兒童新型冠病毒感染之國內外流行狀況

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What is Coronavirus & COVID-19

- Coronaviruses are a large family of viruses, some cause illness in humans, and others cause illness in animals, such as bats, camels, and civets.

- Human coronaviruses cause mild illness, such as the common cold

- Severe acute respiratory syndrome (SARS) is a viral respiratory illness caused by a coronavirus, called SARS-associated coronavirus (SARS-CoV)

- Previous Coronaviruses have included SARS- CoV and MERS-CoV

- Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a new strain of coronavirus that has not been previously identified in humans.

Human Coronavirus Origins

- The most likely ecological reservoirs for coronaviruses are bats, but it is believed that the virus jumped the species barrier to humans from another intermediate animal host.

- This intermediate animal host could be a domestic food animal, a wild animal, or a domesticated wild animal which has not yet been identified.
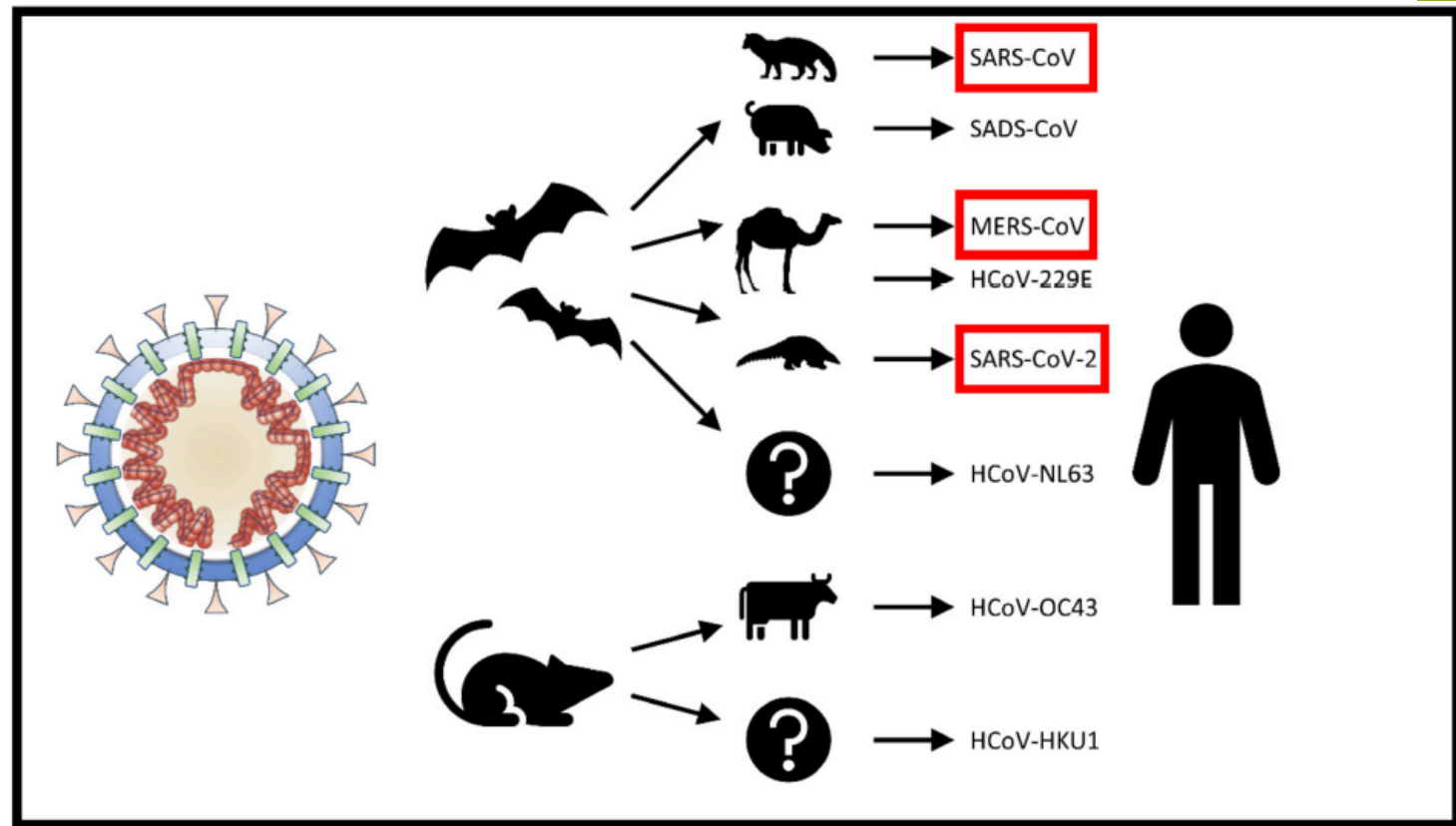
Coronaviruses

- Coronaviruses belong to the Coronaviridae family in the Nidovirales order

- Corona represents crown-like spikes on the outer surface of the virus; thus, it was named as a coronavirus

- Coronaviruses are enveloped viruses, minute in size (65 – 125 nm in diameter) and contain a single-stranded RNA as a nucleic material, size ranging from 26 to 32kbs in length

Nucleocapsid protein

Envelope glycop

RNA

Spike protein (

Membrane glyco

Lipid bilayer
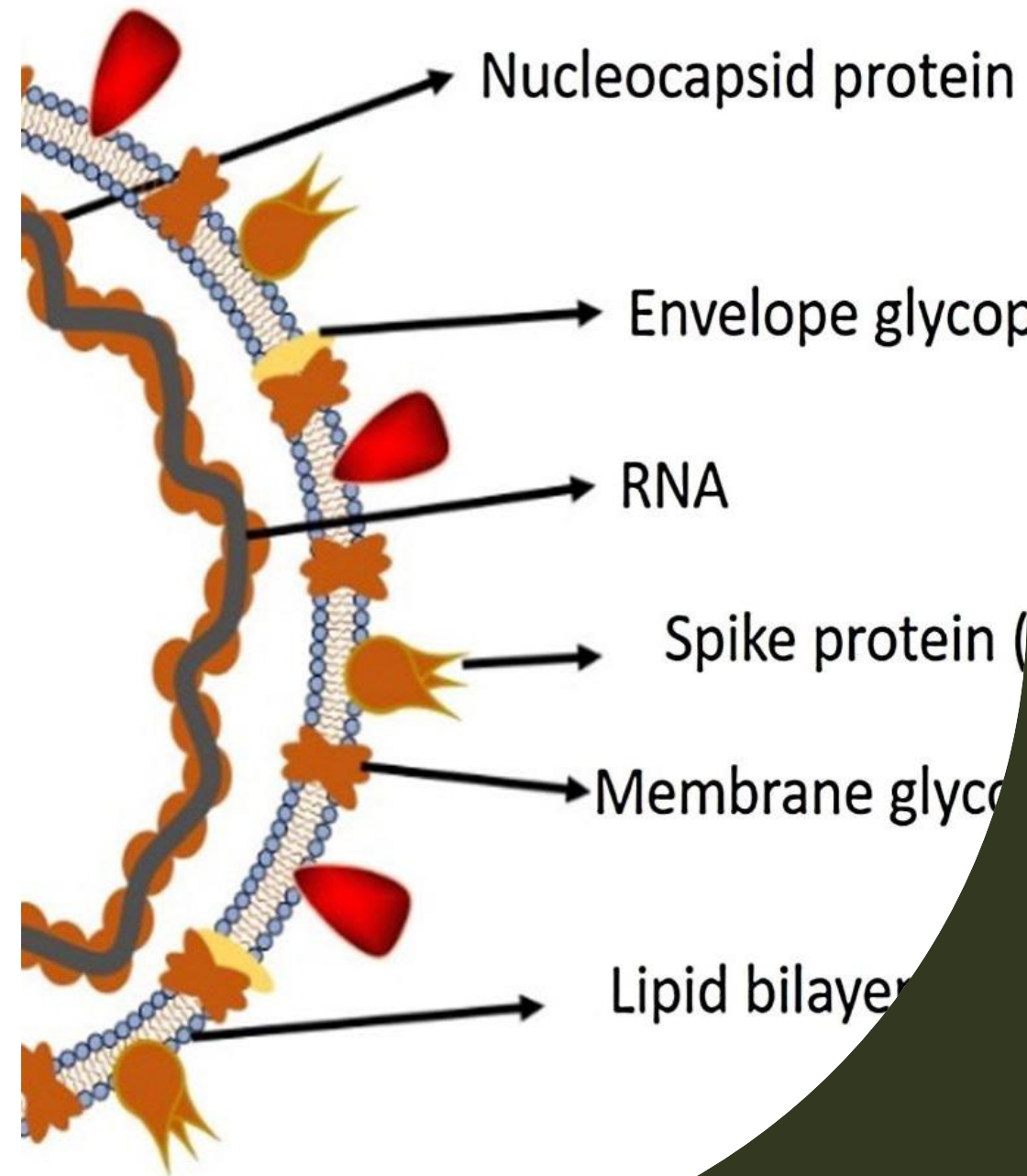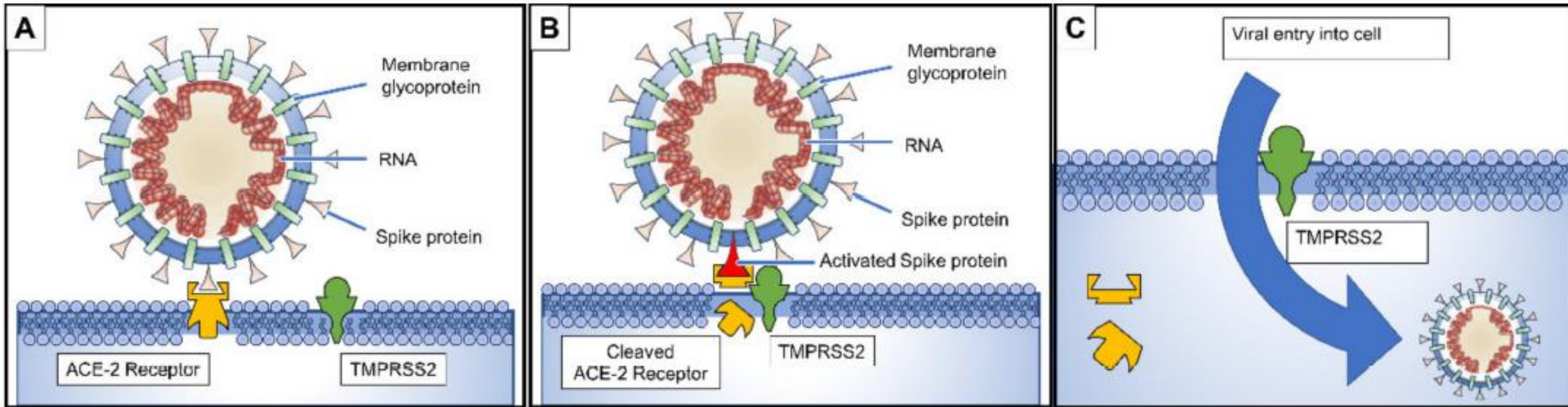
(A) Spike proteins on the surface of the coronavirus bind to angiotensin-converting enzyme 2 (ACE-2) receptors on the surface of the target cell

(B) the type II transmembrane serine protease (TMPRSS2) binds to and cleaves the ACE-2 receptor. In the process, the spike protein is activated

(C) Cleaved ACE-2 and activated spike protein facilitate viral entry. TMPRSS2 expression increases cellular uptake of the coronavirus

COVID-19 Timeline

Dec. 31, 2019

China alerts World Health Organization (WHO) to several cases of pneumonia with no known cause in Wuhan. The disease goes on to be named COVID-19.

