

SCIENTIFIC RESEARCH MONITORING ON COVID-19

22 DECEMBER 2020

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SCIENTIFIC RESEARCH MONITORING ON COVID-19

(ISSUE 322)

Abu Dhabi Public Health Center (ADPHC) is gathering the latest scientific research updates and trends on coronavirus disease (COVID-19) in a daily report. The report provides summaries on breakthrough or updated research on COVID-19 to allow health care professionals and public health professionals get easy and fast access to information.

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Research

Update



Statistics



Articles

Summary

Note : All articles presented in this report represent the authors' views and not necessarily represents Abu Dhabi Public Health Center views or directions. Due the nature of daily posting , some minor language errors are expected.

For further inquiries you may communicate with us as PHP@adphc.gov.ae

RESEARCH UPDATES

The views and opinions expressed in this report are those of the authors and do not reflect the official policy or position of the Abu Dhabi Public Health Center (ADPHC).

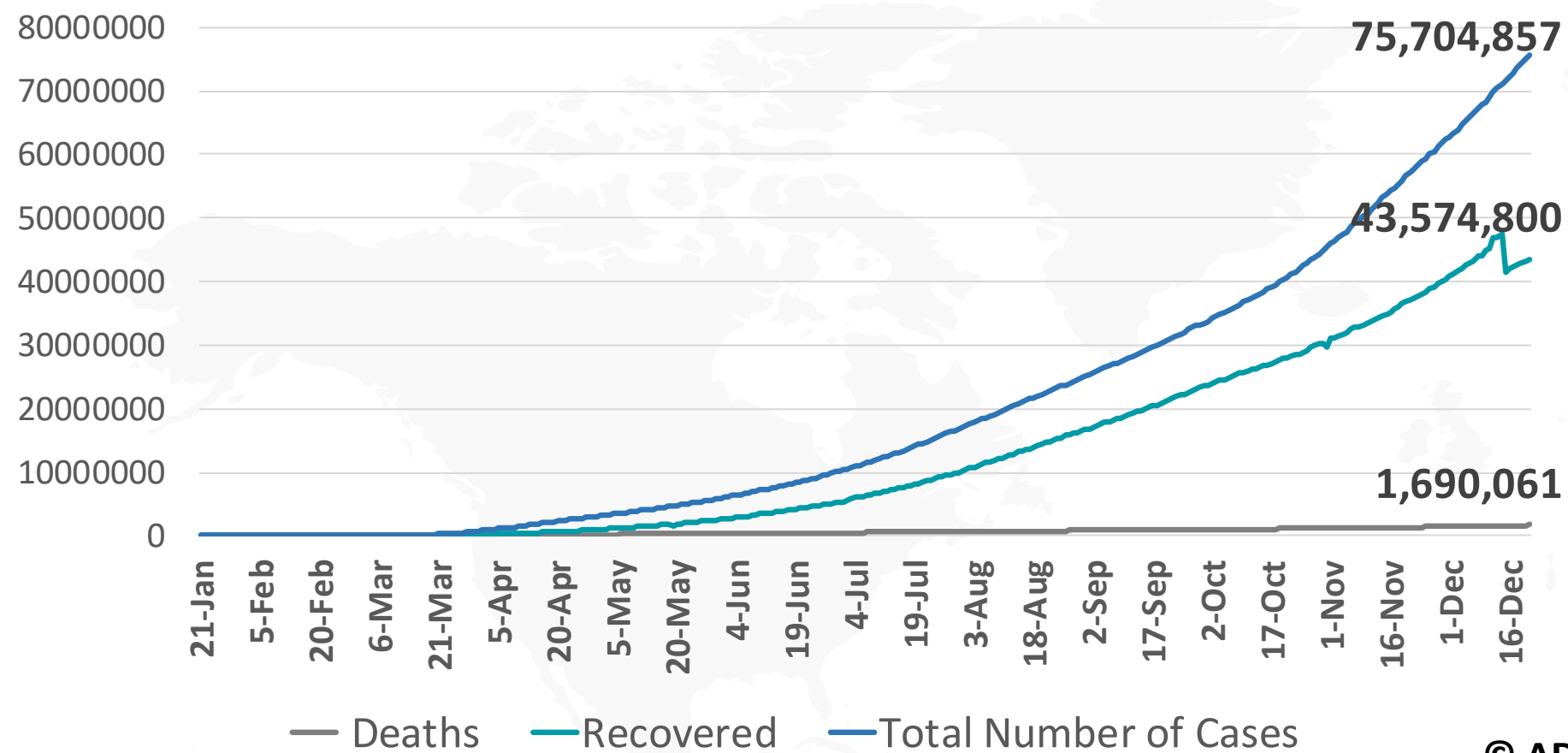
Click on icon to view content

**Public health
response**

**Special report on the UK
detected new variant of SARS-
COV2**



Figure 1: Total Number of Infected, Recovered, and Death Cases



Note: the number of recovered cases in 31st October rechecked from 30 million to 29 million, and in 15th December rechecked from 47 million to 41 million in Johns Hopkins website

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Figure 3: Total Number of Death Due to COVID-19 (china and result of the world)

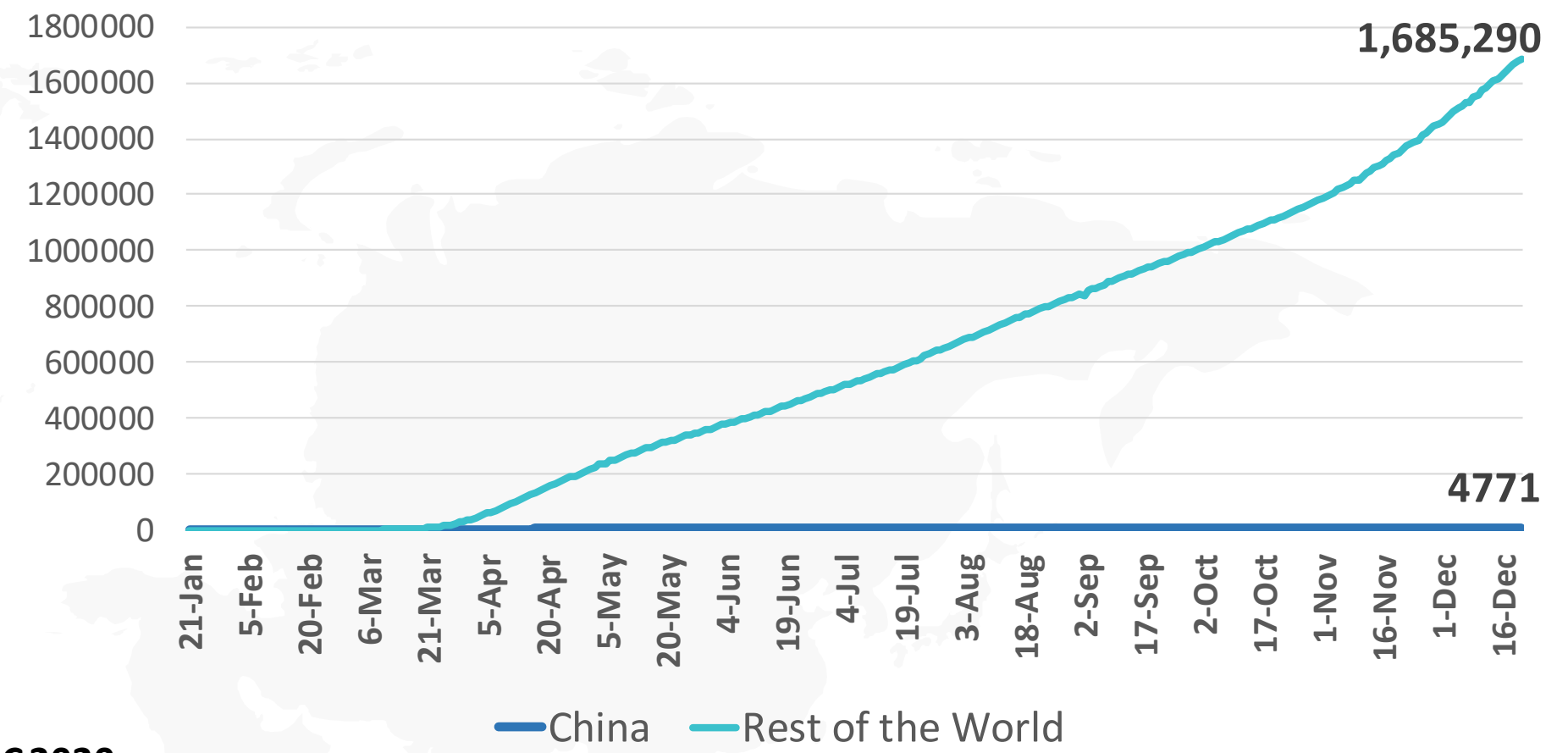


Figure 2: Daily New Infected COVID-19 Cases (China and rest of the world)

