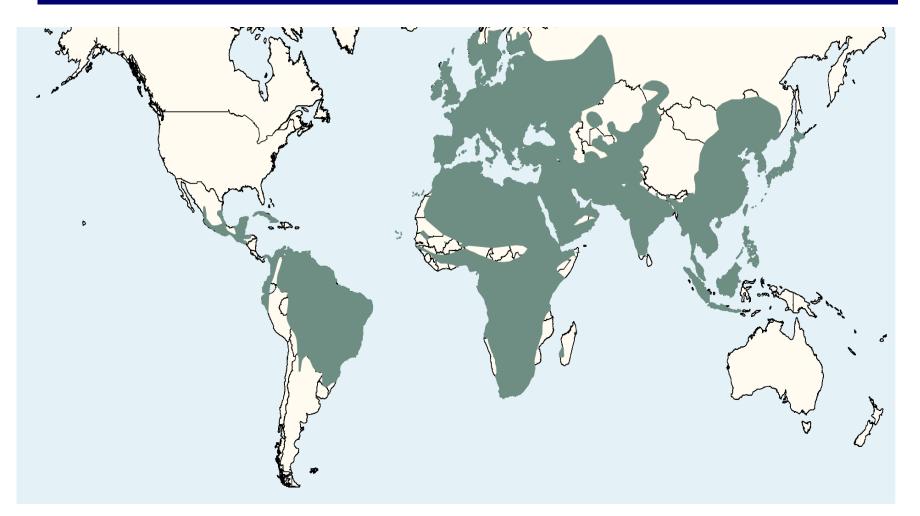
**Country-Specific Indicators** 

	country-specific indicators					
Country	Papers <u>in PubMed</u>	GDP Per <u>Capita (\$)</u>	<u>Risk</u> Index	Papers in PubMed	<u>Risk Index</u>	<u>Non-US Risk</u>
PRC	206	18,465	6.01	33.7	50.3	54.9
USA	129	69,459	1.00	21.1	8.4	
Kenya	6	5,197	0.62	1.0	5.2	5.7
Jordan	9	9,265	0.52	1.5	4.4	4.8
Ghana	5	6,454	0.42	0.8	3.5	3.8
Saudi Arabia	32	47,298	0.36	5.2	3.1	3.3
Australia	34	57,188	0.32	5.6	2.7	2.9
South Africa	8	14,718	0.29	1.3	2.5	2.7
Philippines	5	9,489	0.28	0.8	2.4	2.6
Germany	32	62,507	0.28	5.2	2.3	2.5

#### Source: Author's calculations

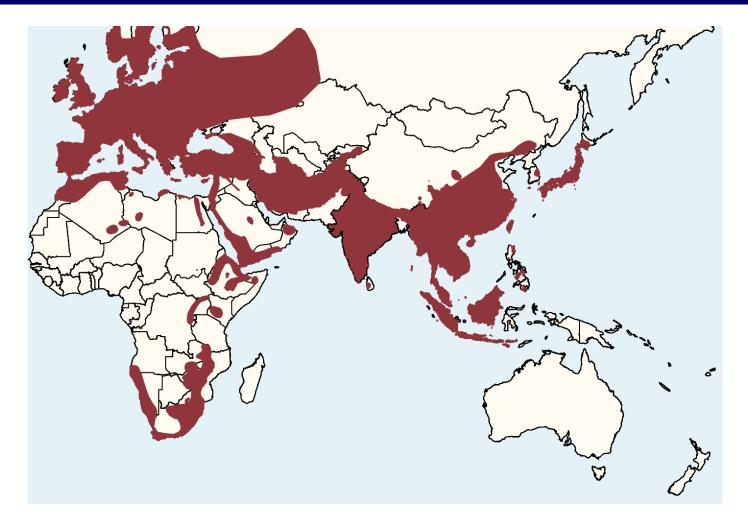
Share of Global Total (%)