Jan. 7

WHO officials announce they have identified a new virus named SARS-CoV-2 that causes COVID-19. It belongs to the coronavirus family, which includes viruses that cause SARS, MERS and the common cold.

Jan. 11

China announces the first death linked to COVID-19.

Jan. 13

WHO reports the first case outside of China in Thailand.

Feb. 26

National Institutes of Health (NIH) begin the first clinical trial in the U.S. for a potential COVID-19 treatment, remdesivir, an antiviral drug originally developed to treat Ebola.

Feb. 29

The FDA took steps to expand novel coronavirus testing to hospital clinical microbiology laboratories.

Mar. 11

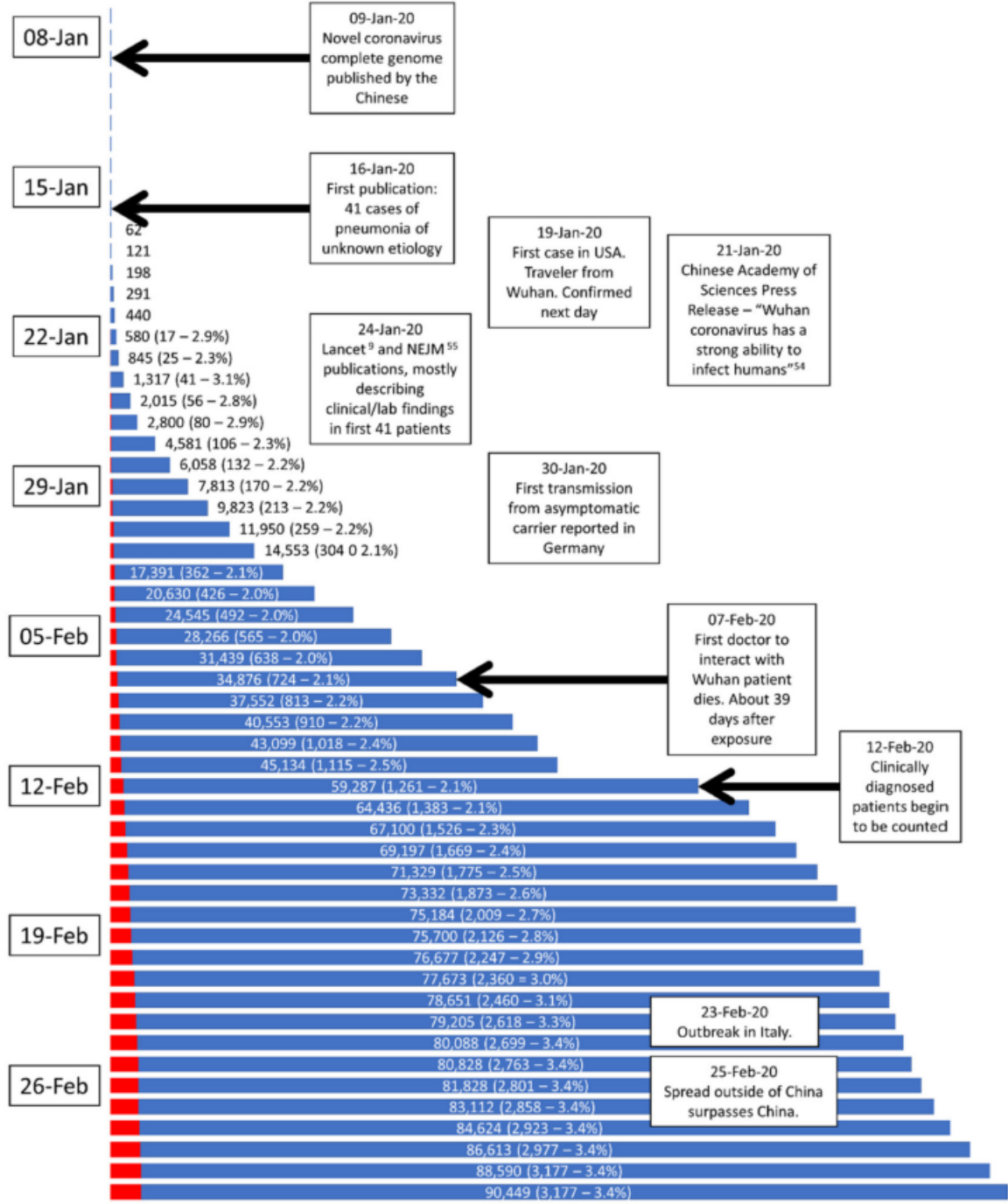WHO declares COVID-19 a pandemic, with more than 100,000 cases and 4,000 deaths in 114 countries.

Apr. 2

Confirmed cases of COVID-19 top 1 million worldwide.

Apr. 10

Global deaths due to COVID-19 top 100,000.

08-Jan

09-Jan-20
Novel coronavirus complete genome published by the Chinese

15-Jan

16-Jan-20
First publication: 41 cases of pneumonia of unknown etiology

62
121
198
291
440

19-Jan-20
First case in USA. Traveler from Wuhan. Confirmed next day

21-Jan-20
Chinese Academy of Sciences Press Release – "Wuhan coronavirus has a strong ability to infect humans"[54]

22-Jan

580 (17 – 2.9%)
845 (25 – 2.3%)

24-Jan-20
Lancet[9] and NEJM[55] publications, mostly describing clinical/lab findings in first 41 patients

1,317 (41 – 3.1%)
2,015 (56 – 2.8%)
2,800 (80 – 2.9%)
4,581 (106 – 2.3%)
6,058 (132 – 2.2%)

29-Jan

7,813 (170 – 2.2%)
9,823 (213 – 2.2%)
11,950 (259 – 2.2%)
14,553 (304 0 2.1%)

30-Jan-20
First transmission from asymptomatic carrier reported in Germany

17,391 (362 – 2.1%)
20,630 (426 – 2.0%)
24,545 (492 – 2.0%)

05-Feb

28,266 (565 – 2.0%)
31,439 (638 – 2.0%)
34,876 (724 – 2.1%)

07-Feb-20
First doctor to interact with Wuhan patient dies. About 39 days after exposure

37,552 (813 – 2.2%)
40,553 (910 – 2.2%)
43,099 (1,018 – 2.4%)
45,134 (1,115 – 2.5%)

12-Feb-20
Clinically diagnosed patients begin to be counted

12-Feb

59,287 (1,261 – 2.1%)
64,436 (1,383 – 2.1%)
67,100 (1,526 – 2.3%)
69,197 (1,669 – 2.4%)
71,329 (1,775 – 2.5%)
73,332 (1,873 – 2.6%)
75,184 (2,009 – 2.7%)

19-Feb

75,700 (2,126 – 2.8%)
76,677 (2,247 – 2.9%)
77,673 (2,360 = 3.0%)
78,651 (2,460 – 3.1%)
79,205 (2,618 – 3.3%)
80,088 (2,699 – 3.4%)

23-Feb-20
Outbreak in Italy.

80,828 (2,763 – 3.4%)
81,828 (2,801 – 3.4%)
83,112 (2,858 – 3.4%)

25-Feb-20
Spread outside of China surpasses China.

26-Feb

84,624 (2,923 – 3.4%)
86,613 (2,977 – 3.4%)
88,590 (3,177 – 3.4%)
90,449 (3,177 – 3.4%)

SARS-CoV-2 Variant Classifications and Definitions

- Variant of Interest (VOI)

  A variant with specific genetic markers that have been associated with changes to receptor binding, reduced neutralization by antibodies generated against previous infection or vaccination, reduced efficacy of treatments, potential diagnostic impact, or predicted increase in transmissibility or disease severity.

- Variant of Concern (VOC)

  A variant for which there is evidence of an increase in transmissibility, more severe disease (e.g., increased hospitalizations or deaths), significant reduction in neutralization by antibodies generated during previous infection or vaccination, reduced effectiveness of treatments or vaccines, or diagnostic detection failures.