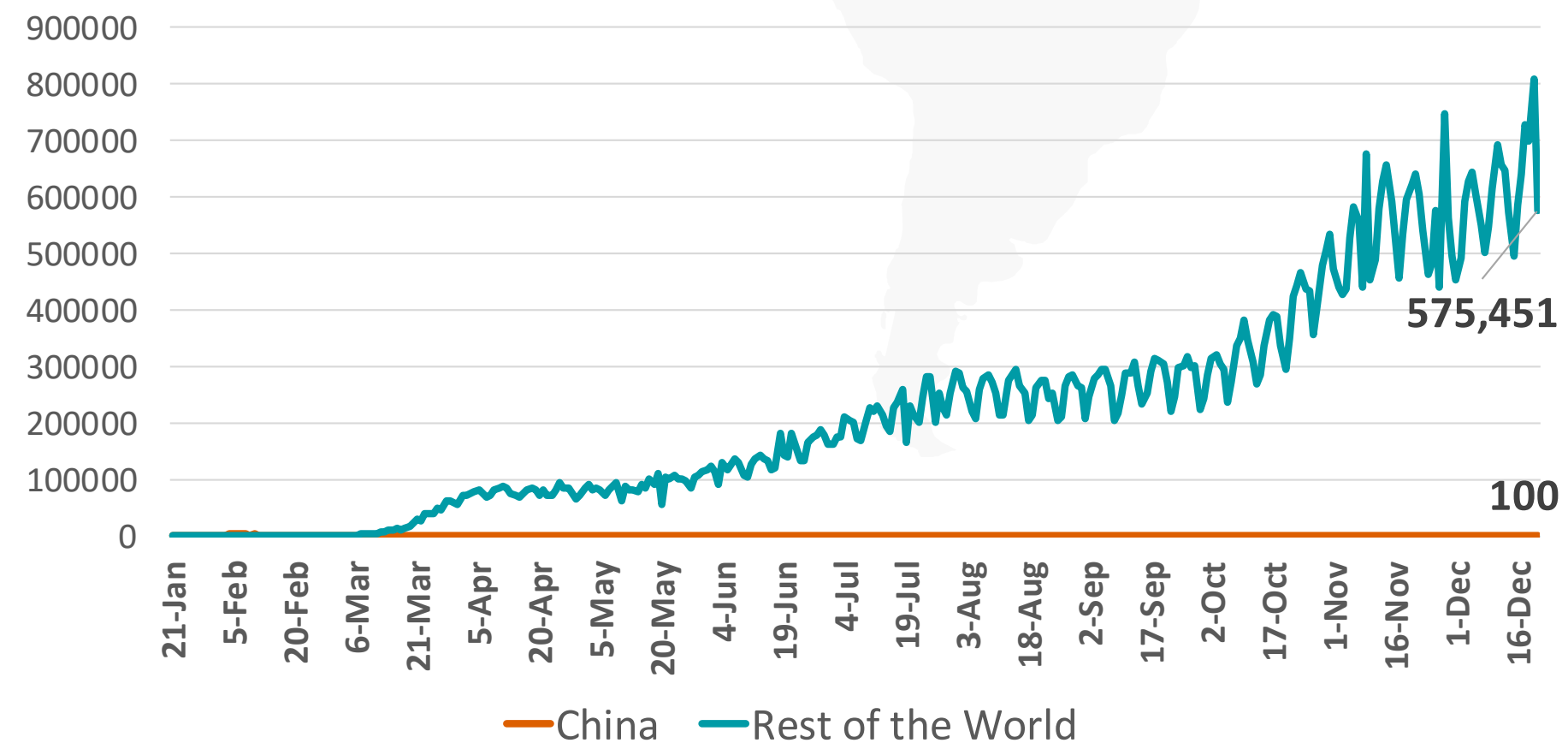


Figure 4: Global Daily New Deaths Due to COVID-19

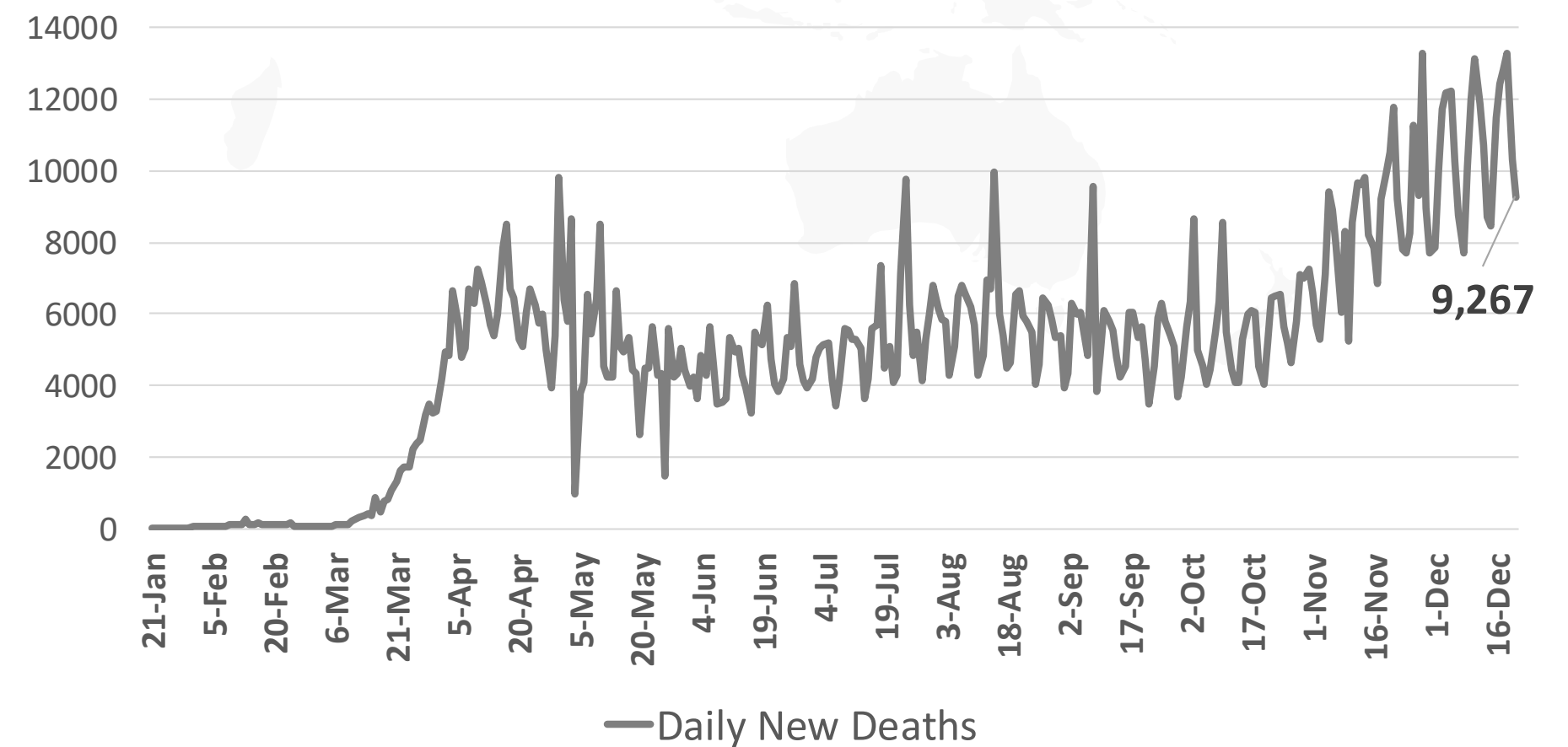
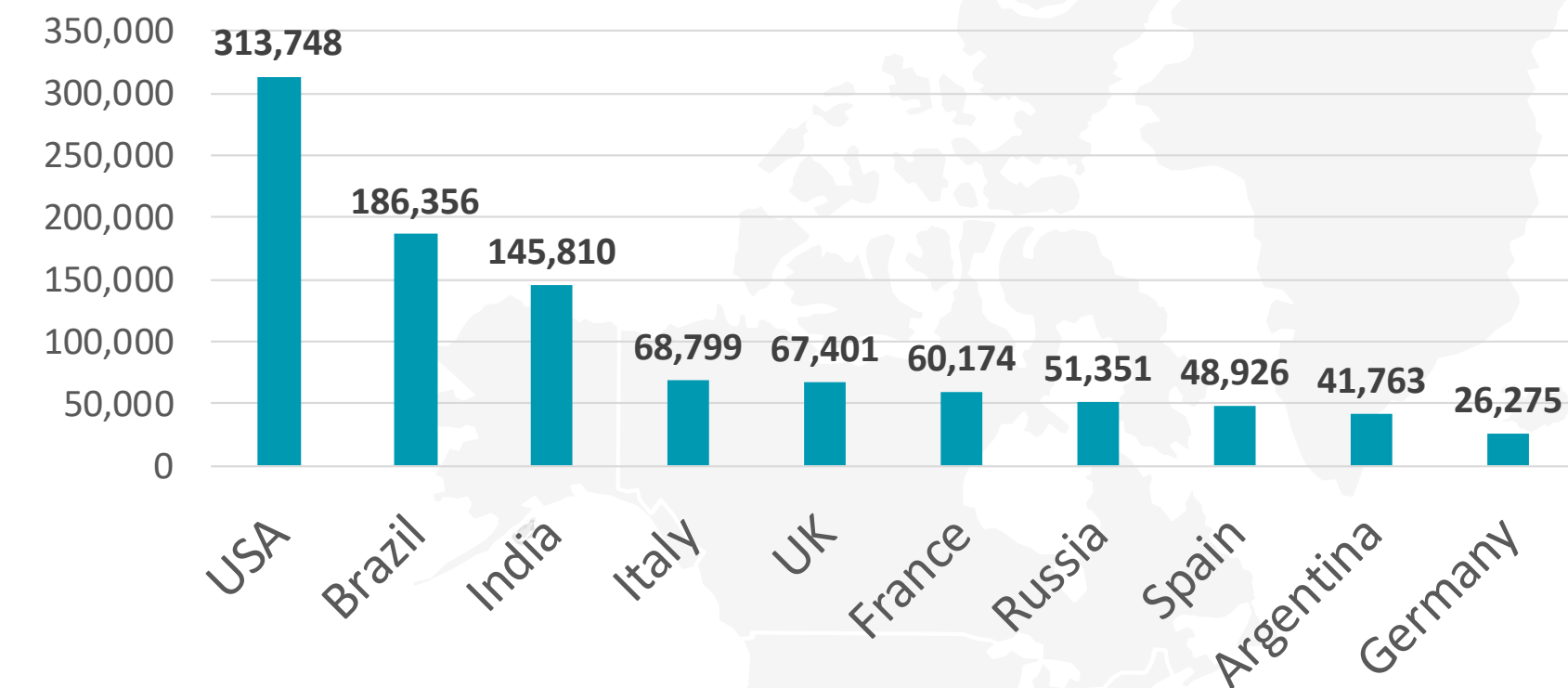
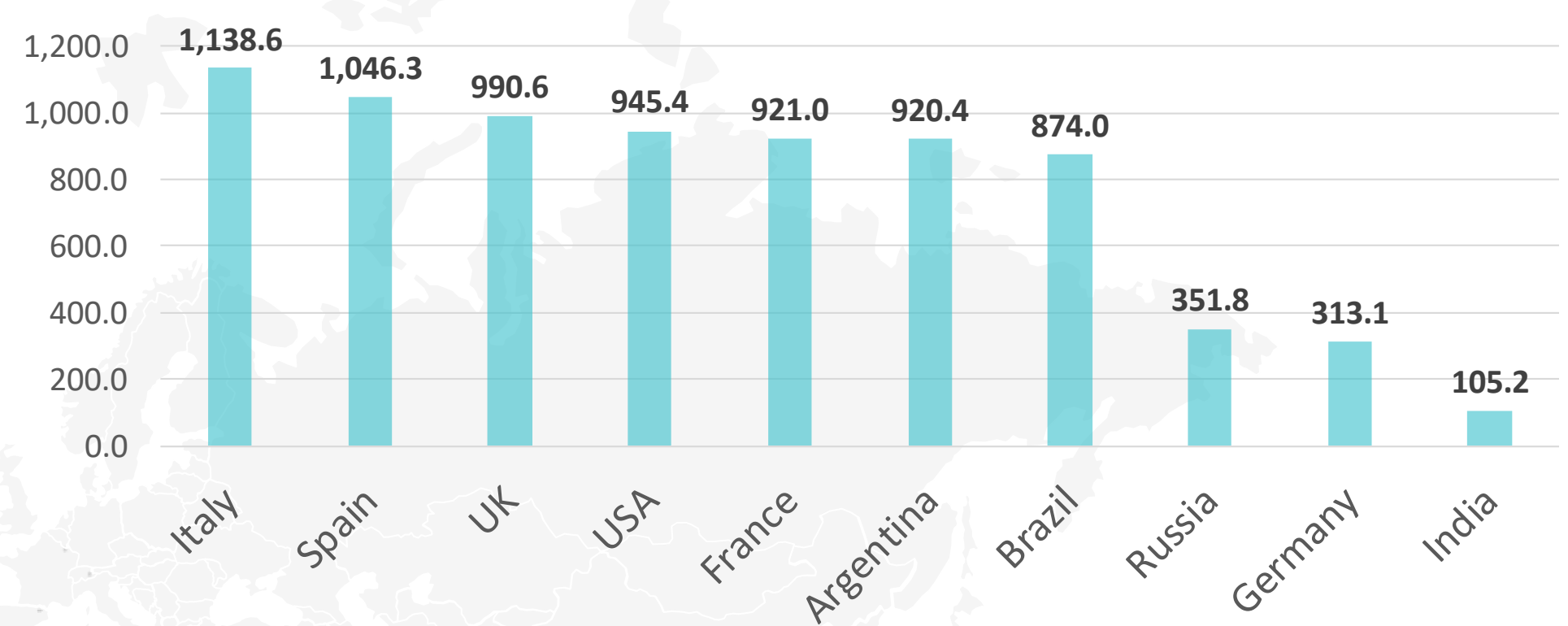


Figure 5: Top 10 Countries in the Total Number of Cases Due to COVID-19

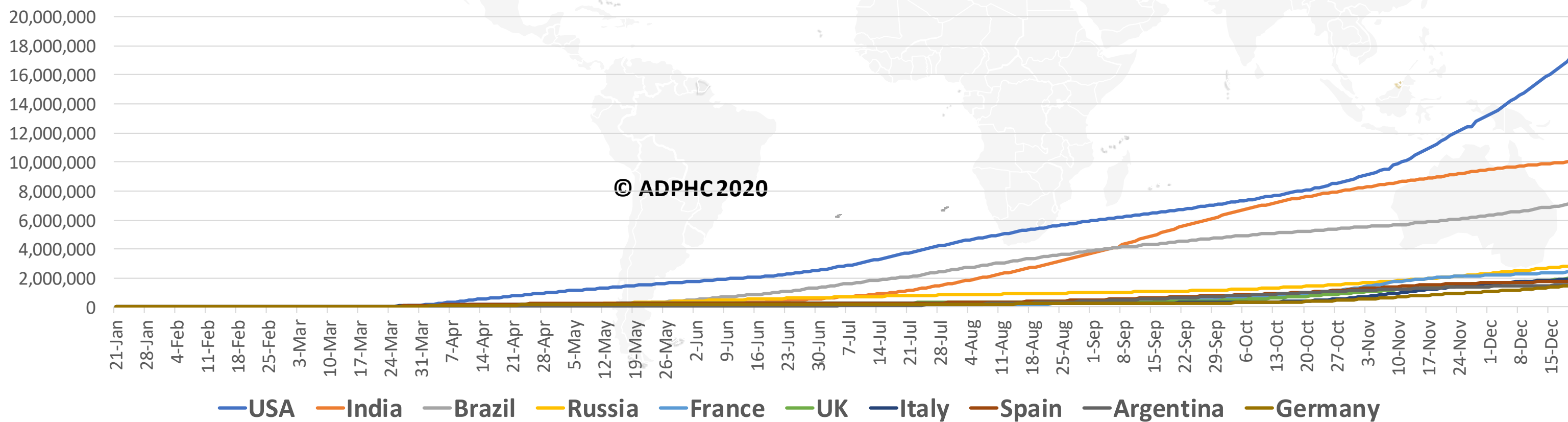
TOTAL DEATHS



DEATHS PER MILLION



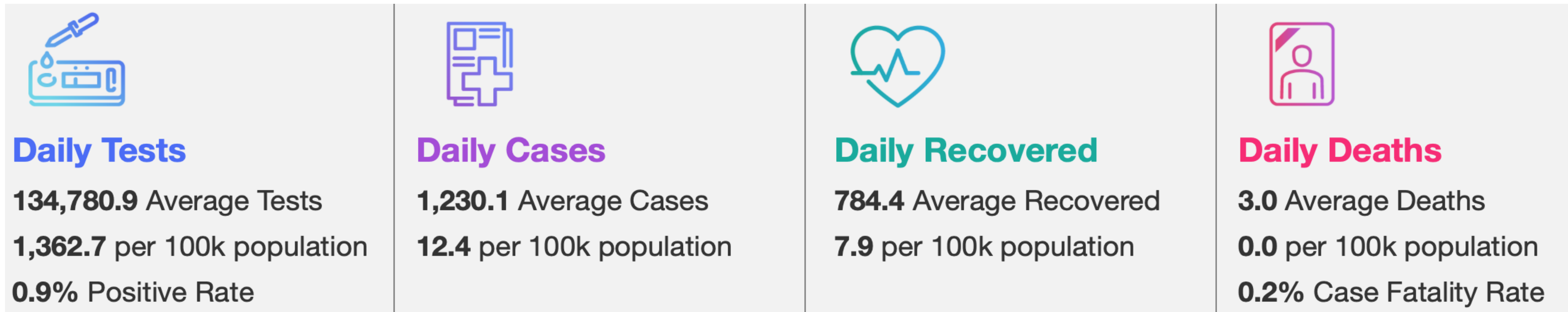
TOTAL INFECTED CASES



USA	17,515,091
India	10,055,560
Brazil	7,213,155
Russia	2,877,727
France	2,431,237
UK	2,040,151
Italy	1,953,185
Spain	1,797,236
Argentina	1,537,169
Germany	1,510,652