# The Global Distribution of Bat Species with MERS-Related Viruses



Source: Frutos et al. (2021), Wu et al. (2023), IUCN RedList

#### The Global Distribution of Bat Species with SARS-Related Viruses



Source: Frutos et al. (2021), Wu et al. (2023), IUCN RedList

## Assessing the Risk of a Bat-Related Zoonotic Outbreak in PRC

#### Population in 2019 (millions)

Geographic Range of Bat Host Species	PRC	Total	Ratio (%)
All Coronaviruses	1,415.9	7,742.3	18.3
SARS-Related Viruses	1,009.8	5,207.9	19.4
<b>MERS-Related Viruses</b>	1,415.9	7,134.3	19.8

#### Source: Author's calculations

# Why Did the Pandemic Start in Wuhan?

• Hypothesis A: Assess the geographic distribution of research on bat-related coronaviruses in PRC.

• Hypothesis Z: Assess the geographic distribution of wild and farmed raccoon dogs in PRC.

## **Bat-Related Viral Research in Wuhan**

- During 2011-2013 WIV led expeditions to an abandoned mineshaft in Yunnan province (just a short distance from China's southern border with Laos and Vietnam), where they collected fecal swabs from six species of bats and identified several novel SARS-like virus.
- WIV conducted molecular analysis showing that these viruses were highly similar to the SARS-CoV virus, with nucleotide sequence identity of 95 to 96%.
- WIV researchers used cutting-edge methods to modify viral genomes, produce chimeras and cDNA clones, and compare the *in vitro* efficiency of viral variants using cell cultures.
- WIV's work was generally performed in BSL-2 labs, although one study involving international coauthors was conducted using a BSL-3 lab.
- Wuhan had an agglomeration of other researchers engaged in collecting specimens and molecular analysis of bat-related viruses.

# Wild Raccoon Dogs



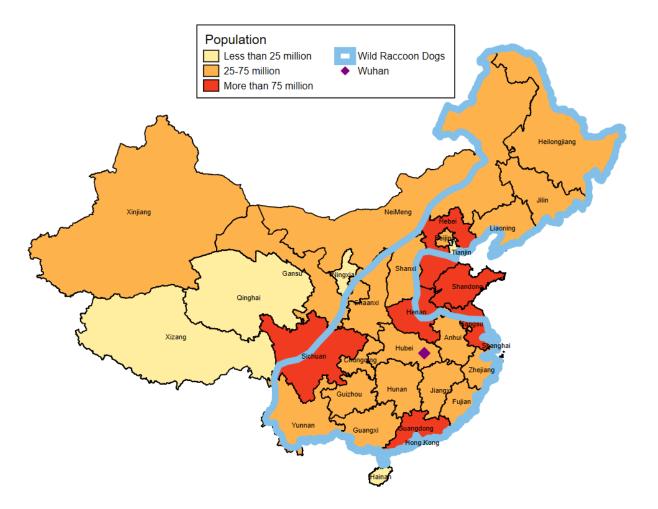
Source: Kaarina Kauhala (2022)

#### Wild Raccoon Dogs



Source: Kaarina Kauhala (2022)

# The Range of Wild Raccoon Dogs in PRC

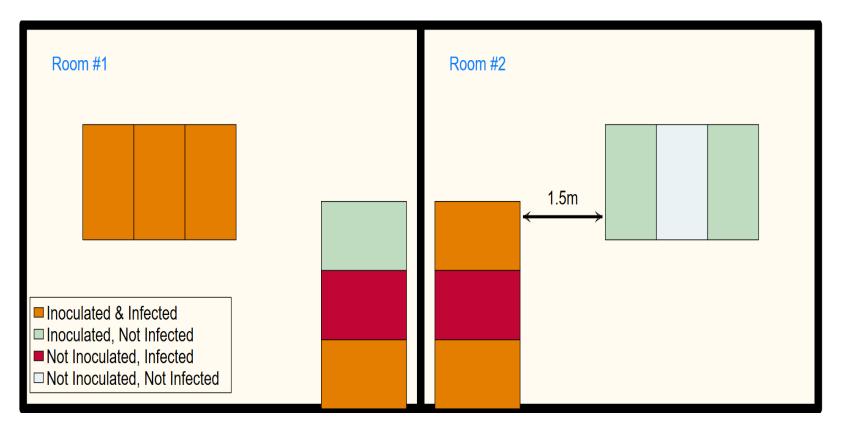


Source: IUCN Redlist data compiled by Kauhala & Saeki (2015)