Variant of Concern (VOC) _ updated 24 May 2021

Lineage + additional mutations	Country first detected (community)	Spike mutations of interest	Year and month first detected	Evidence for impact on transmissibility	Evidence for impact on immunity	Evidence for impact on severity	Transmission in EU/EEA
B.1.1.7	United Kingdom	N501Y, D614G, P681H	September 2020	Yes (v) [1]	Unclear [2]	Yes (v) [3, 4]	Dominating
B.1.1.7+E484K	United Kingdom	E484K, N501Y, D614G, P681H	December 2020	Yes (v) [1]	Neutralisation (v) [2, 5]	Yes (v) [3]	Outbreaks
B.1.351	South Africa	K417N, E484K, N501Y, D614G, A701V	September 2020	Yes (v) [6]	Escape (v) [7, 8]	Yes (v) [4, 9]	Community
P.1	Brazil	K417T, E484K, N501Y, D614G, H655Y	December 2020	Yes (v) [10]	Neutralisation (v) [11]	Yes (v) [4]	Community
B.1.617.2	India	L452R, T478K, D614G, P681R	December 2020	Yes (v) [12-14]	Escape (v) [15]		Community

VOC (renamed by WHO, 31 May 2021)

WHO label	Pango lineage	GISAID clade/lineage	Nextstrain clade	Earliest documented samples	Date of designation
Alpha	B.1.1.7	GRY (formerly GR/501Y.V1)	20I/S:501Y.V1	United Kingdom, Sep-2020	18-Dec-2020
Beta	B.1.351	GH/501Y.V2	20H/S:501Y.V2	South Africa, May-2020	18-Dec-2020
Gamma	P.1	GR/501Y.V3	20J/S:501Y.V3	Brazil, Nov-2020	11-Jan-2021
Delta	B.1.617.2	G/452R.V3	21A/S:478K	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021

Variant of Concern (VOC) _ updated 24 May 2021

Lineage + additional mutations	Country first detected (community)	Spike mutations of interest	Year and month first detected	Evidence for impact on transmissibility	Evidence for impact on immunity	Evidence for impact on severity	Transmission in EU/EEA
B.1.525	Nigeria	E484K, D614G, Q677H	December 2020		Neutralisation (m) [5]		Community
B.1.427/B.1.429	USA	L452R, D614G	September 2020	Unclear [12]	Neutralisation (v) [12]		Sporadic/Travel
P.3	The Philippines	E484K, N501Y, D614G, P681H	January 2021	Yes (m) [1]	Neutralisation (m) [5]		Sporadic/Travel
B.1.616	France	V483A, D614G, H655Y, G669S	February 2021	Detection (c) [13]			Single outbreak
B.1.617.1	India	L452R, E484Q, D614G, P681R	December 2020	Yes (v) [14]	Neutralisation (v) [15, 17]		Outbreaks
B.1.617.3	India	L452R, E484Q, D614G, P681R	February 2021	Yes (m) [1]	Neutralisation (m) [5, 12]		Not detected
B.1.620	Unclear (b)	S477N, E484K, D614G, P681H	February 2021		Neutralisation (m) [5, 14]		Outbreaks
B.1.621	Colombia	R346K, E484K, N501Y, D614G, P681H	January 2021	Yes (m) [1]	Neutralisation (m) [5]		Sporadic/Travel

VOI (renamed by WHO, 31 May 2021)

WHO label	Pango lineage	GISAID clade/lineage	Nextstrain clade	Earliest documented samples	Date of designation
Epsilon	B.1.427/B.1.429	GH/452R.V1	20C/S.452R	United States of America, Mar-2020	5-Mar-2021
Zeta	P.2	GR	20B/S.484K	Brazil, Apr-2020	17-Mar-2021
Eta	B.1.525	G/484K.V3	20A/S484K	Multiple countries, Dec-2020	17-Mar-2021
Theta	P.3	GR	20B/S:265C	Philippines, Jan-2021	24-Mar-2021
Iota	B.1.526	GH	20C/S:484K	United States of America, Nov-2020	24-Mar-2021
Kappa	B.1.617.1	G/452R.V3	21A/S:154K	India, Oct-2020	4-Apr-2021

Where B.1.1.7 (UK Variant) Has Been Found
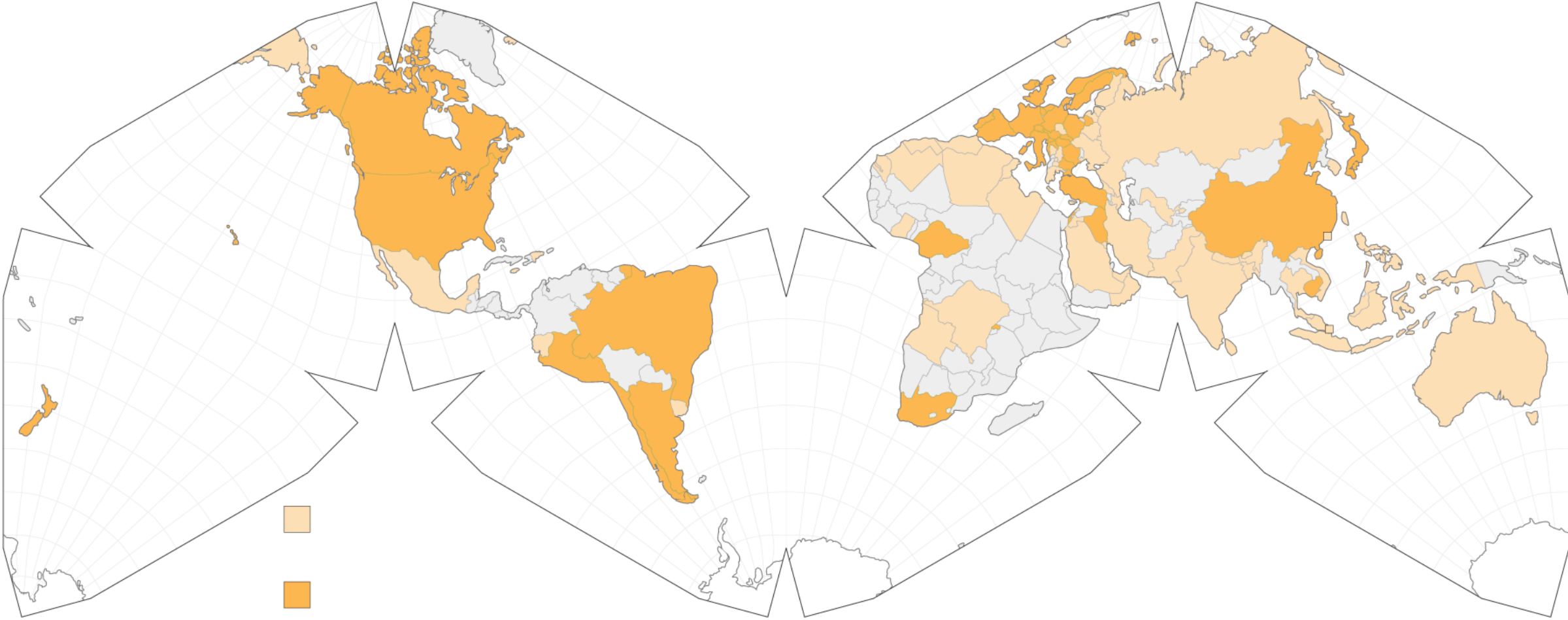
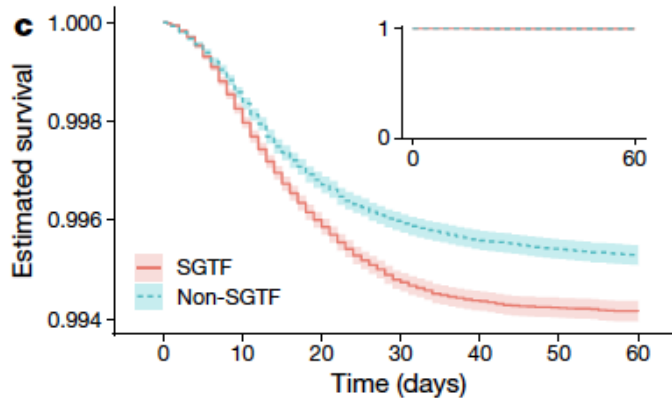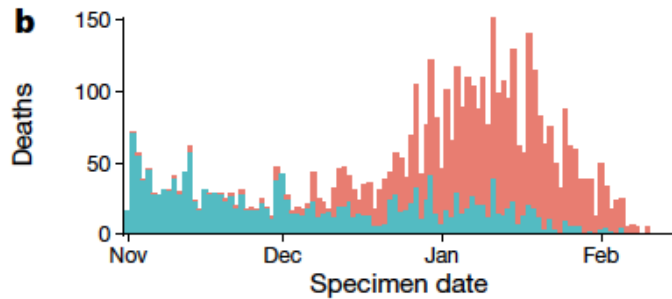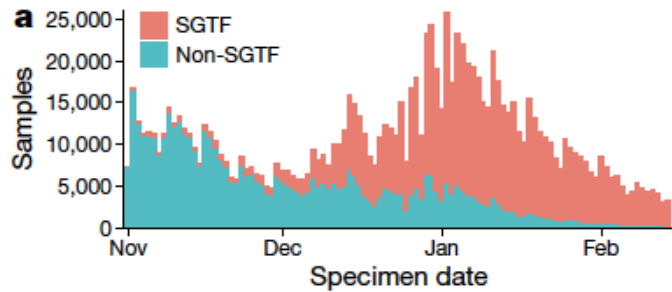# Increased Transmissibility in UK Variant

Table 1. Estimates of increased reproduction number for VOC 202012/01. Means and 95% CIs (GLMM) or 95% CrIs (R_t regression, transmission model) are shown. GLMM models do not estimate a baseline growth rate or reproduction number. Increases in the reproduction number assume a generation interval of 5.5 days. See table S1 for full details.

Model type	Model	Model assumptions	Data	Geography	Baseline growth rate	Additive increase in growth rate, Δr	Baseline reproduction number	Multiplicative increase in reproduction number
GLMM	1a	Separate-slopes multinomial spline model*	Sequence	Regions of UK	—	0.104 [0.100, 0.108]	—	77% [73, 81]
GLMM	1b	Common-slope multinomial model*	Sequence	Lower-tier local authorities of UK	—	0.093 [0.091, 0.095]	—	67% [65, 69]
GLMM	2h	Separate-slope binomial spline model†	S gene target failure‡	Regions of England	—	0.109 [0.107, 0.111]	—	83% [81, 84]
R_t regression	4a	Regional time-varying baseline	S gene target failure	Upper-tier local authorities of England	0.007 [0.002, 0.012]	0.067 [0.060, 0.073]	1.04 [1.01, 1.07]	43% [38, 48]
R_t regression	4b	Regional static baseline	S gene target failure	Upper-tier local authorities of England	0.007 [0.002, 0.012]	0.085 [0.079, 0.091]	1.04 [1.01, 1.07]	57% [52, 62]
Transmission model	5a	Increased transmissibility	S gene target failure‡	Regions of England	−0.001 [−0.017, 0.012]	0.118 [0.067, 0.168]	1.01 [0.94, 1.09]	82% [43, 130]
GLMM	3a	Common-slope binomial model†	Sequence	Regions of Denmark	—	0.080 [0.067, 0.092]	—	55% [45, 66]
GLMM	3b	Common-slope binomial model†	Sequence + RT-PCR rescreening	Regions of Switzerland	—	0.101 [0.092, 0.109]	—	74% [66, 82]
GLMM	3c	Common-slope binomial model†	S gene target failure‡	States of USA	—	0.084 [0.080, 0.088]	—	59% [56, 83]

*VOC 202012/01 versus B.1.177.   †VOC 202012/01 versus all other variants.   ‡Binomial counts adjusted for the true positive rate (proportion of S gene target failures that are VOC 202012/01), estimated from misclassification model (for UK) or a binomial GLMM fitted to sequencing data of S gene target failures (for US).