Figure 6: COVID-19 Status in the UAE (Federal Competitiveness and Statistics Authority Dashboard)



TOTAL NUMBER OF INFECTED AND RECOVERED CASES DUE TO COVID-19 REPORTED BY THE UAE

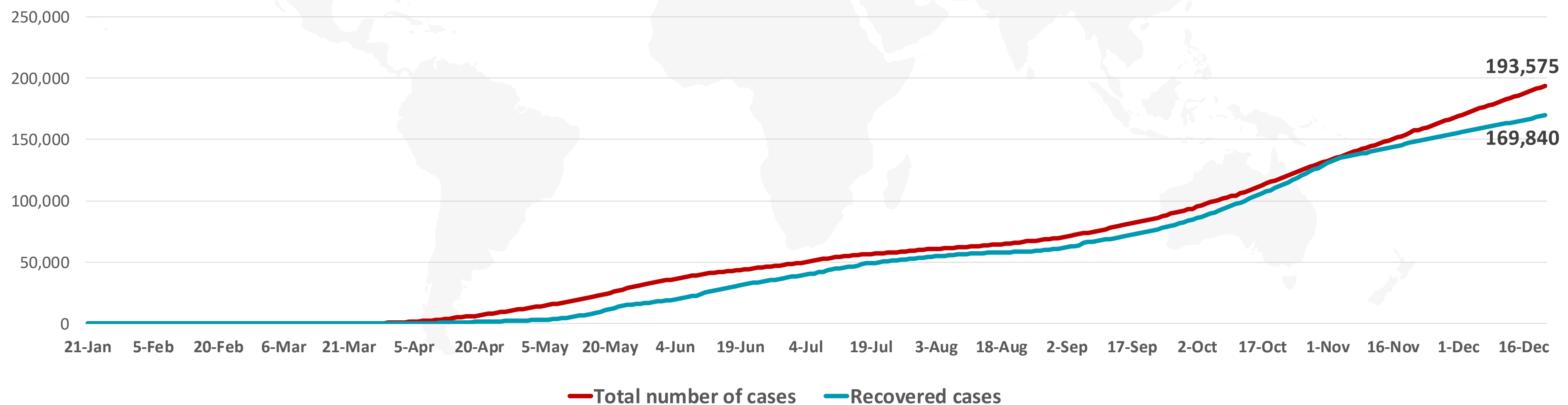
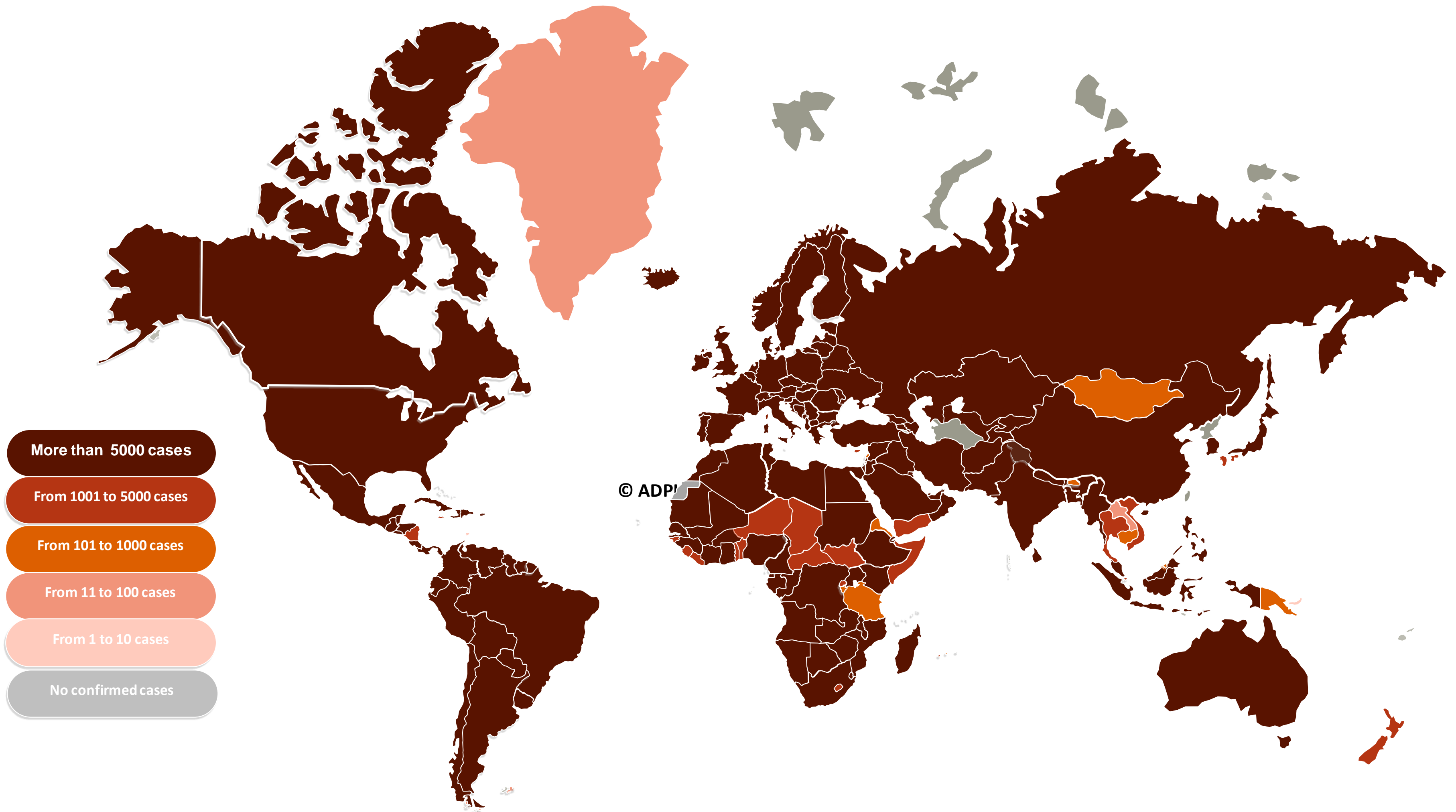


Figure 7A : Global Distribution of COVID-19 Cases



More than 5000 cases

From 1001 to 5000 cases

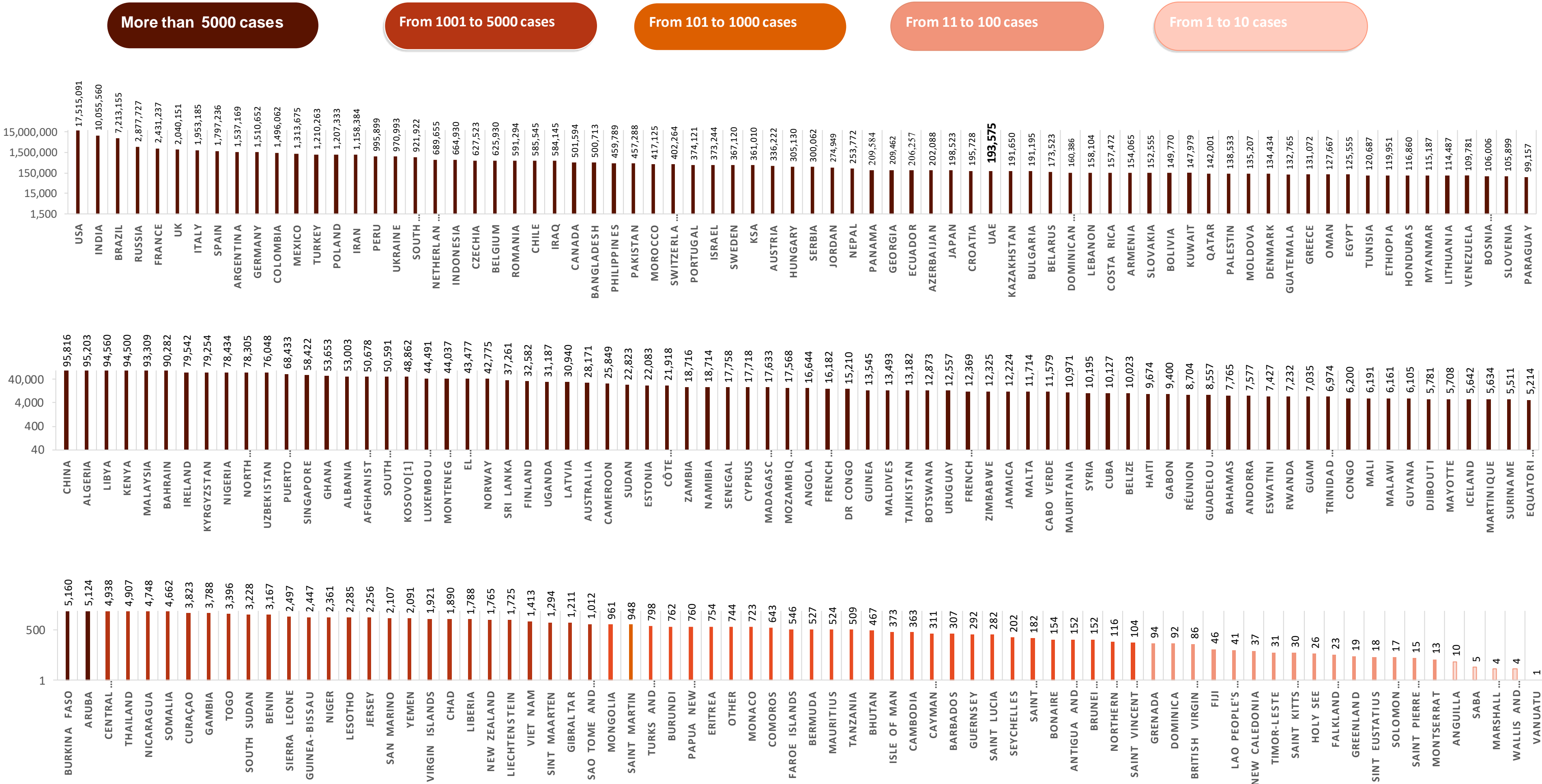
From 101 to 1000 cases

From 11 to 100 cases

From 1 to 10 cases

No confirmed cases

Figure 7B: Bar Chart Illustrates the Global Distribution of COVID19 Cases



Other*: includes cases and deaths reported under the international conveyance (Diamond Princess)

Graphs published by Abu Dhabi Public Health Center 2020 | Data resources: [WHO](#)

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Figure 8: Global Distribution of COVID-19 Cases per Region