### Friederich Loeffler Laboratory Insel Reims, Germany



## SARS-CoV-2 Infection and Transmissibility in Raccoon Dogs



Source: Freuling et al. (2021)

#### **Raccoon Dogs on Fur Farms**



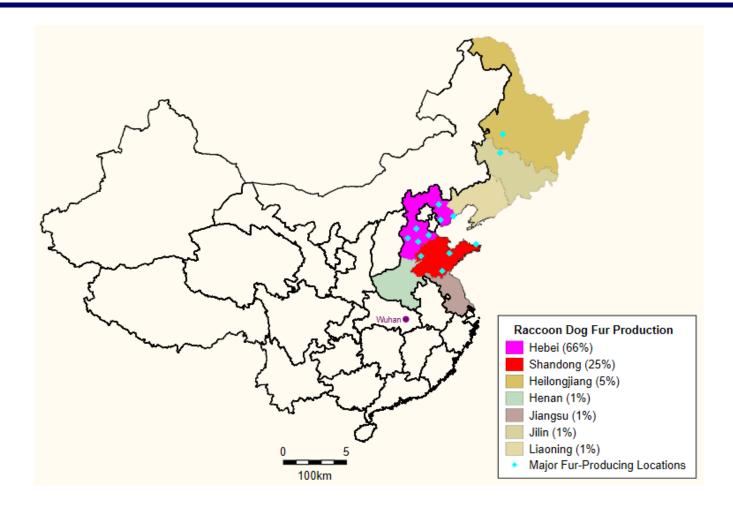
Source: ActAsia (2018)

#### **Raccoon Dogs on Fur Farms**



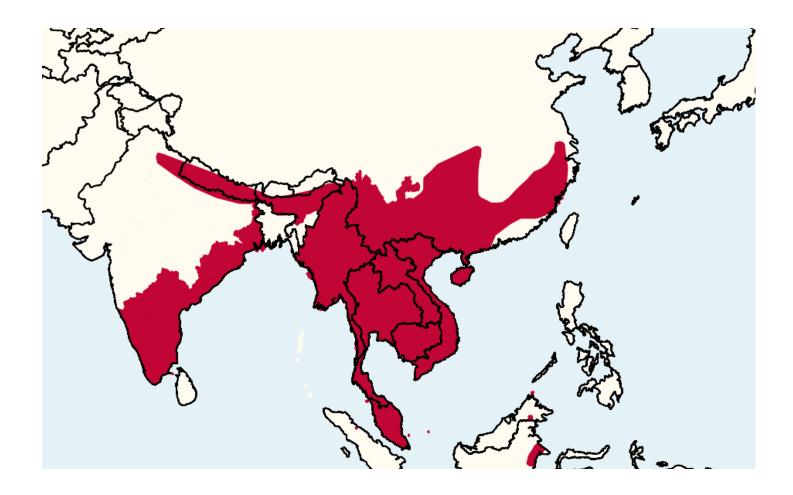
Source: ActAsia (2018)