DOI: https://doi.org/10.1126/science.abg3055

Increased Mortality in Cases of UK Variant

Table 1 | Absolute 28-day mortality risk for B.1.1.7

Sex	Age (years)	Baseline mortality	Mortality risk for B.1.1.7	
			SGTF for complete cases	p_{VOC} IPW
Female	1–34	0.00069%	0.0011% (0.00096–0.0012%)	0.0011% (0.00097–0.0012%)
	35–54	0.033%	0.050% (0.045–0.056%)	0.052% (0.046–0.059%)
	55–69	0.18%	0.28% (0.25–0.31%)	0.29% (0.26–0.33%)
	70–84	2.9%	4.4% (4.0–4.9%)	4.6% (4.0–5.1%)
	85 and older	13%	19% (17–21%)	20% (18–22%)
Male	1–34	0.0031%	0.0047% (0.0042–0.0052%)	0.0049% (0.0043–0.0055%)
	35–54	0.064%	0.099% (0.089–0.11%)	0.10% (0.090–0.12%)
	55–69	0.56%	0.86% (0.77–0.95%)	0.89% (0.78–1.0%)
	70–84	4.7%	7.2% (6.4–7.9%)	7.4% (6.6–8.3%)
	85 and older	17%	25% (23–27%)	26% (23–29%)

The absolute mortality risk is expressed as the case fatality ratio (%) among individuals testing positive in the community. The baseline risk (that is, for pre-existing SARS-CoV-2 variants) is derived using linked deaths within 28 days for all individuals testing positive in the community from 1 August to 31 October 2020. Adjusted risks are presented for the SGTF analysis for complete cases and for the misclassification-adjusted (p_{VOC}) IPW analysis, which yielded the lowest and highest mortality estimates, respectively, of the main models assessed (Fig. 2a–d).

DOI: https://doi.org/10.1038/s41586-021-03426-1

B.1.617.2 COVID (India Variant), More Transmissible
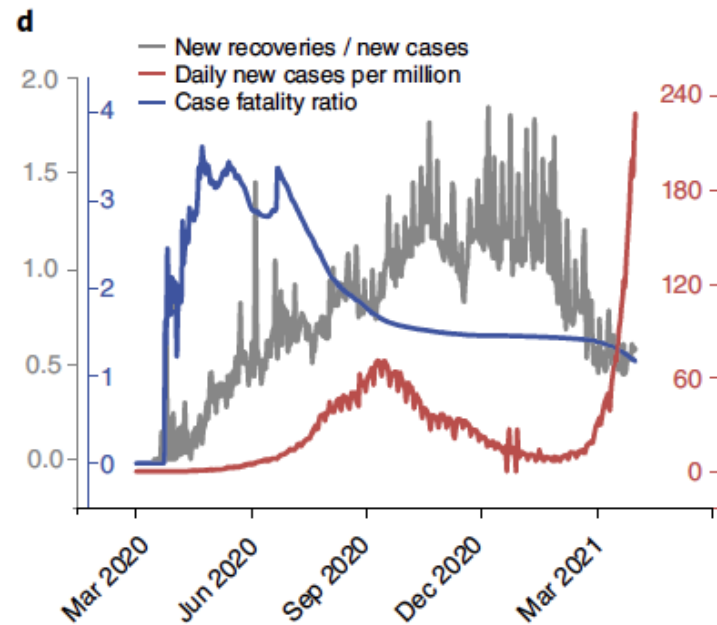
	New WHO Name	Transmissibility	Immune Evasiveness	Vaccine Effectiveness^
Ancestral		—	—	✓
D614G		+	—	✓
B.1.1.7	Alpha	+++	—	✓
B.1.351	Beta	+	++++	✓
P.1	Gamma	++	++	✓
B.1.429	Epsilon	+	+	✓
B.1.526	Iota	+	+	✓
B.1.617.2	Delta	++++*	++#	✓

*Relative transmissibility to B.1.1.7 yet to be fully defined
^Effectiveness from real world evidence vs. severe illness, not all vaccines are effective vs all variants, and importance of 2-doses, especially for B.1.617.2 for which 1 dose of mRNA or AZ is only ~30% effective # May carry more immune escape than P.1, to be determined

DOI: https://doi.org/10.1038/s41591-021-01397-4

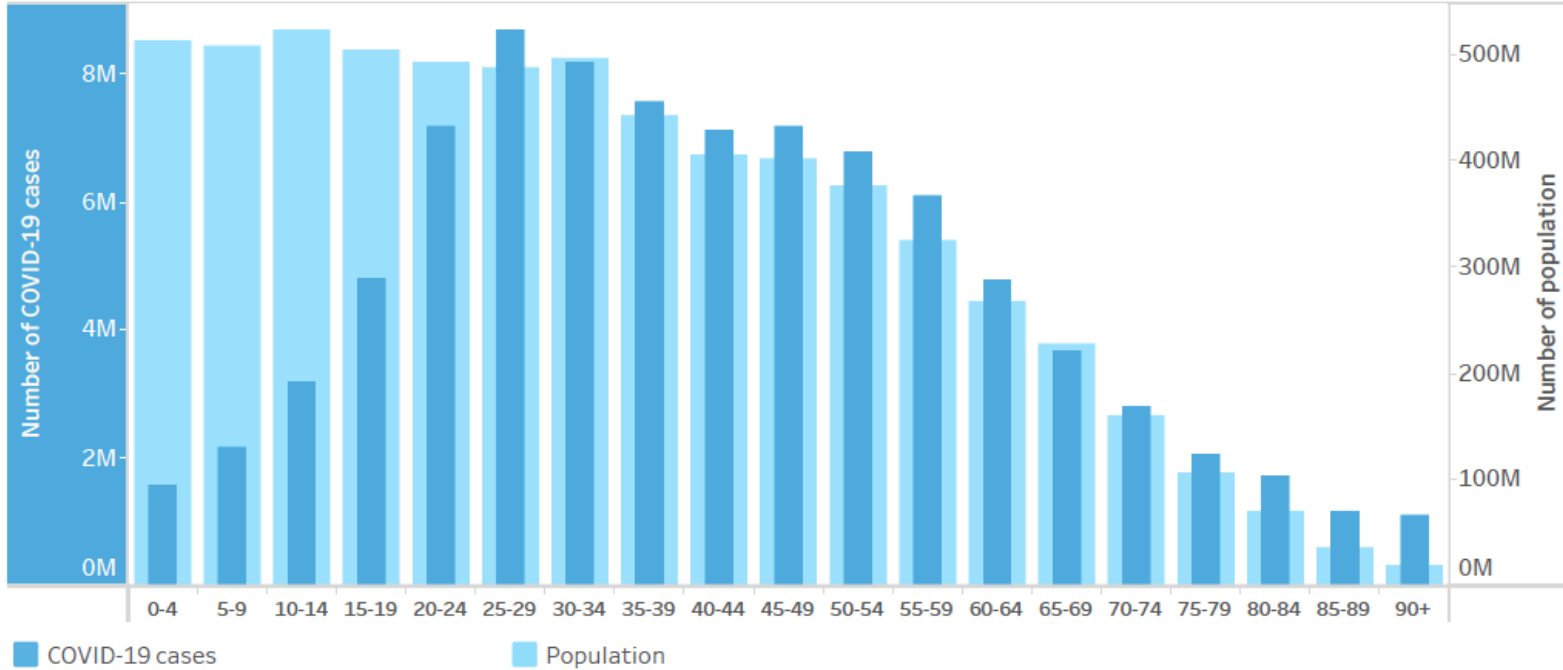# Geographic Distribution (Worldwide)