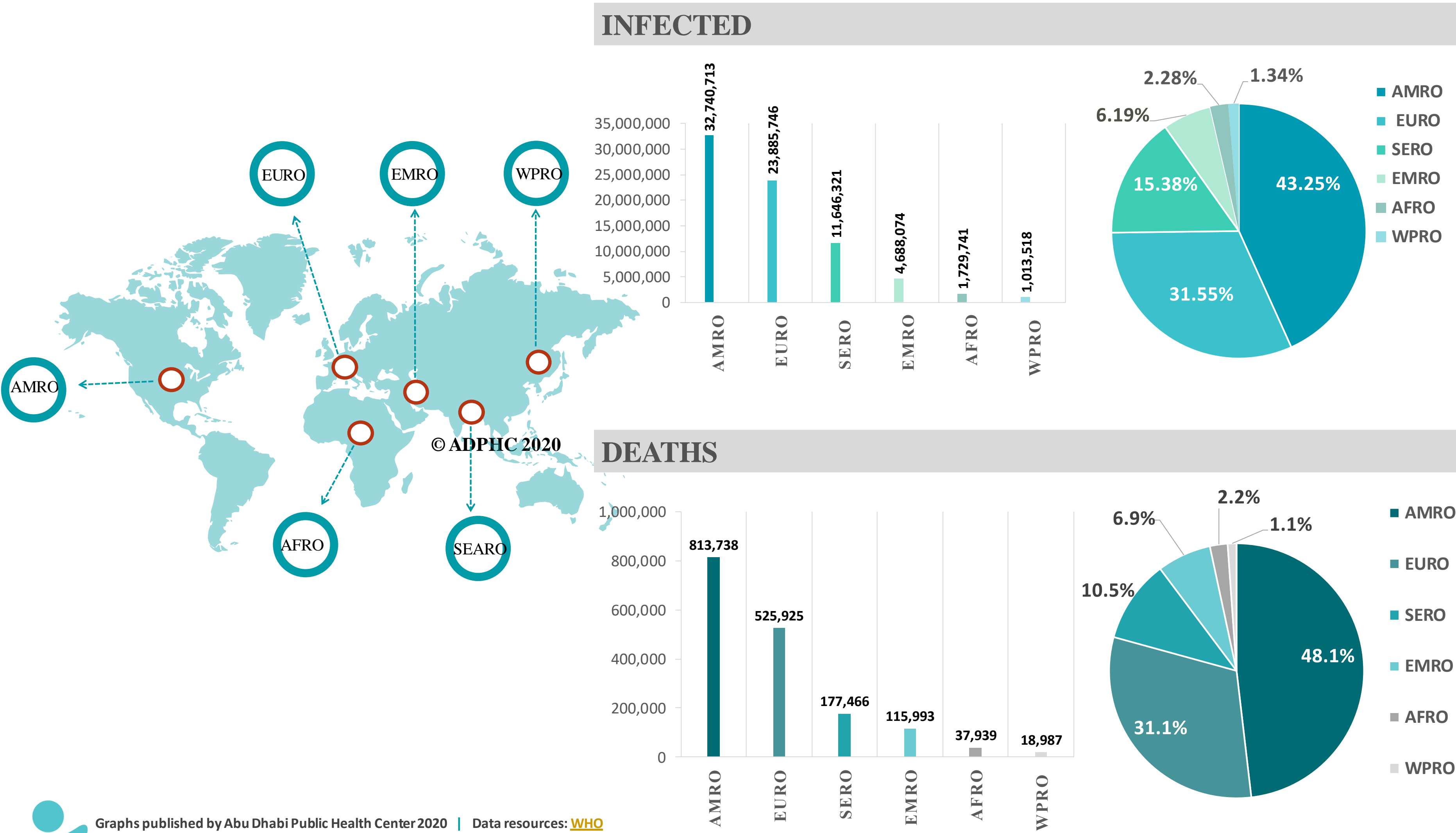
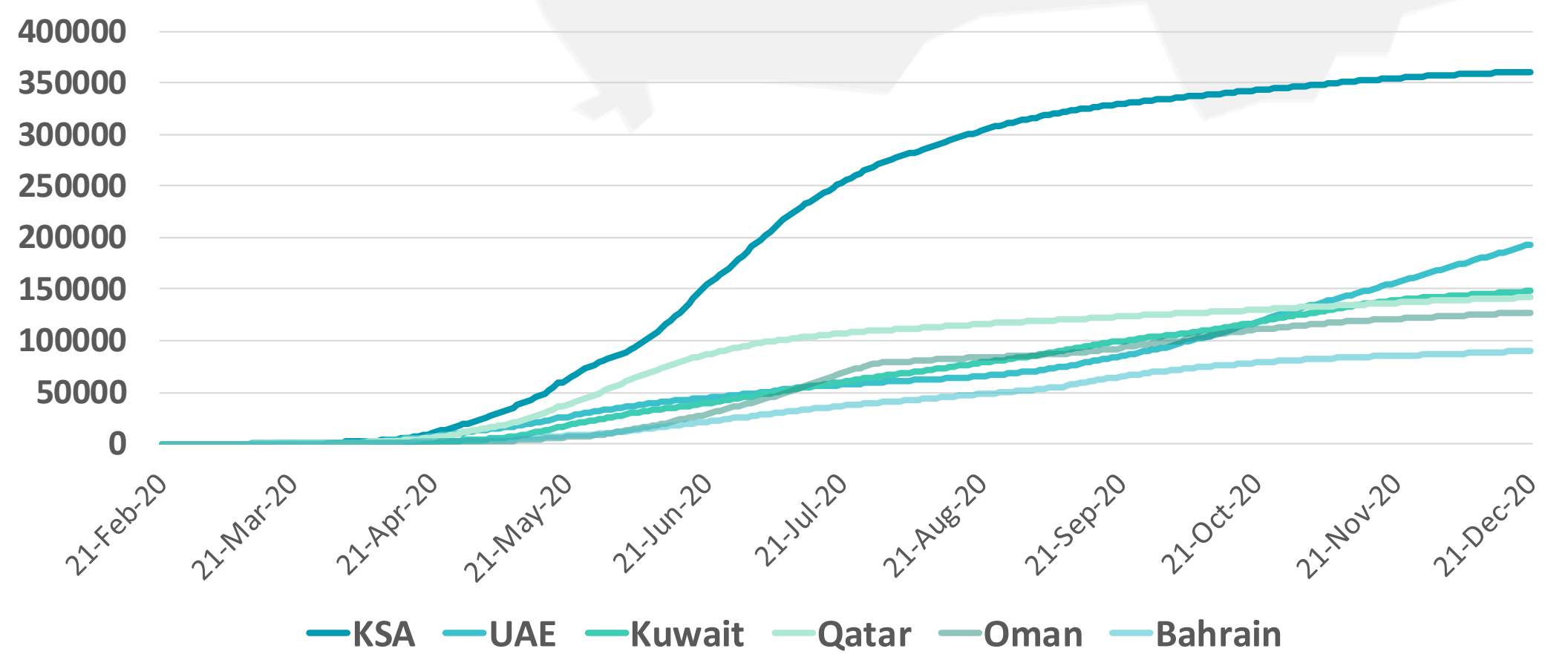
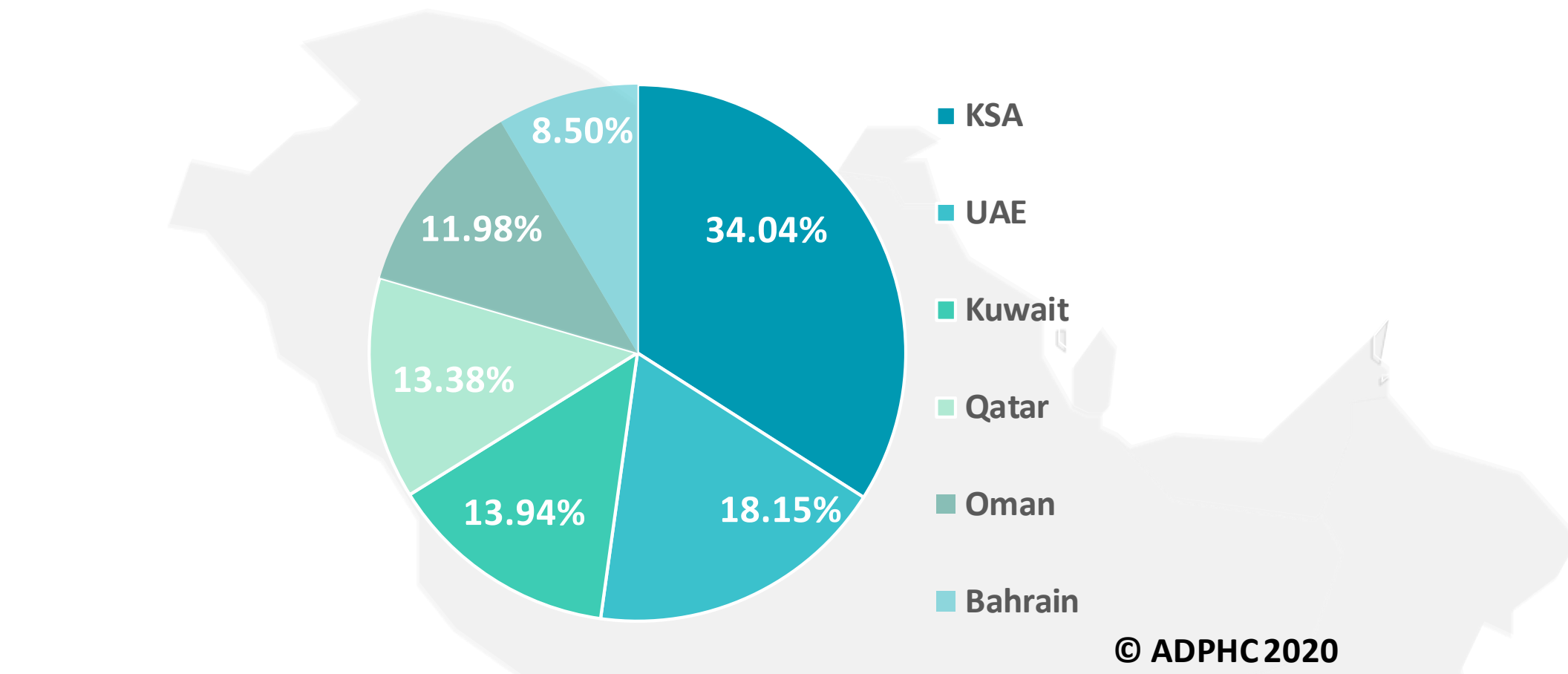
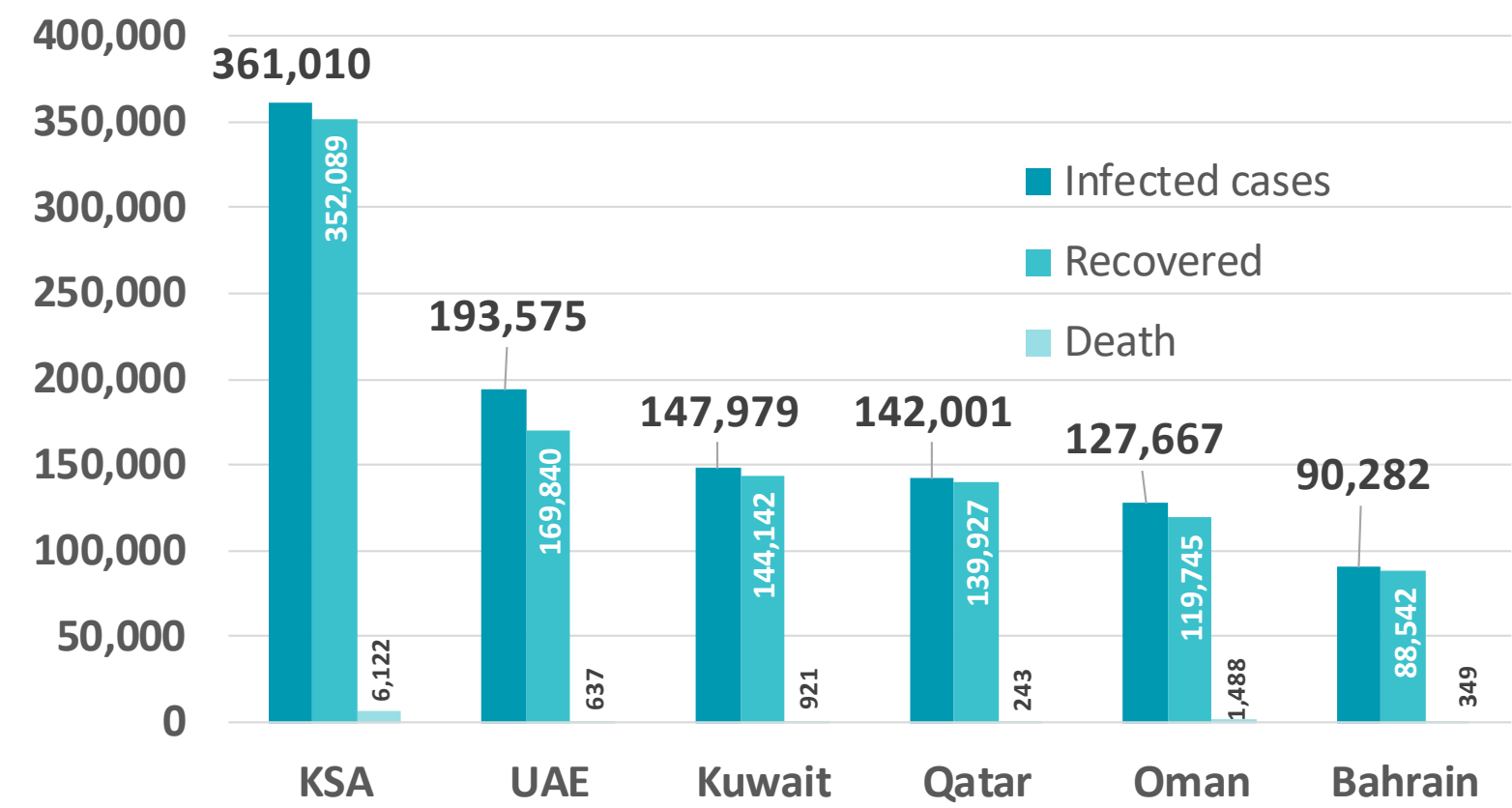


Figure 9: Comparative Analysis of the Distribution of COVID-19 Cases in GCC Countries