## The Geographical Distribution of Raccoon Dog Fur Farms in PRC



Source: China Leather Industry Association data for 2019

#### The Distribution of Bat Species with SARS-CoV-2 Related Viruses



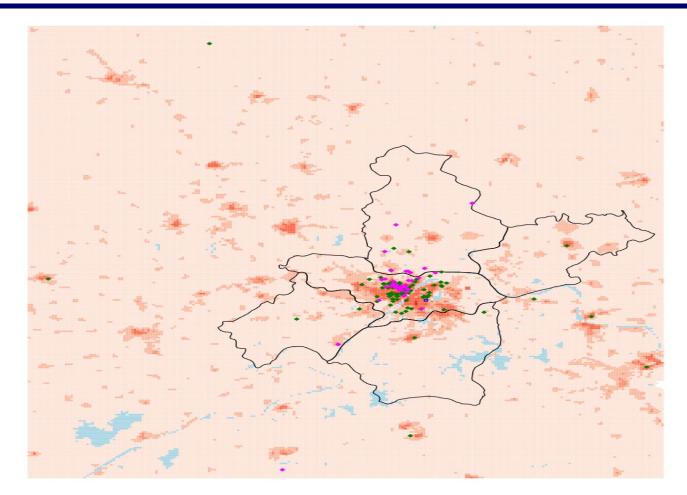
Source: Frutos et al. (2021), Wu et al. (2023), IUCN RedList

# What about the Spatiotemporal Pattern of Early Cases in Wuhan?

• Hypothesis A: Early COVID cases that were unlinked to the Huanan Market would be more frequent on the east bank of the Yangtze River, near the BSL-2 and BSL-3 labs conducting bat viral research.

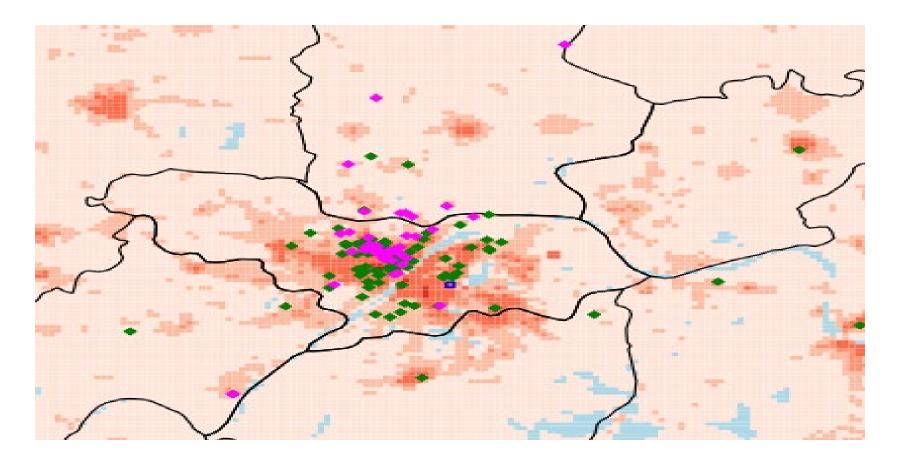
• Hypothesis Z: The distribution of unlinked cases would be roughly similar to the distribution of cases that were linked to the Huanan Market.

## The Distribution of Early COVID Cases in the Wuhan Area



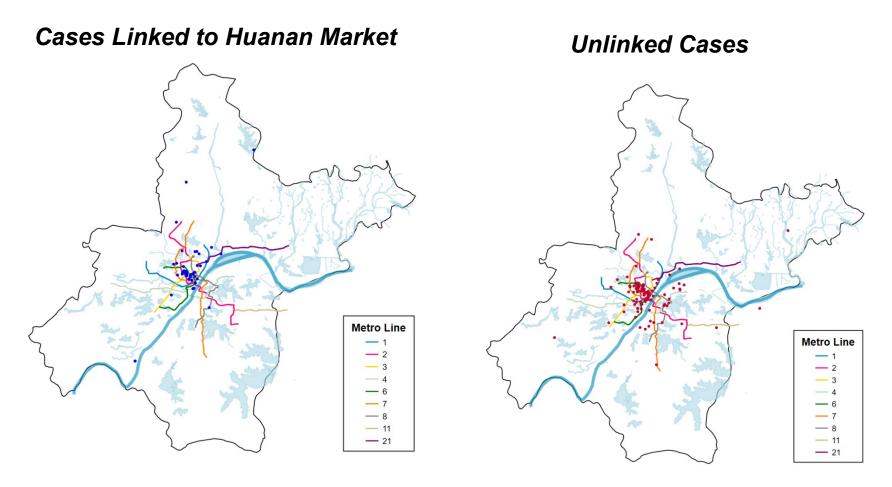
*Note: magenta = linked cases, green = unlinked cases Sources: WHO (2021), UN Population Division (2023)* 