https://gisanddata.maps.arcgis.com/apps/dashboards/bda7594740fd40299423467b48e9ecf6
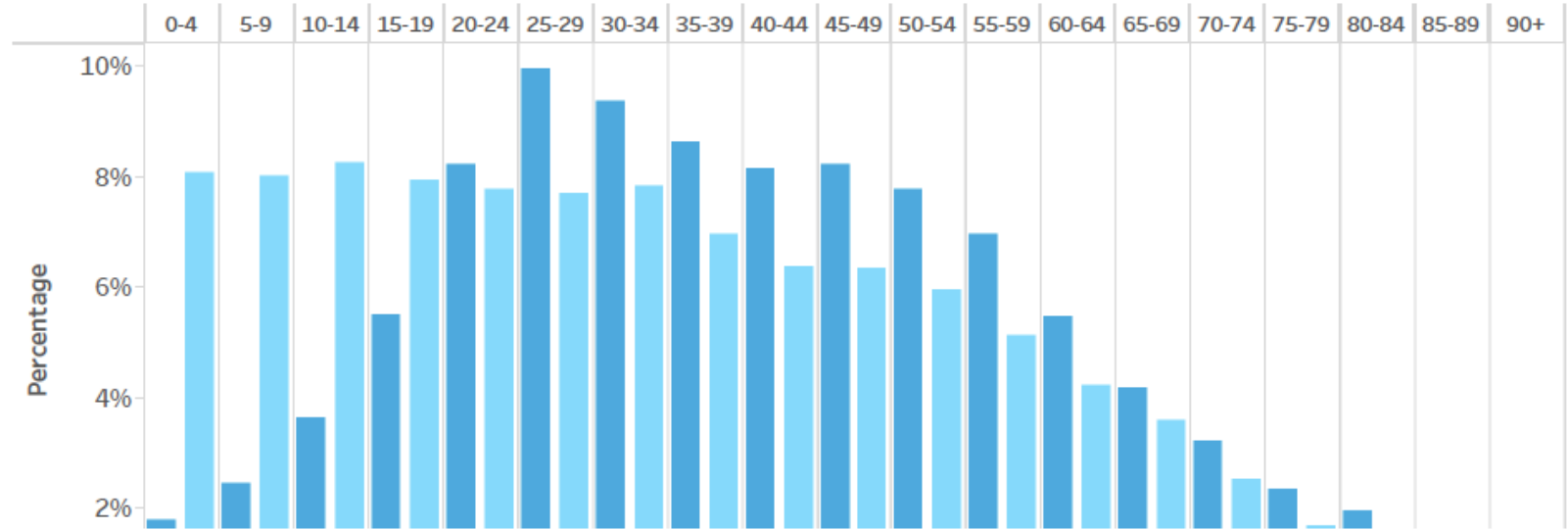https://sedac.ciesin.columbia.edu/mapping/popest/covid-19
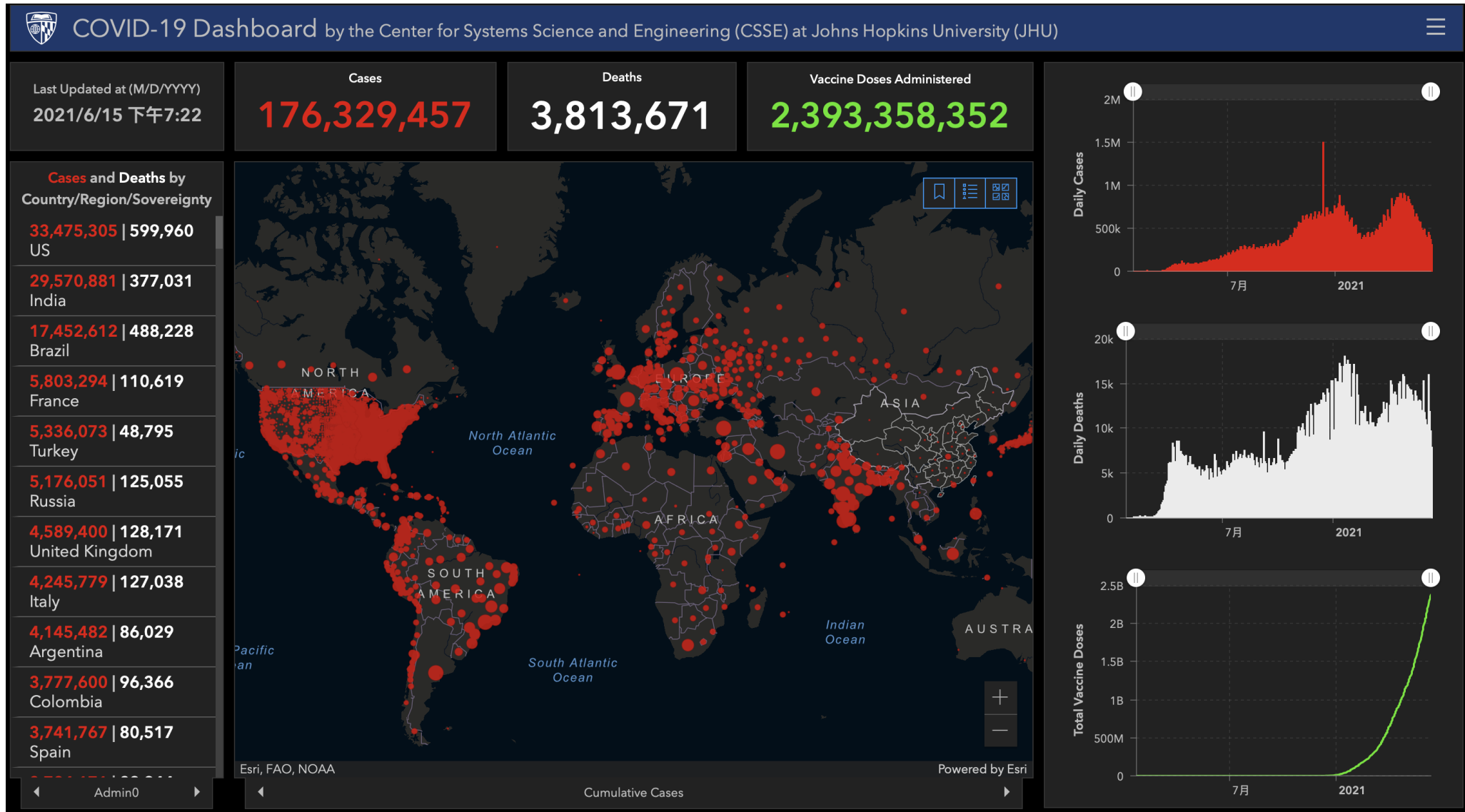
COVID-19 cases and population by 5-year age groups (in numbers) in 100 countries

COVID-19 in Children (Global)

COVID-19 cases and population by 5-year age groups (in per cent) in 100 countries

COVID-19 HOSPITALIZATION AND DEATH BY AGE

FACTORS THAT INCREASE COMMUNITY SPREAD AND INDIVIDUAL RISK

- CROWDED SITUATIONS
- CLOSE / PHYSICAL CONTACT
- ENCLOSED SPACE
- DURATION OF EXPOSURE

Rate ratios compared to 18-29 year olds	0-4 years	5-17 years	18-29 years	30-39 years	40-49 years	50-64 years	65-74 years	75-84 years	85+ years
HOSPITALIZATION[1]	4x lower	9x lower	Comparison Group	2x higher	3x higher	4x higher	5x higher	8x higher	13x higher
DEATH[2]	9x lower	16x lower	Comparison Group	4x higher	10x higher	30x higher	90x higher	220x higher	630x higher

ACTIONS TO REDUCE RISK OF COVID-19
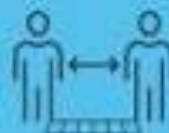
- WEARING A MASK
- SOCIAL DISTANCING (6 FT GOAL)
- HAND HYGIENE
- CLEANING AND DISINFECTION

[1] Data source: COVID-NET (https://www.cdc.gov/coronavirus/2019-ncov/covid-data/covidview/index.html, accessed 08/06/20). Numbers are unadjusted rate ratios.

[2] Data source: NCHS Provisional Death Counts (https://www.cdc.gov/nchs/nvss/vsrr/COVID19/index.htm, accessed 08/06/20). Numbers are unadjusted rate ratios.

cdc.gov/coronavirus

CS319360-A 08/10/2020

Geographic Distribution (Domestic data)

https://nidss.cdc.gov.tw/nndss/Diagram?id=19CoV

全國 嚴重特殊傳染性肺炎 本土病例 地理分佈 (2021年-2021年)
[發病日 2021/01/01-2021/12/31]
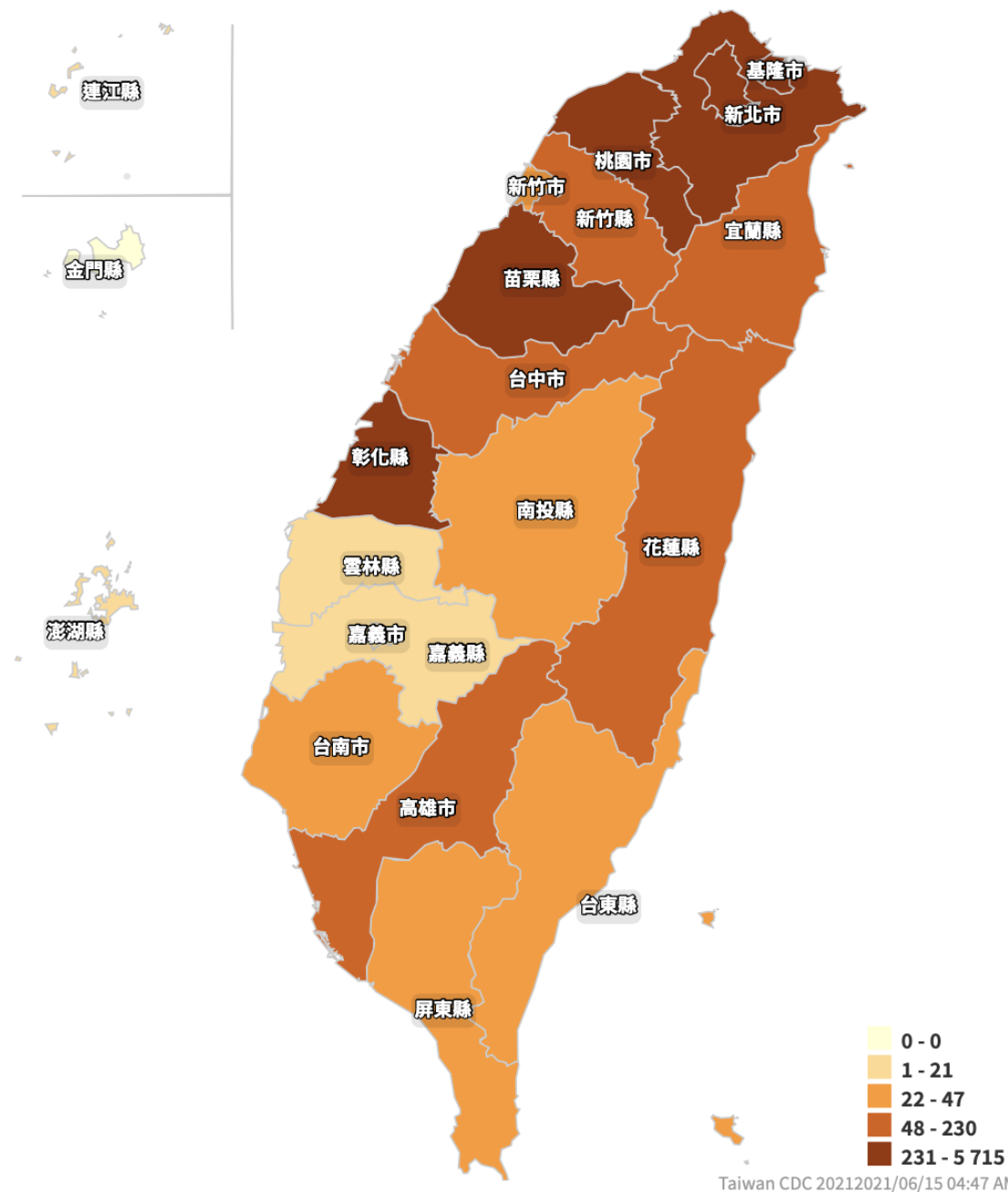
Age-specific Trend of Domestic Data