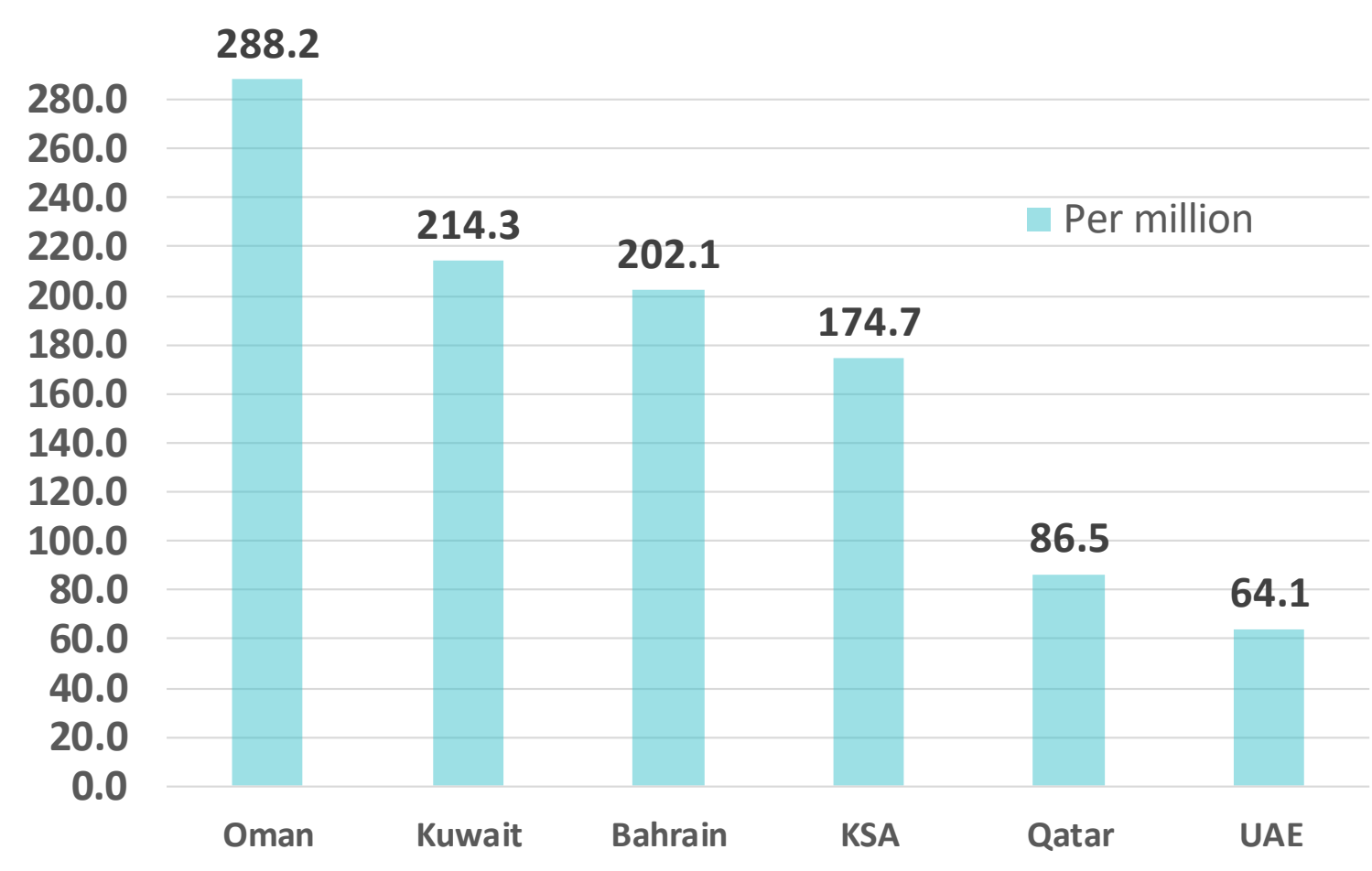
TOTAL NUMBER OF INFECTED CASES



TOTAL NUMBER OF INFECTED, RECOVERED AND DEATHS



DEATHS PER MILLION



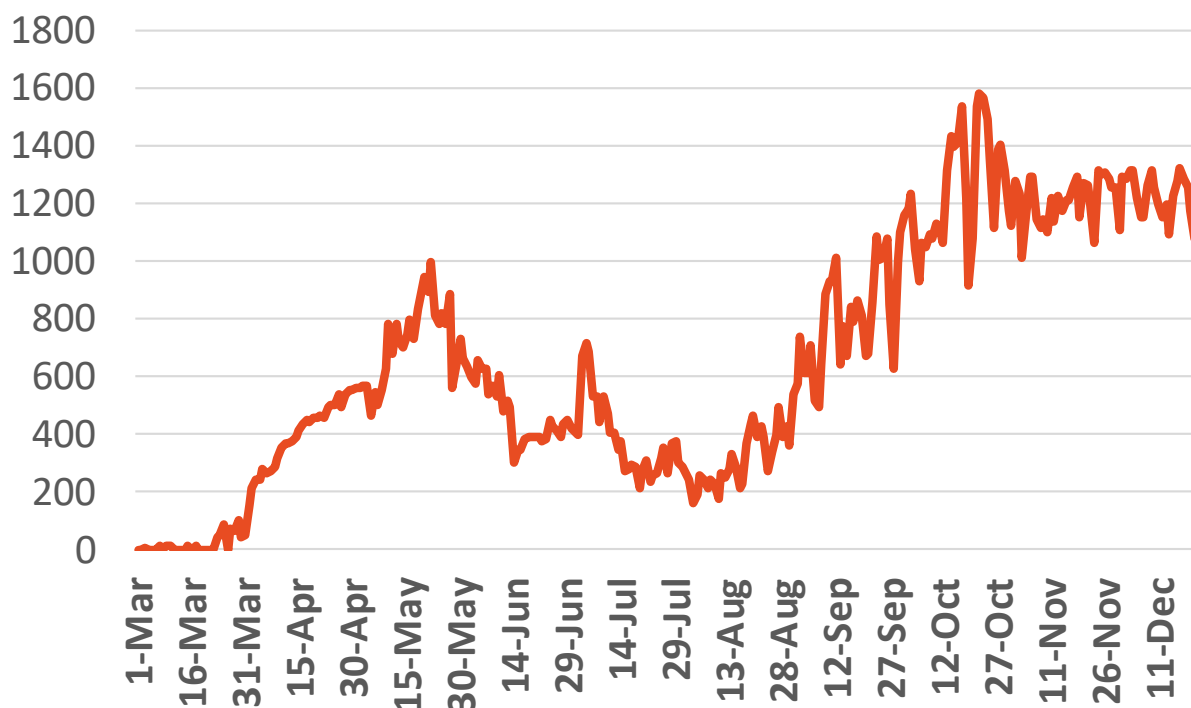
Graphs published by Abu Dhabi Public Health Center 2020 | Data resources: [John Hopkins](#), [WHO](#)

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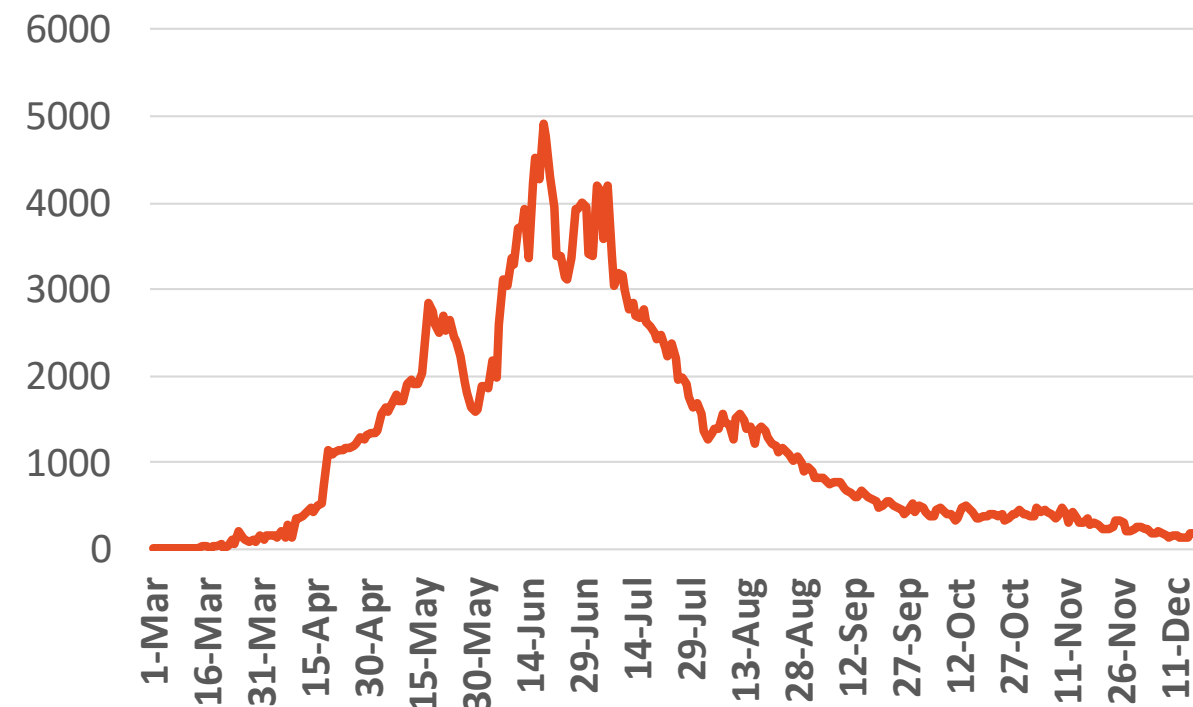
Figure 10: Comparative Analysis of the Distribution of COVID-19 New Cases in GCC Countries

UAE



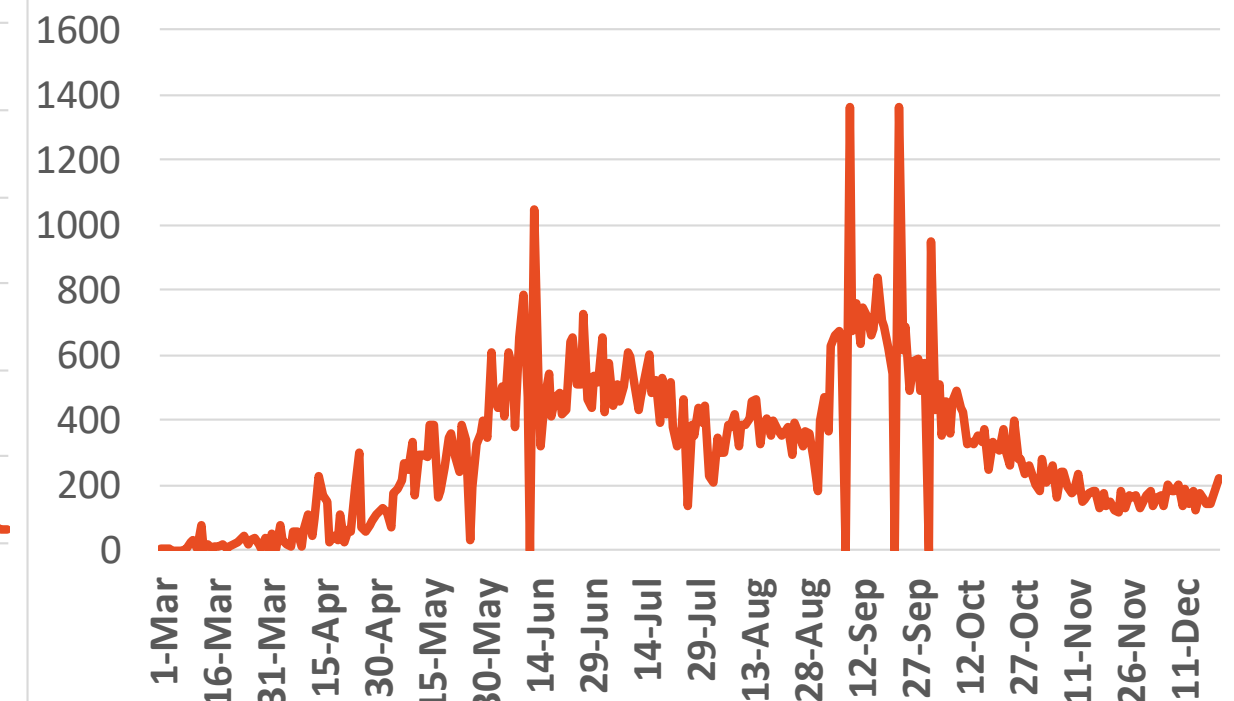
Source : National Emergency Crisis and Disaster Management Authority