## The Distribution of Early COVID Cases in the Central Core of Wuhan



*Note: magenta = linked cases, green = unlinked cases Sources: WHO (2021), UN Population Division (2023)* 

## The Distribution of Early COVID Cases in the Central Core of Wuhan



Source: WHO (2021)

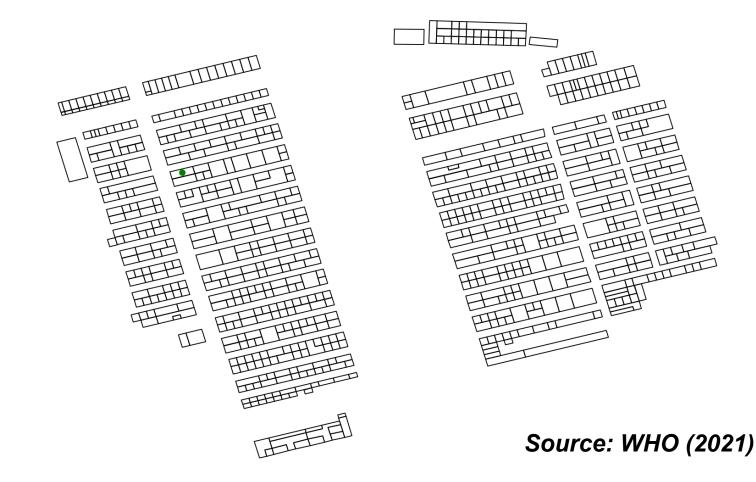
# What about the Spatiotemporal Pattern of Cases at Huanan Market?

• Hypothesis A: Cases where vendors were infected would be strongly linked to prior cases and time of infection, not distance to stalls selling wild mammals.

• Hypothesis Z: Cases where vendors were infected would mainly be determined by distance to stalls selling wild animals, not to the spread of infections outside the market.

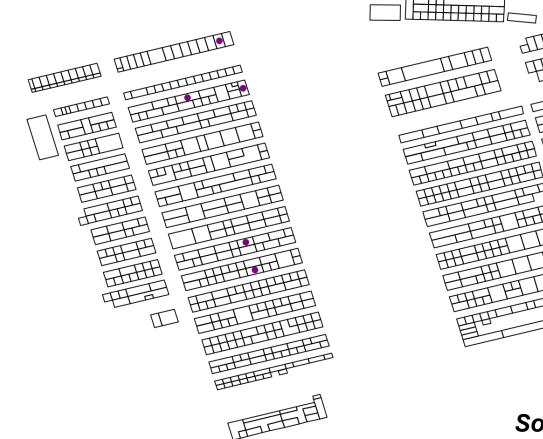
## The Spatiotemporal Pattern of Vendor Cases at Huanan Market

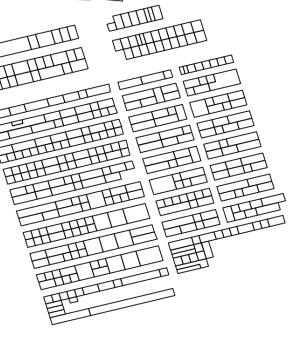
13 December 2019



## The Spatiotemporal Pattern of Vendor Cases at Huanan Market

#### 20 December 2019





Source: WHO (2021)

## The Spatiotemporal Pattern of Vendor Cases at Huanan Market

27 December 2019



Source: WHO (2021)

#### Kaarina Kauhala (1954-2022)



#### Source: Helsinki Sanomat (2023)