全國 嚴重特殊傳染性肺炎 本土病例及境外移入病例 年齡別發生率趨勢圖 (2020年1週-2021年24週)

https://nidss.cdc.gov.tw/nndss/Diagram?id=19CoV

https://sedac.ciesin.columbia.edu/mapping/popest/covid-19

— 2020   — 2021
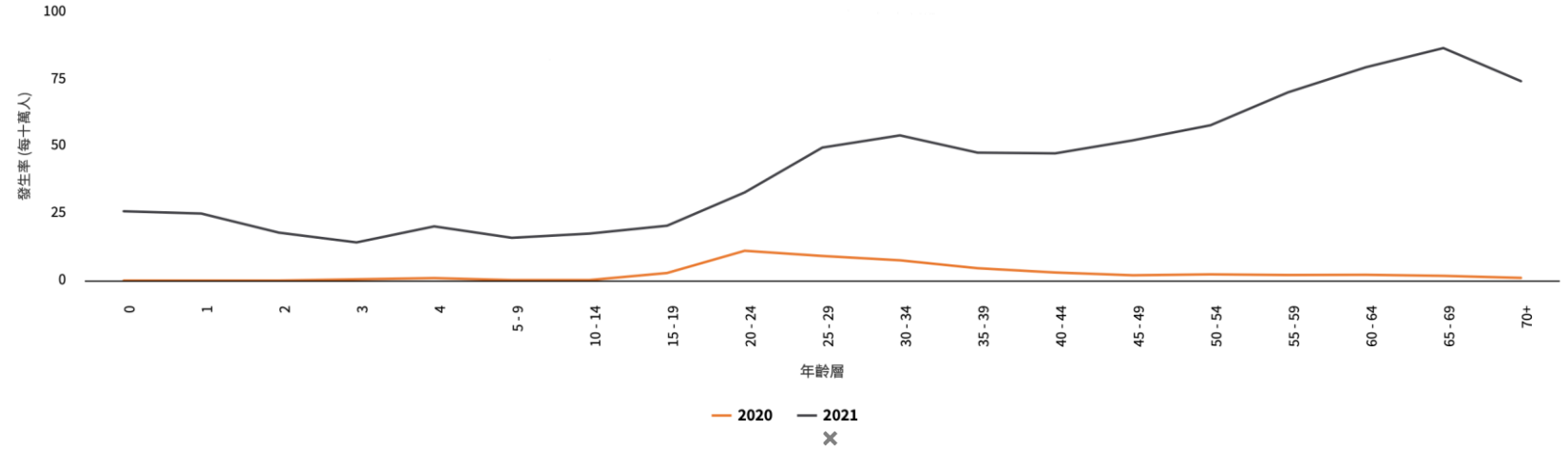
COVID-19 Statistics for Taiwan

| Cases | Deaths | Cases & Deaths |

Cases and Deaths with 7 day Moving Averages

1m **3m** 6m YTD 1y All

● Cases   — Cases 7 Day   ● Deaths   — Deaths 7 Day
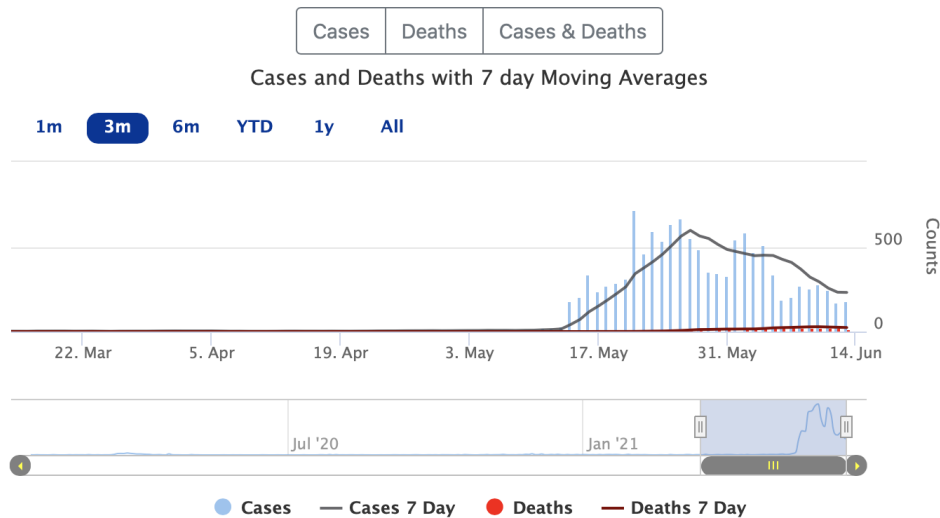
Prevalence

	TOTAL	PAST 7 DAYS
CASES	13,106	1,615
PER 100K PPL	56	7
PER CAPITA	1 in 1,786	1 in 14,491

Mortality

	TOTAL	PAST 7 DAYS
DEATHS	452	166
PER 100K PPL	2	1
PER CAPITA	1 in 51,775	1 in 140,979

Last updated on 6/15/2021. Per 100k proportions were calculated using SEDAC's 2020 GPW population data. Source of COVID-19 Data: Johns Hopkins University Center for Systems Science and Engineering (CSSE).

2021 台灣近期本土Covid-19病例與死亡累計 ｜ 年齡分配 ｜ 6月13日

（5月1日之後）

病例數與死亡數

確診數

確診致死率

死亡數

Age	確診數	死亡數	致死率
0-9	331	0	
10-19	389	0	
20-29	1054	0	
30-39	1617	5	0.3%
40-49	1730	6	0.3%
50-59	2219	30	1.4%
60-69	2472	112	4.5%
70+	1639	270	16.5%

Data: Taiwan CECC, MOHW, g0v
Authors: Chase W. Nelson 倪誠志, Ming-Hsueh Lin 林明學
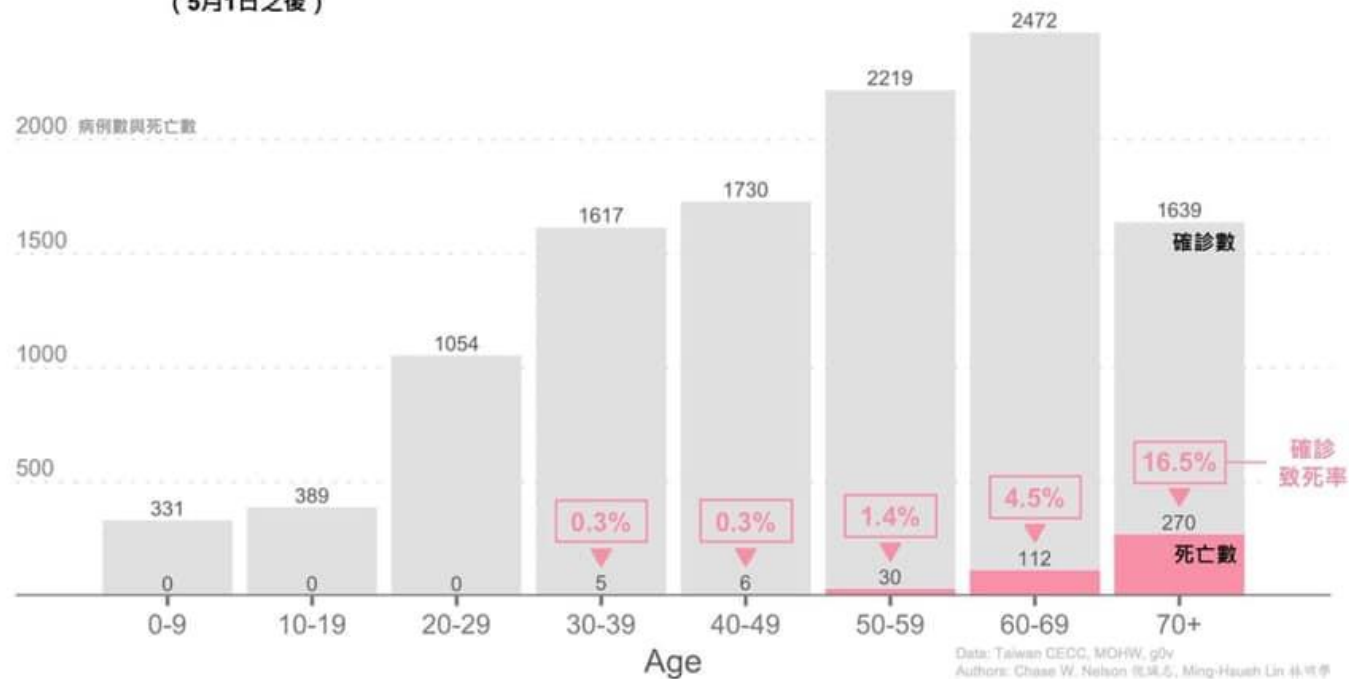
表1 2021/4/20-6/13的COVID-19年齡別本土確診病例人數、重症人數、死亡人數、重症率及致死率

年齡(歲)	確診病例人數 (%)	重症人數	死亡人數	重症率	致死率
0-9	340 (2.9%)	1	0	0.3%	0%
10-19	401 (3.5%)	2	0	0.5%	0%
20-29	1,076 (9.3%)	26	0	2.4%	0%
30-39	1,641 (14.1%)	78	5	4.8%	0.3%
40-49	1,768 (15.2%)	165	6	9.3%	0.3%
50-59	2,249 (19.3%)	371	30	16.5%	1.3%
60-69	2,500 (21.5%)	707	117	28.3%	4.7%
70-79	1,166 (10.0%)	496	134	42.5%	11.5%
80+	495 (4.3%)	213	133	43.0%	26.9%

表2 2021/4/20前後的COVID-19年齡別本土確診病例人數、重症率及致死率

年齡(歲)	2021/4/19以前			2021/4/20以後		
	確診病例人數	重症率	致死率	確診病例人數	重症率	致死率
0-49	44 (57.1%)	2.3%	0%	5,226 (44.9%)	5.2%	0.2%
50-69	26 (33.8%)	38.5%	11.5%	4,749 (40.8%)	22.7%	3.1%
70+	7 (9.1%)	42.9%	28.6%	1,661 (14.3%)	42.7%	16.1%

COVID-19 in Children (Global)

COVID-19 death rate by age group
Death rate due to COVID-19 (all cases)