KSA



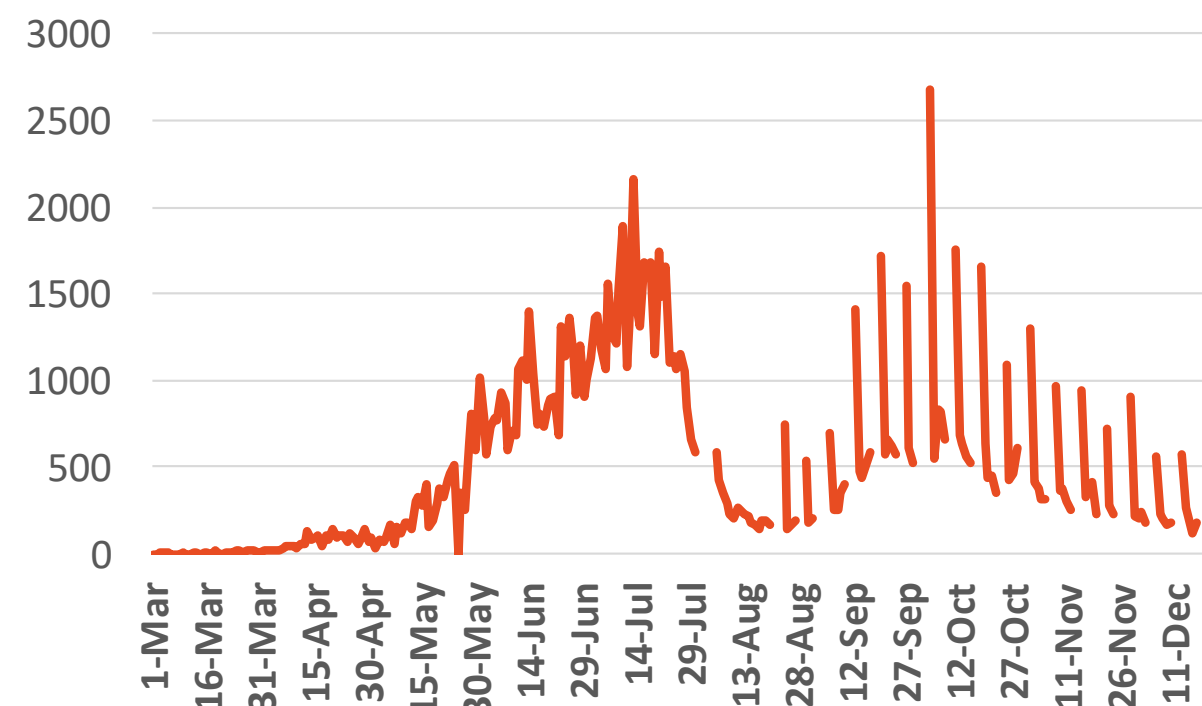
Source : KSA ministry of health

Bahrain



Source :WHO

Oman



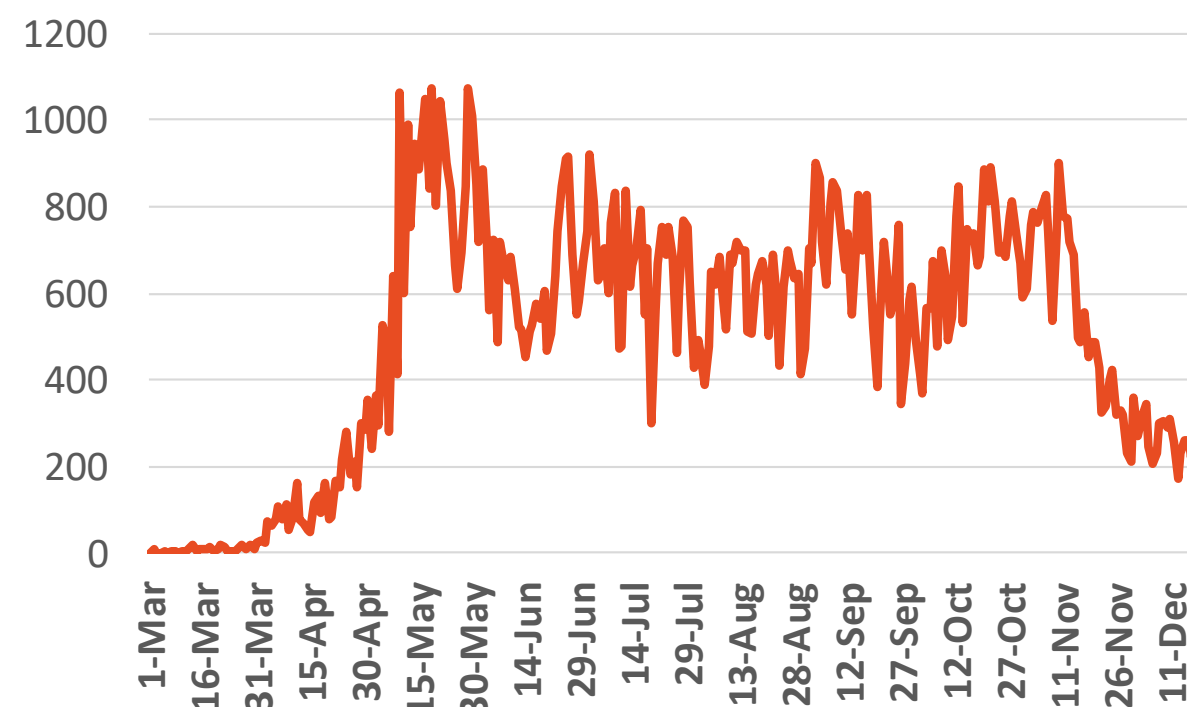
Source :Oman ministry of health

*No announced statistic data from 31 JUL to 4 AUG, 21,23,28,30 AUG 2020, 5,11,12,18,19,25,26,30 SEP,1,2,9,10,16,17,23,24,30,21 OCT, 6,7,13,14,17,20,21,25,26,6 DEC

*No announced statistic data on weekends and official holidays.

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Kuwait



Source : Kuwait ministry of health

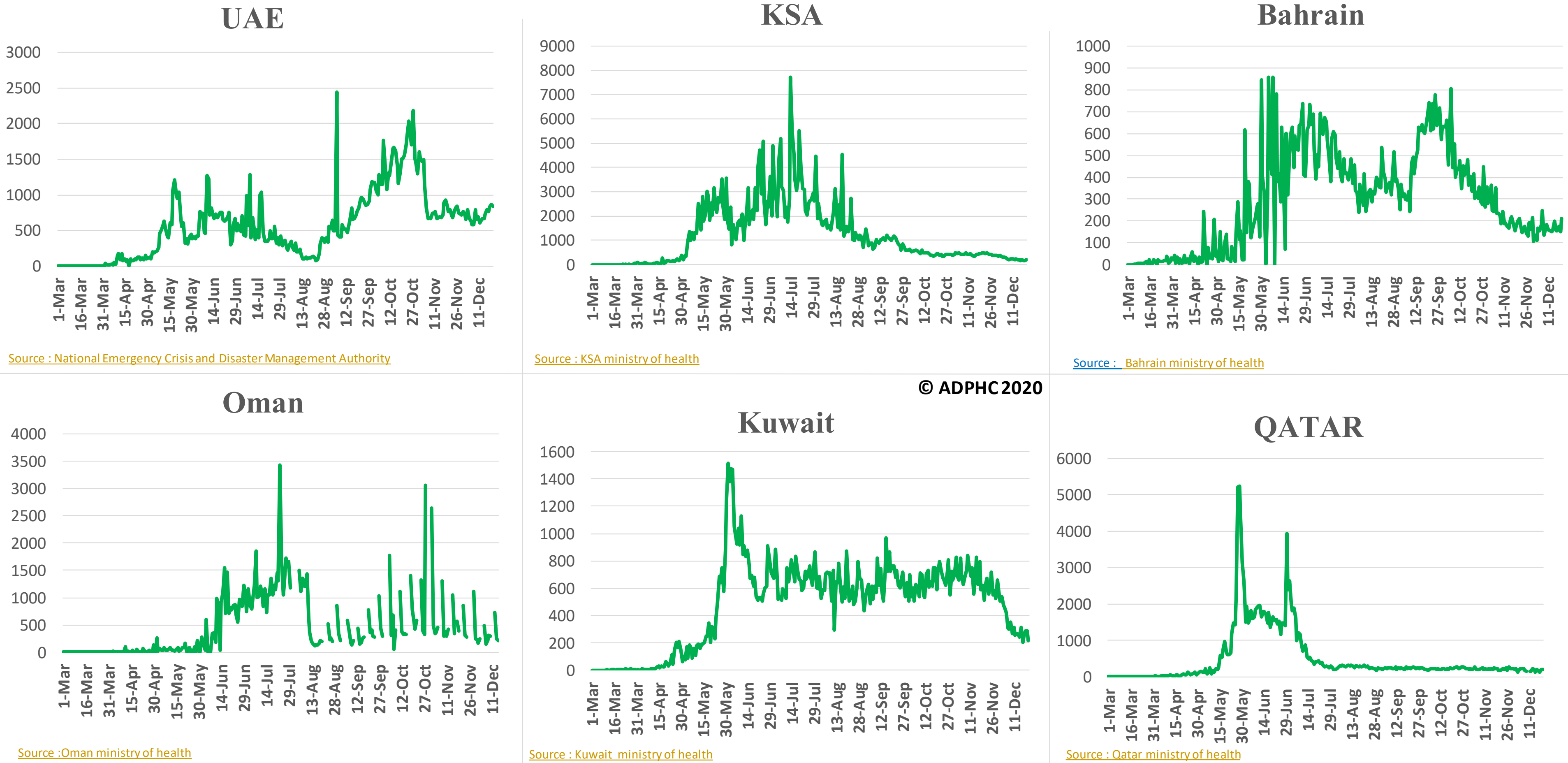
Qatar



Source : Qatar ministry of health



Figure 11: Comparative Analysis of the Distribution of COVID-19 Newly Recovered Cases in GCC Countries



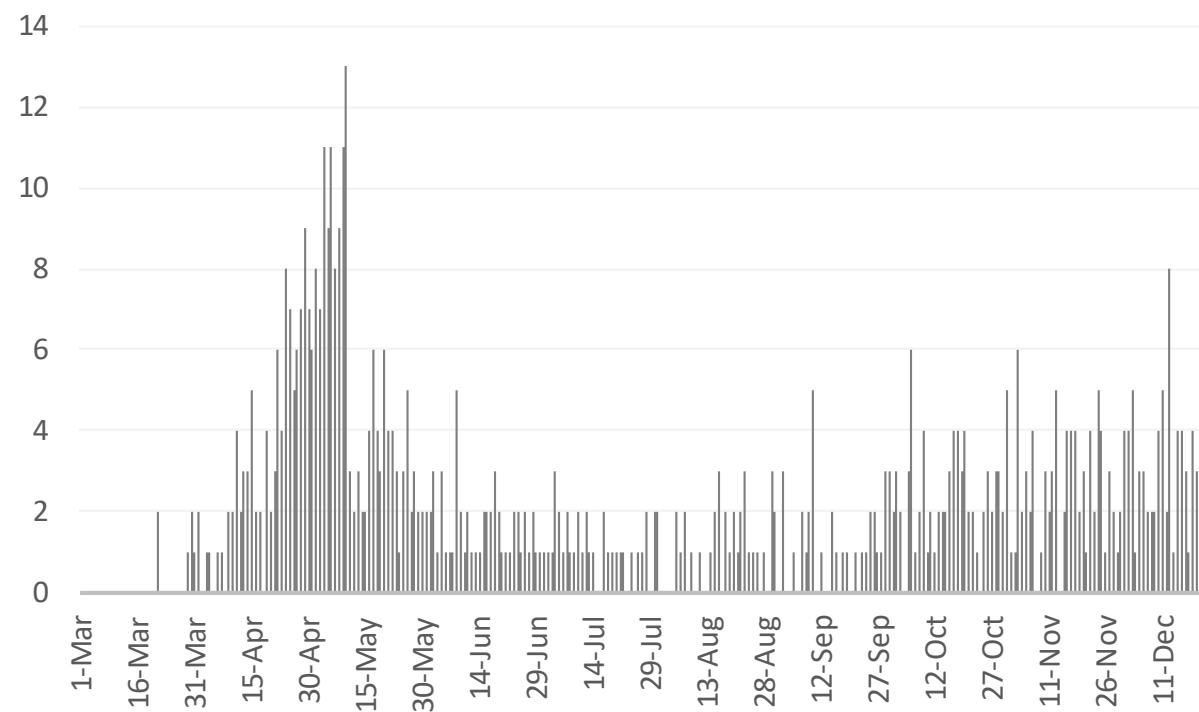
*No announced statistic data from 31 JUL 4 AUG, 21,23,28,30 AUG 2, 4 5,11,12,18,19,25,26,30 SEP,1,2,9,10,16,17,23,24,30,21 OCT, 6,7,13,14,17,20,21, 25,26,6 DEC

*No announced statistic data on weekends and official holidays.



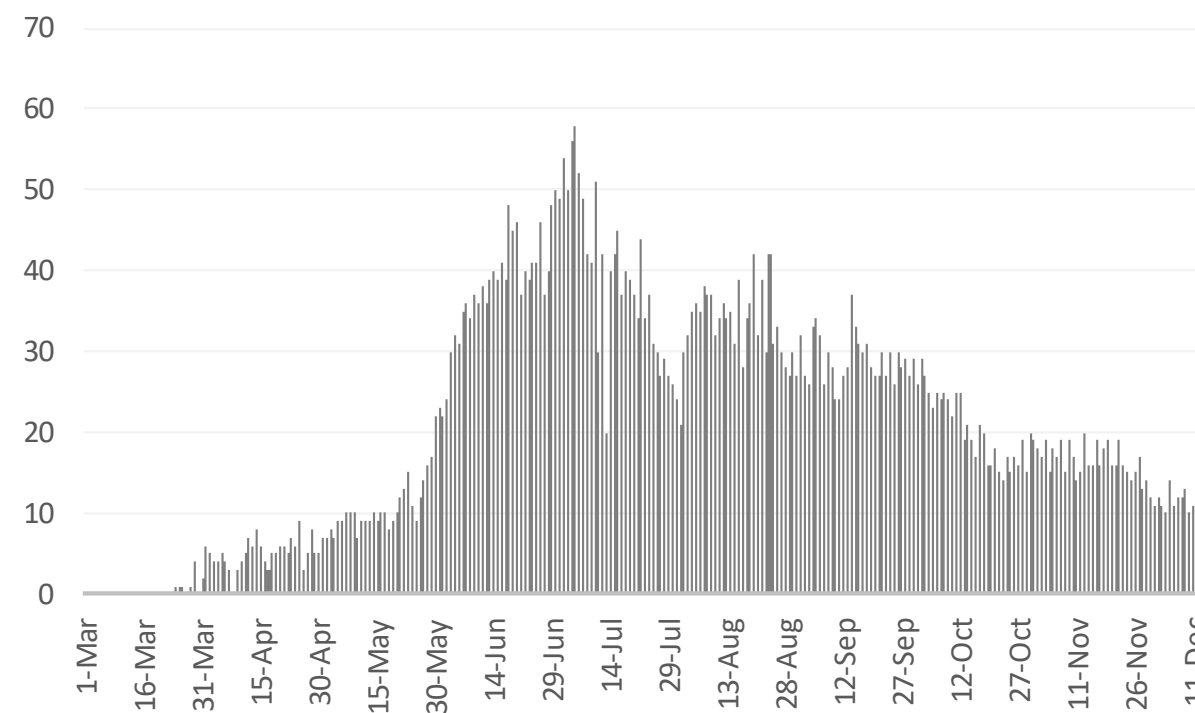
Figure 12: Comparative Analysis of the Distribution of COVID-19 New Death Cases in GCC Countries

UAE



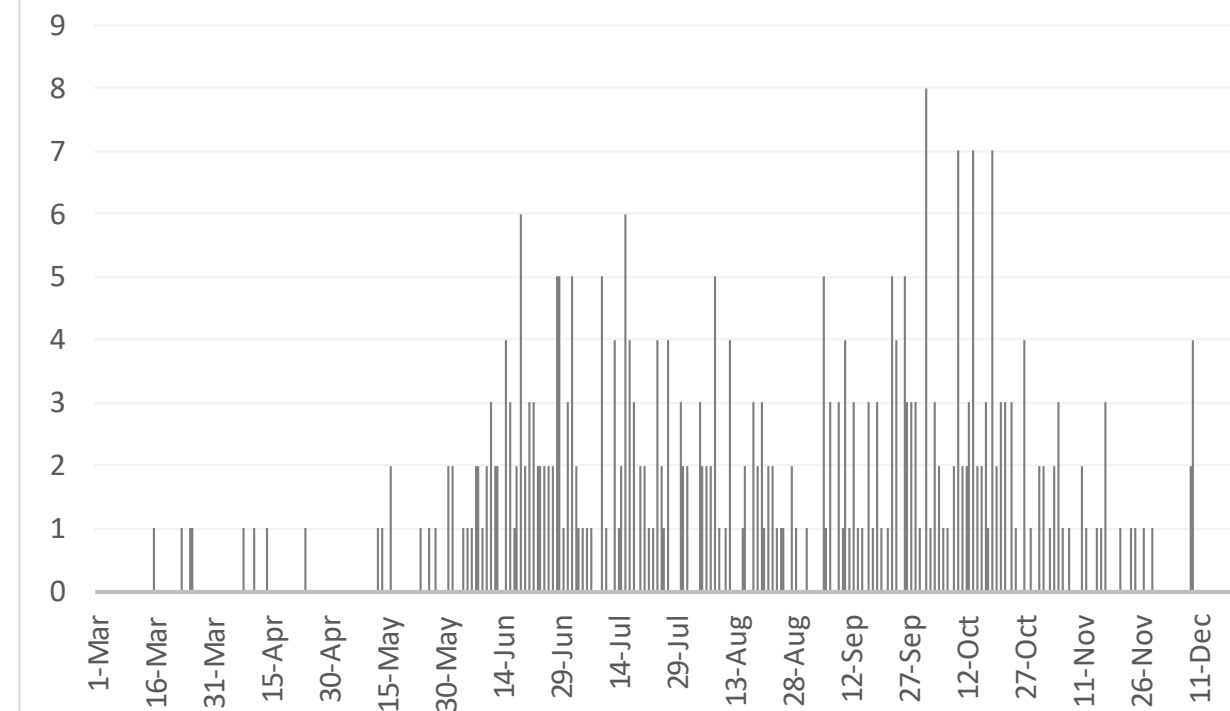
Source : National Emergency Crisis and Disaster Management Authority

KSA



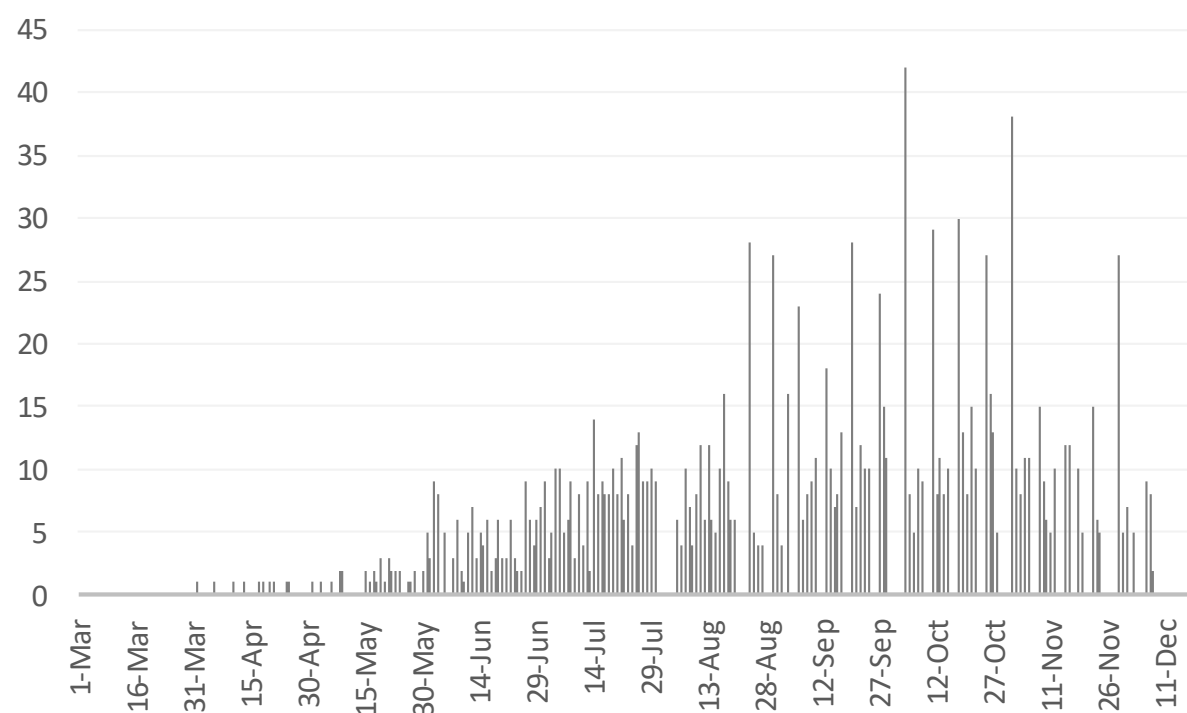
Source : KSA ministry of health

Bahrain



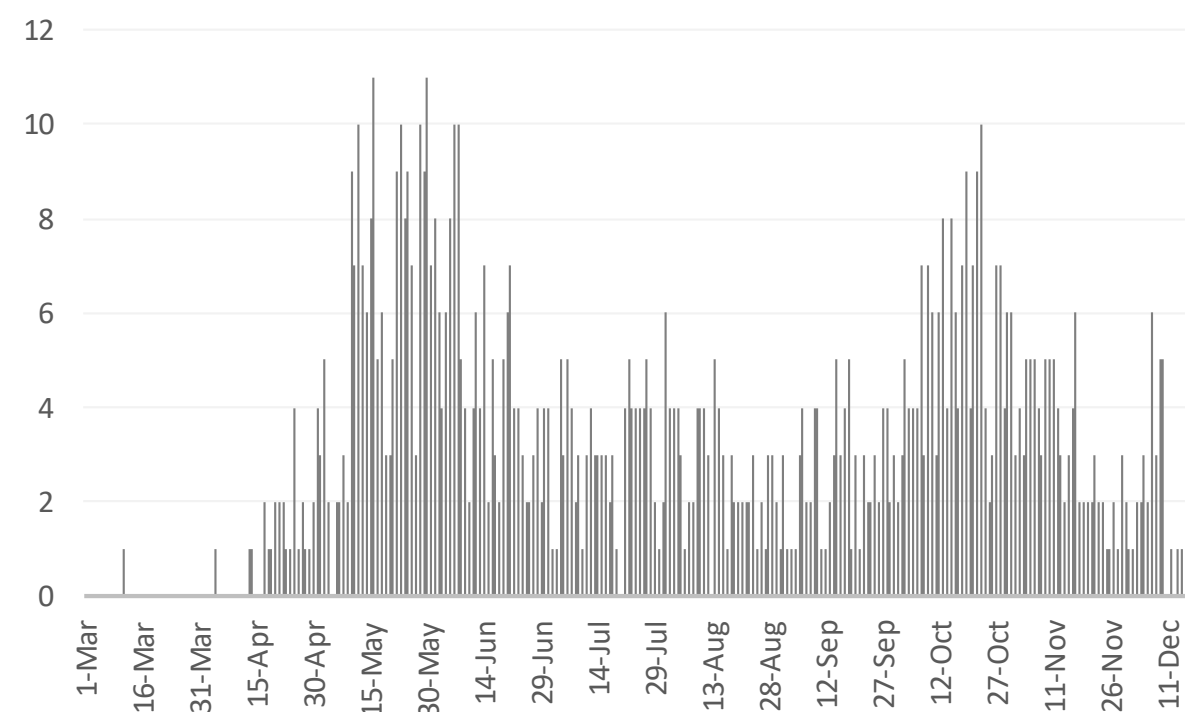
Source :WHO

Oman



Source :Oman ministry of health

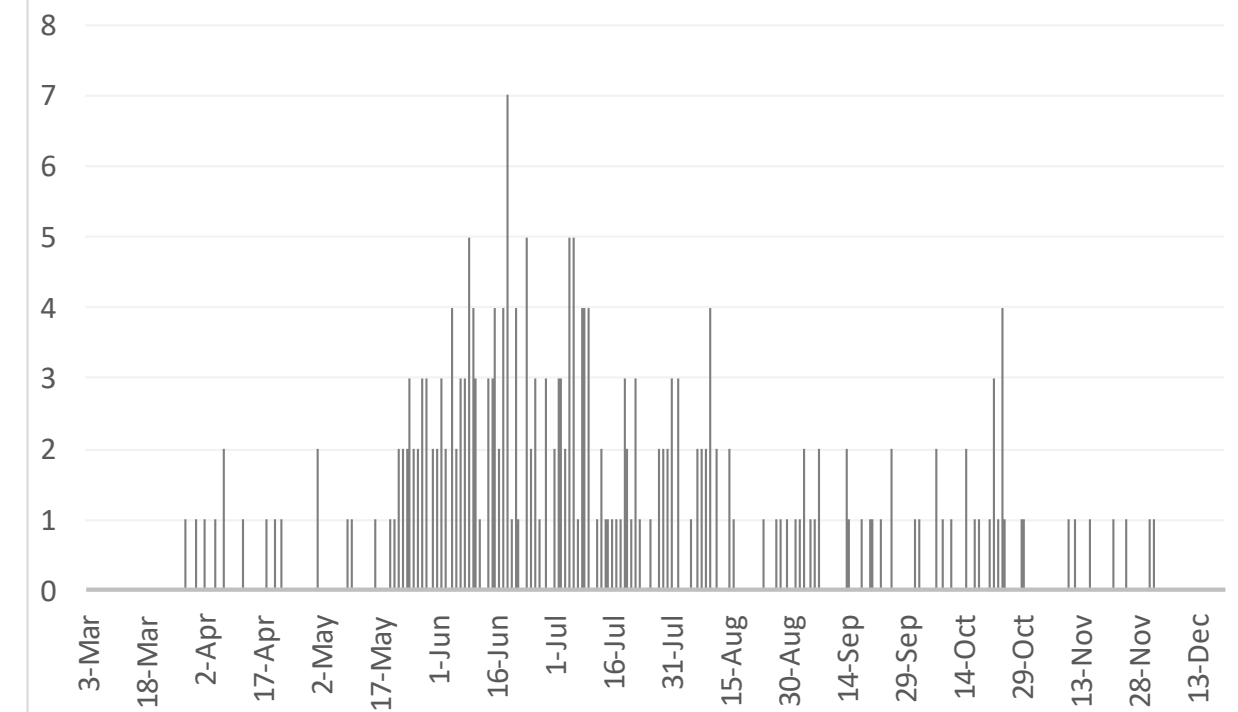
Kuwait



Source : Kuwait ministry of health

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Qatar



Source : Qatar ministry of health

*No announced statistic data from 31 JUL 4 AUG, 21,23,28,30 AUG 2, 4 5,11,12,18,19,25, 26,30 SEP,1,2,9,10,16,17,23,24,30,21 OCT, 6,7,13,14,17,20,21,25,26,6 DEC

*No announced statistic data on weekends and official holidays.