Age group

Age group	Death rate
80+	14.8%
70-79	8.0%
60-69	3.6%
50-59	1.3%
40-49	0.4%
30-39	0.2%
20-29	0.2%
10-19	0.2%
0-9	No fatalities recorded
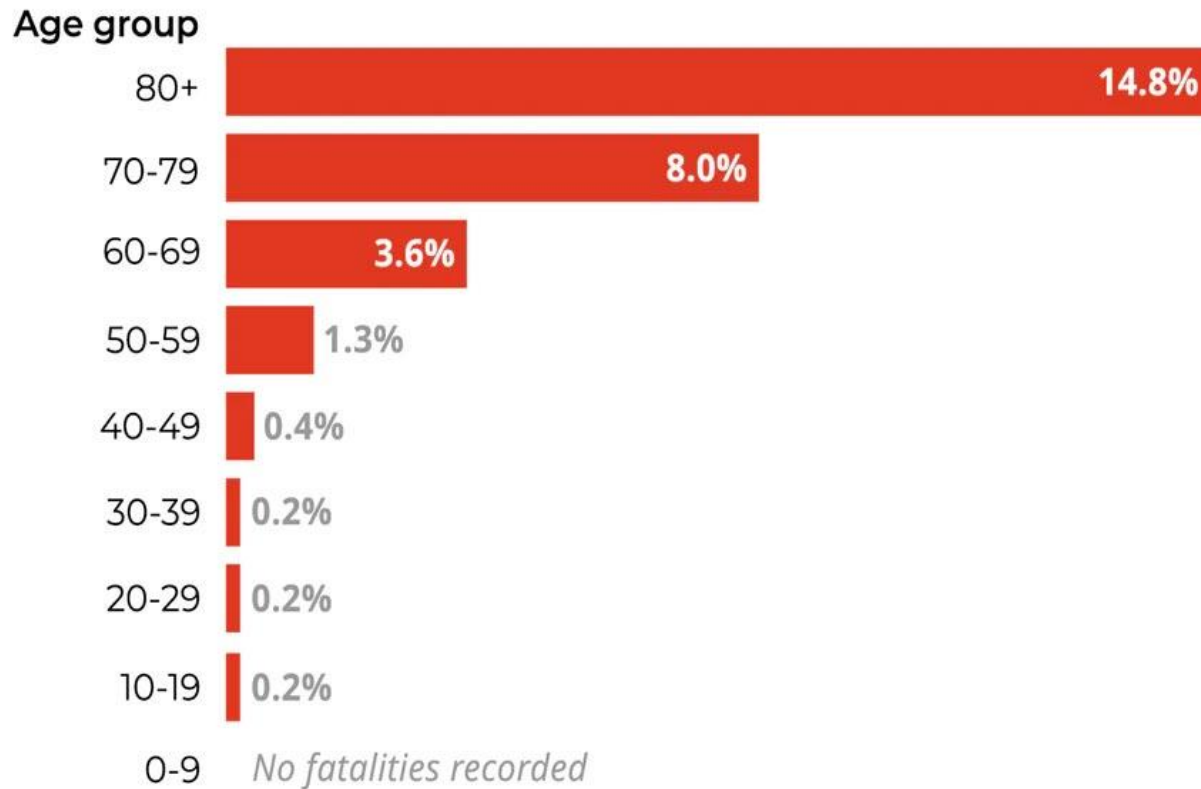
Source: Author provided

Severity of illness in children with COVID-19

- Critical 1.2%
- Severe 2.1%
- Asymptomatic 14.2%
- Moderate 46.0%
- Mild 36.3%

COVID-19 in Children (Global)

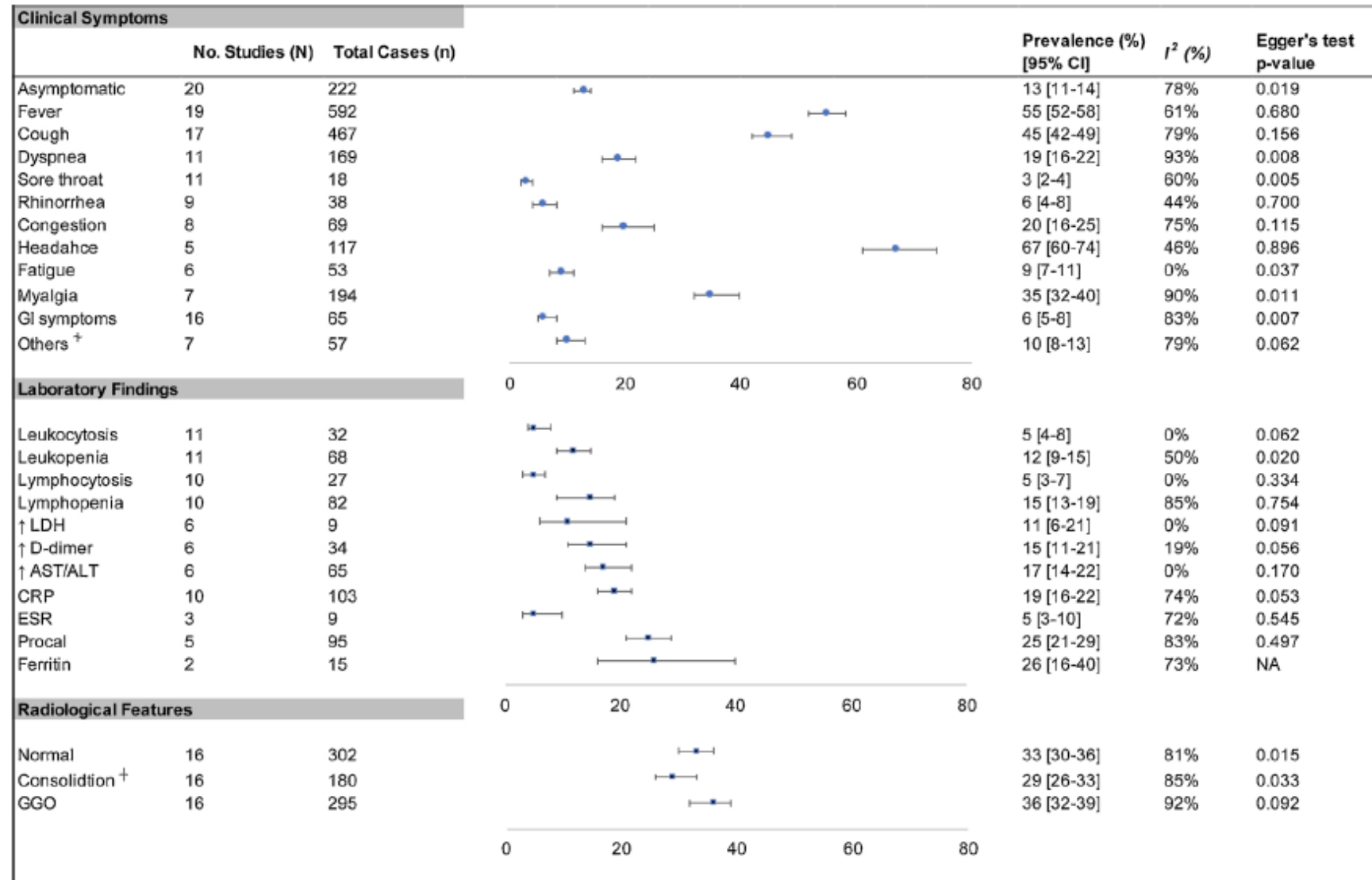| Clinical Symptoms	No. Studies (N)	Total Cases (n)		Prevalence (%) [95% CI]	I² (%)	Egger's test p-value
Asymptomatic	20	222		13 [11-14]	78%	0.019
Fever	19	592		55 [52-58]	61%	0.680
Cough	17	467		45 [42-49]	79%	0.156
Dyspnea	11	169		19 [16-22]	93%	0.008
Sore throat	11	18		3 [2-4]	60%	0.005
Rhinorrhea	9	38		6 [4-8]	44%	0.700
Congestion	8	69		20 [16-25]	75%	0.115
Headahce	5	117		67 [60-74]	46%	0.896
Fatigue	6	53		9 [7-11]	0%	0.037
Myalgia	7	194		35 [32-40]	90%	0.011
GI symptoms	16	65		6 [5-8]	83%	0.007
Others +	7	57		10 [8-13]	79%	0.062
Laboratory Findings						
Leukocytosis	11	32		5 [4-8]	0%	0.062
Leukopenia	11	68		12 [9-15]	50%	0.020
Lymphocytosis	10	27		5 [3-7]	0%	0.334
Lymphopenia	10	82		15 [13-19]	85%	0.754
↑ LDH	6	9		11 [6-21]	0%	0.091
↑ D-dimer	6	34		15 [11-21]	19%	0.056
↑ AST/ALT	6	65		17 [14-22]	0%	0.170
CRP	10	103		19 [16-22]	74%	0.053
ESR	3	9		5 [3-10]	72%	0.545
Procal	5	95		25 [21-29]	83%	0.497
Ferritin	2	15		26 [16-40]	73%	NA
Radiological Features						
Normal	16	302		33 [30-36]	81%	0.015
Consolidtion +	16	180		29 [26-33]	85%	0.033
GGO	16	295		36 [32-39]	92%	0.092

TABLE 3 Demography, clinical characteristics and outcomes of SARS-CoV-2 in children

Study	Patients n	Median Age	Infants (0-1 yrs) n (%)	Male n (%)	Positive SARS-CoV-2 RT-PCR n (%)	Underlying medical conditions n (%)	No symptoms n (%)	Fever n (%)	Respiratory (cough/SOB) n (%)	Pneumonia n (%)	GI (vomiting/diarrhea) n (%)	Hospitalized n (%)	ICU care/mechanical ventilation n (%)	Mortality n (%)
Zachariah et al.[17] (New York)	50	11	14 (34)	27 (54)	50 (100)	33 (67)	0 (0)	40 (80)	23 (46)/17 (34)	-	7 (14)	50 (100)	-/9 (18)	1 (2)
Götzinger et al.[18] (Europe)	582	5	230 (40)d	311 (53)	582 (100)	145 (25)	92 (16)	379 (65)	313 (54)/-	93/198 (47)	128 (22)	363 (62)	48 (8)/25 (4)	4 (1)
Garazzino et al.[16] (Italy)	168	2.3	66 (39)	94 (56)	168 (100)	33 (20)	4 (3)	138 (32)	82 (49)/16 (10)	75 (45)	9 (5)/22 (13)	110 (65)	2 (1)/2 (1)	0 (0)
Swann et al.[50] (UK)	651	4.6	225 (35)	367 (56)	651 (100)	276 (42)	0 (0)	431/617 (70)	233/599 (39)/173/570 (30)	-	179/564 (32)	651 (100)	116/632 (18)/58/620 (9)	6/627 (1)
Dong et al.[5] (China)	2143	7	379 (18)	1213 (57)	731 (34)	-	94 (4)	-	-	-	-	-	-	-
Han et al.[4] (South Korea)	91	11	6 (7)	53 (58)	91 (100)	6 (7)	20 (22)	62 (68)	54 (60)	-	16 (18)	91 (100)a	0 (0)/0 (0)	0 (0)
Shekerdemian et al.[51] (USA/Canada)	48	13	8 (17)	25 (52)	48 (100)	40 (83)	1 (2)	-	35 (73)	-	1 (2)	48 (100)	48 (100)/18 (38)	2 (4)
Cura Yayla et al.[19] (Turkey)	220	10	-	105 (48)	220 (100)b	22 (10)	55 (26)	89 (41)	79 (36)/9 (4)	74 (34)	9 (4)/17 (8)	220 (100)	3 (1)	2 (1)
Lu et al.[20] (Wuhan)	171	6.7	31 (18)	104 (61)	171 (100)	-	27 (16)	71 (42)	83 (49)/49 (29)	111 (65)	11 (6)/15 (9)	-	3 (2)/3 (2)	1 (1)
Parri et al.[52] (Italy)	100	3.3	40 (40)	57 (57)	100 (100)	27 (27)	21 (21)	28/54 (52)	44 (44)/11 (11)	20 (20)	10 (10)	67 (67)	-/1 (1)	0 (0)
Yonker et al.[21] (MA, USA)	49	12.7	2 (4)	23 (47)	49 (100)	-	0 (0)	25 (51)	23 (47)/8 (16)	-	3 (6)/3 (6)	-	-	-

COVID-19 in Children (China)

TABLE 2 Different Severity of Illness by Age Group

Age Group, y[a]	Asymptomatic, n (%)	Mild, n (%)	Moderate, n (%)	Severe, n (%)	Critical, n (%)	Total, n
<1	7 (1.9)	204 (54.2)	125 (33.2)	33 (8.8)	7 (1.9)	376
1–5	15 (3.1)	245 (49.9)	195 (39.7)	34 (6.9)	2 (0.4)	491
6–10	30 (5.8)	277 (53.3)	191 (36.7)	22 (4.2)	0 (0.0)	520
11–15	27 (6.5)	198 (48.1)	170 (41.3)	14 (3.4)	3 (0.7)	412
>15	15 (4.5)	164 (49.1)	145 (43.4)	9 (2.7)	1 (0.3)	334
Total	94 (4.4)	1088 (51.0)	826 (38.7)	112 (5.3)	13 (0.6)	2133

January 16, 2020, to February 8,2020

COVID-19 in Children (China)

**TABLE 1** Characteristics of Children's COVID-19 Cases in China

Characteristics	All Cases	Confirmed	Suspected	P
Age, median (interquartile range)	7 (2–13)	10 (4–15)	6 (2–12)	<.001
Age group, n (%)				
<1	379 (17.6)	85 (11.7)	291 (20.7)	<.001
1–5	491 (23.0)	137 (18.8)	354 (25.2)	
6–10	522 (24.5)	170 (23.4)	352 (25.0)	
11–15	412 (19.3)	180 (24.7)	232 (16.5)	
>15	334 (15.6)	156 (21.4)	178 (12.6)	
Sex, n (%)				
Male	1208 (56.6)	418 (57.4)	790 (56.1)	.575
Female	927 (43.4)	310 (42.6)	617 (43.9)	
Severity of illness, n (%)				
Asymptomatic	94 (4.4)	94 (12.9)	0 (0.0)	—
Mild	1088 (51.0)	314 (43.1)	774 (55.0)	<.001
Moderate	826 (38.7)	298 (40.9)	528 (37.5)	
Severe	112 (5.2)	18 (2.5)	94 (6.7)	
Critical	13 (0.6)	3 (0.4)	10 (0.7)	
Missing	2 (0.1)	1 (0.2)	1 (0.1)	
Days from symptom onset to diagnosis				
Median (interquartile range)	2 (1–5)	3 (1–5)	2 (0–4)	<.001
Range	0–42	0–42	0–36	—
Province, n (%)				
Hubei	981 (46.0)	229 (31.5)	752 (53.4)	<.001
Surrounding areas[a]	396 (18.5)	154 (21.1)	242 (17.2)	
Other	758 (35.5)	345 (47.4)	413 (29.4)	
Total	2135	728 (34.1)	1407 (65.9)	—

Characteristics	Non-hospitalized cohort (total N = 11,634)		Hospitalized cohort (total N = 672)		P-value	Standardized mean difference
	Patient count	Mean ± SD or proportion	Patient count	Mean ± SD or proportion		
Age (years)	11,634	9.4 ± 5.6	672	9.0 ± 6.2	0.13	0.06
Age groups					<0.001	0.53
Infant (0–1 years)	1345	11.6%	73	10.9%		
Toddlers (1–3 years)	933	8.0%	85	12.6%		
Preschoolers (3–5 years)	959	8.2%	65	9.7%		
Middle childhood (6–11 years)	3146	27.0%	127	18.9%		
Adolescents (≥ 12 years)	5256	45.1%	317	47.1%		
Male	5954	51.2%	343	51.0%	0.94	0.002
Female	5678	48.8%	329	49.0%		
Race/ethnicity						
Non-Hispanic Whites	6064	52.1%	243	36.2%	<0.001	0.18
Non-Hispanic Blacks	3066	26.4%	223	33.2%	<0.001	0.21
Hispanic	1889	16.2%	133	19.8%	<0.001	0.16
Non-Hispanic Asians	273	2.3%	19	2.8%	0.43	0.03
Other	342	2.9%	54	8.0%	0.04	0.08
Comorbidities						
Cardiovascular	94	0.8%	102	15.2%	<0.001	0.54
Gastrointestinal	334	2.9%	121	18.0%	<0.001	0.51
Hematologic or immunologic	57	0.5%	45	6.7%	<0.001	0.30
Malignancy	51	0.4%	34	5.1%	<0.001	0.29
Metabolic	79	0.8%	69	10.3%	<0.001	0.38
Neurological and Neuromuscular	252	2.2%	92	13.7%	<0.001	0.44
Congenital or genetic defects	127	1.1%	191	28.4%	<0.001	0.83
Renal and urologic	175	1.5%	87	13.0%	<0.001	0.45
Respiratory	2,310	19.9%	189	28.1%	<0.001	0.20

COVID-19 in Children (US)

Frequency of Symptoms: Stratified by Hospitalization Status
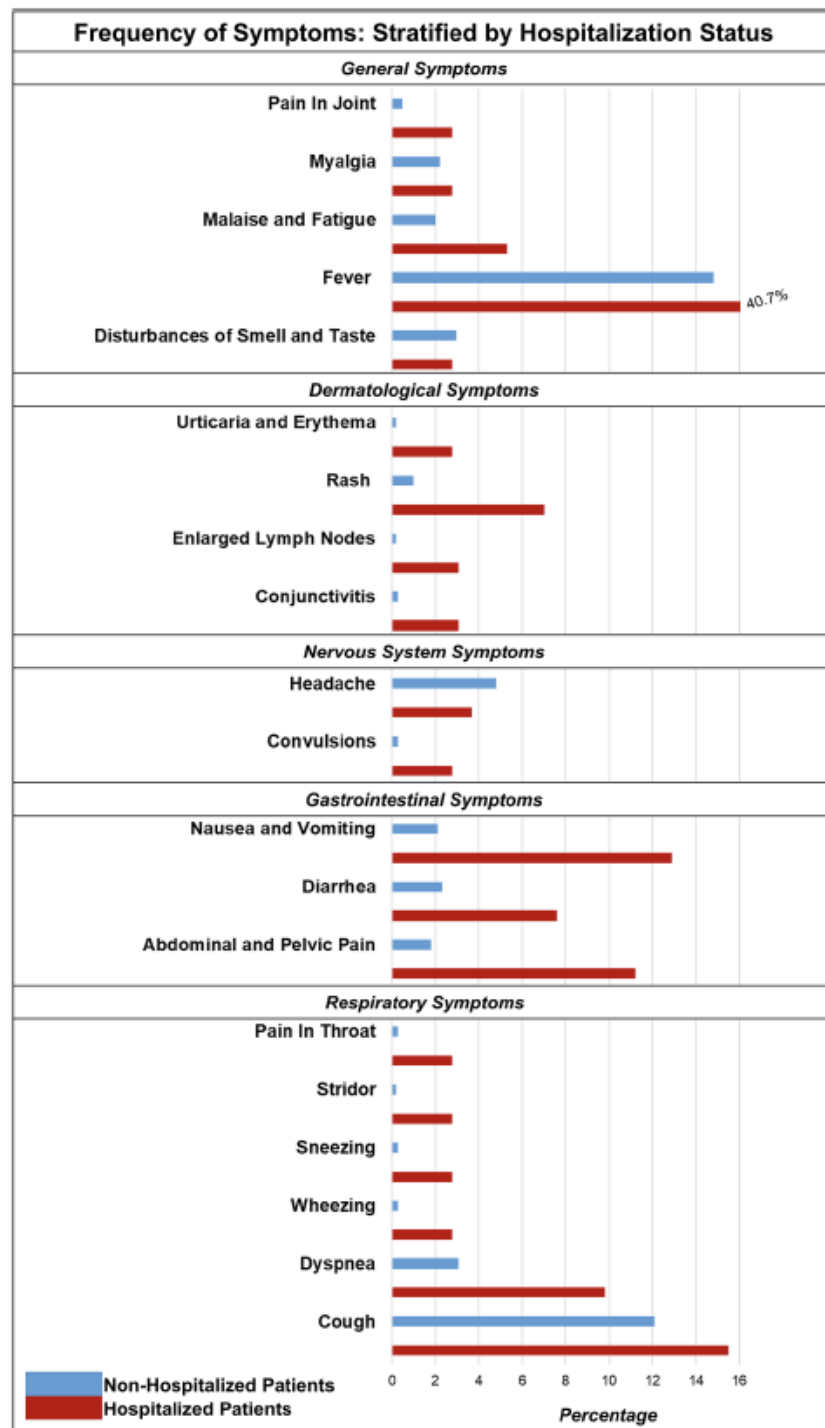
COVID-19 in Children (US)

COVID-19 in Children (US)

Impact of the COVID-19 Pandemic on Children

- Illness

- *Education*

- *Mental health*

- *Health and Development*

Impact on Education

Children and youth **out of school** due to **COVID-19 closures**

89%
of the world's student population
*As of March 2020

1.52 billion
children and youth

including
743 million
girls.

Young people classified as **NEET***

267 million

2/3
are young women.

NEET | "Not in Education, Employment, or Training". A person who is unemployed, not in school or vocational training.

Impact on Mental Health

- Mental health visits saw a 24% increase for children ages 5 to 11, and 31% for older minors.

- More vulnerable to mental health conditions such as depression and anxiety due to the pandemic and its consequences,

Impact on Health and Development

- Stressful pressures such as these can negatively impact a child's neurological development, especially in infancy or early childhood → depression in adulthood

- Elevated maternal death and infant mortality (disrupted access to healthcare and food)

Thank for Your Attention !