EPIDEMIC SITUATION IN THE UNITED KINGDOM

FROM 21 JAN TO 21 DEC 2020

Figure 1: Total Cumulative Cases Of COVID19

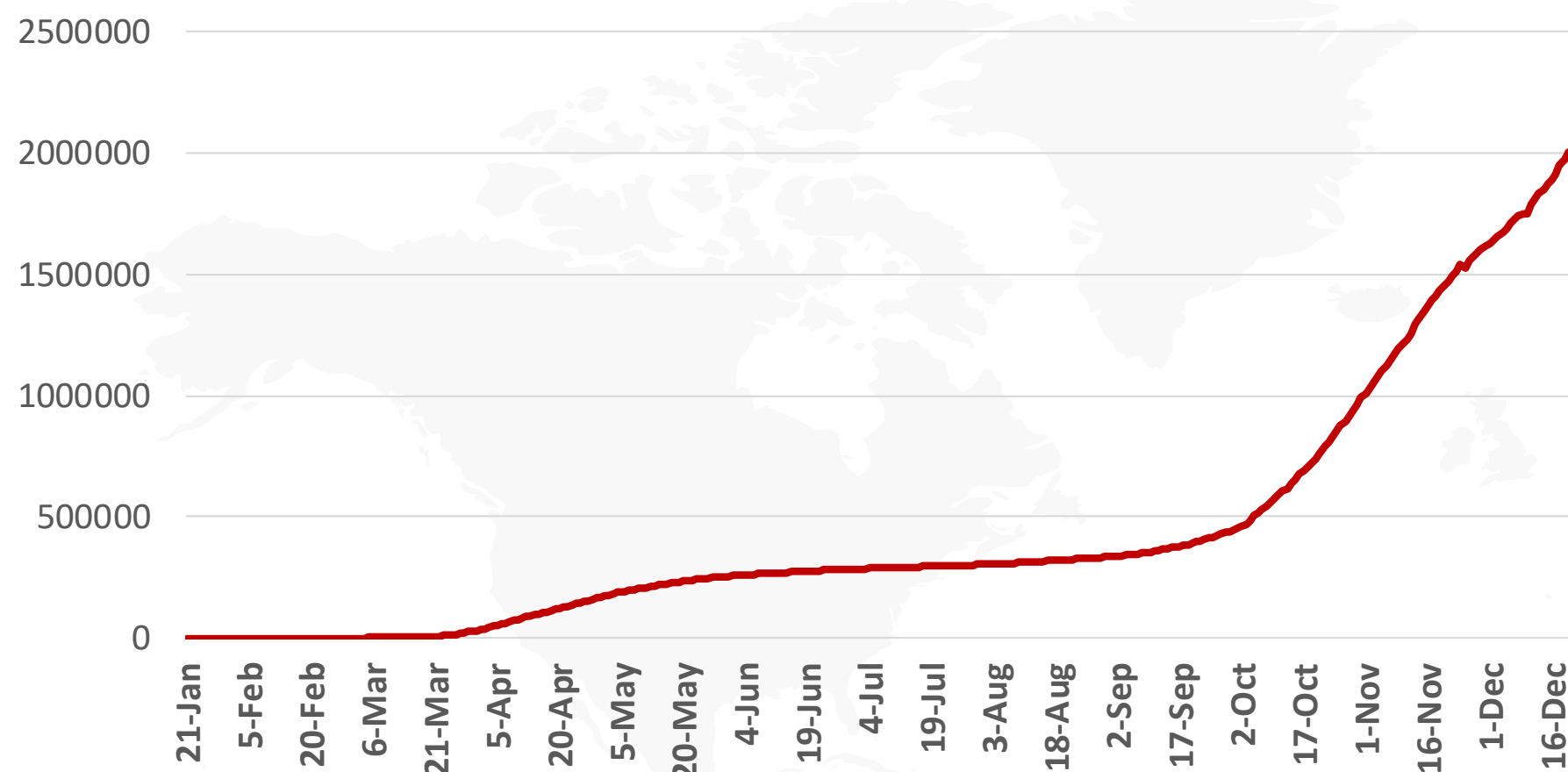
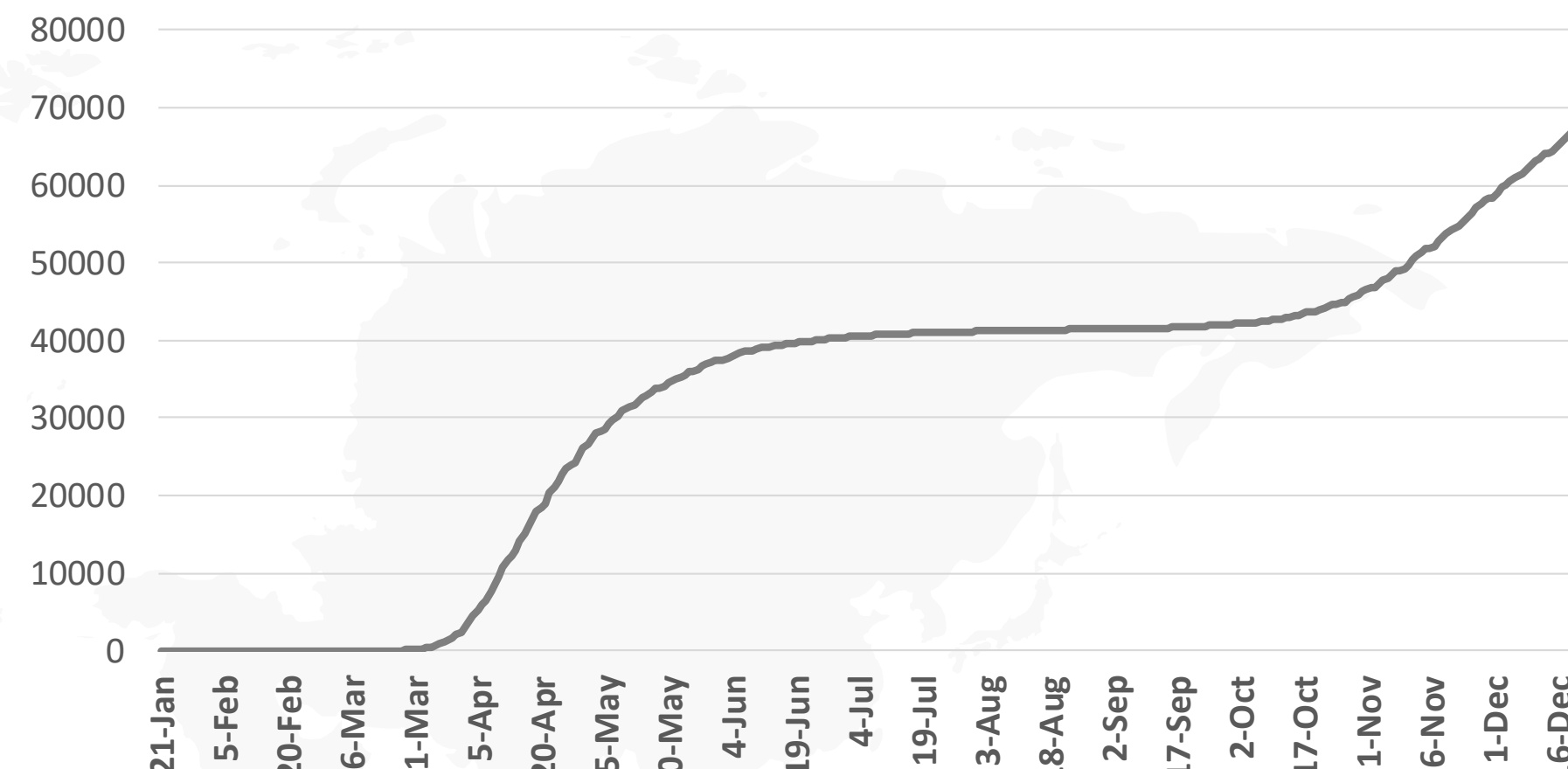
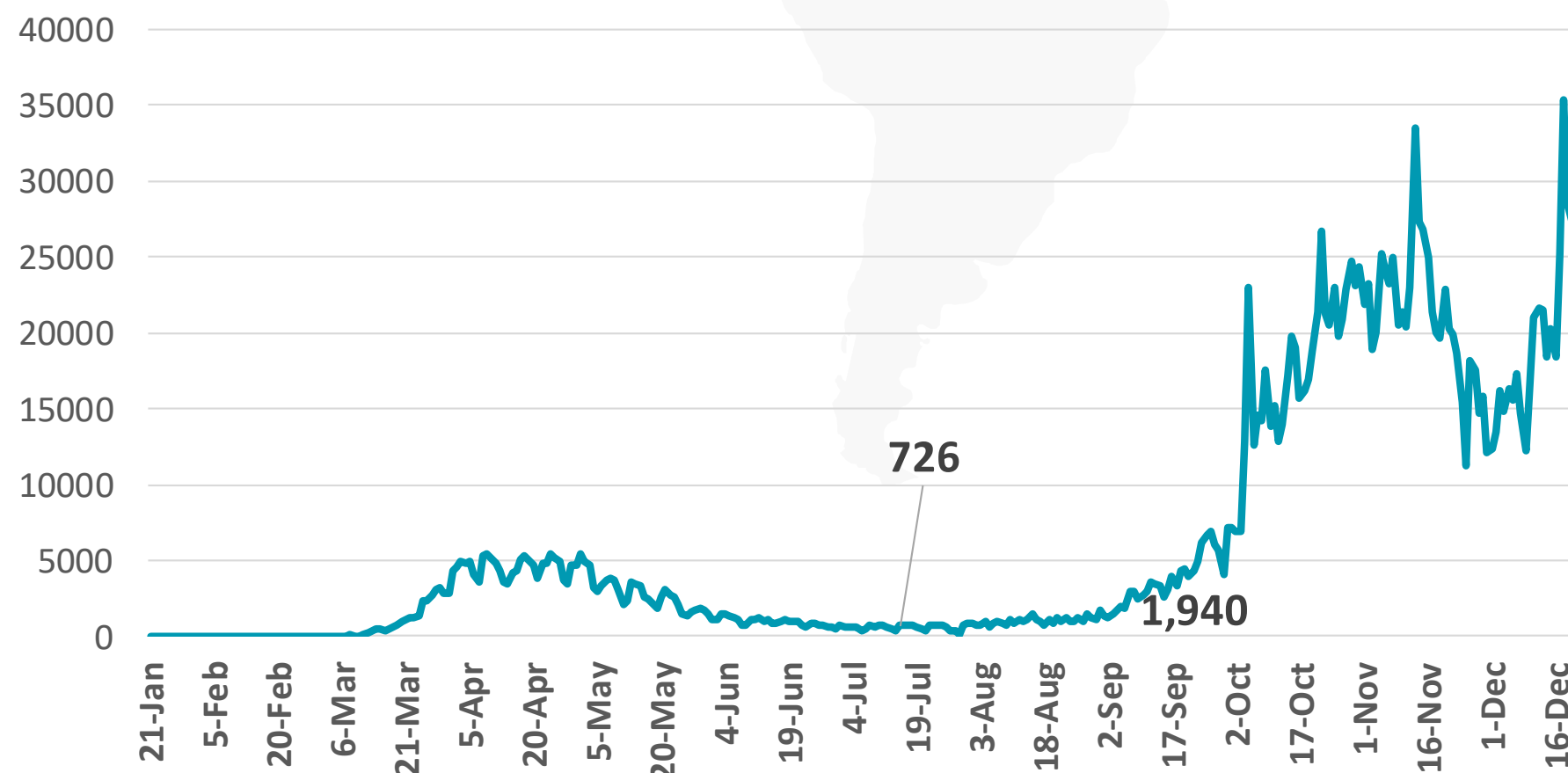


Figure 2: Total Number of Death Due to COVID-19



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Figure 3: DAILY new infected cases of COVID19



20 cases per 100k people

7 Day Moving Average IS 1.7 [DATE 21.12.2020](#)

Total recovered	N/A
Active cases	N/A
Serous Critical	1,364
Total cases/ 1M pop	30,468
Total death/ 1M pop	994
Total Tests	50,851,151
Total Tests/1M pop	747,215
Population	68,054,268

Graphs published by Abu Dhabi Public Health Center 2020 | Data resources: [John Hopkins](#), [WHO](#)

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Article 1

Threat Assessment Brief: Rapid increase of a SARS-CoV-2 variant with multiple spike protein mutations observed in the United Kingdom

Published

21 DEC 2020 , the [European CDC](#)

- Over the last few weeks, the UK has faced a rapid increase in COVID-19 cases in South East England, leading to enhanced epidemiological and virological investigations. Analysis of viral genome sequence data identified a large proportion of cases belonged to a new single phylogenetic cluster.
- The new variant is defined by multiple spike protein mutations (**deletion 69-70, deletion 144, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H**) present as well as mutations in other genomic regions. (*This variant is referred to in the UK as SARS-CoV-2 VUI 202012/01 (Variant Under Investigation, year 2020, month 12, variant 01)*). While it is known and expected that viruses constantly change through mutation leading to the emergence of new variants, preliminary analysis in the **UK suggests that this variant is significantly more transmissible than previously circulating variants:**
- Estimated increase of the reproductive number (R) by 0.4 or greater with an estimated increased transmissibility of up to 70%.
- This new variant has emerged at a time of the year when there has traditionally been increased family and social mixing.

Potential impact on severity of disease in a population or group

- There is no indication at this point of increased infection severity associated with the new variant.**
- Other countries affected:** A few cases with the new variant have to date been reported by Denmark and the Netherlands and, according to media reports, in Belgium.





Continued

Potential impact on SARS-CoV-2 diagnostics

- The UK reports that the deletion 69-70 in the spike protein of the **variant** causes a **negative result from S-gene RT-PCR assays** applied in some laboratories in the UK .
- Assays targeting the S-gene are not widely used for primary detection.
- Relying only on the S-gene for primary detection of SARS-CoV-2 infection using RT-PCR is not recommended because mutations are more likely to occur in this gene.

Potential impact on occurrence of variant viruses to increase frequency of reinfections

- there is as yet no evidence that there is a resulting impact on **increased risk for reinfection or lower vaccine effectiveness**
- Four probable reinfections have been identified amongst 915 subjects with this variant but further work is needed to compare this reinfection rate with comparable data sets. ([NERVTAG](#)).

Possible impact on vaccine match and effectiveness

- The new virus variant displays several mutations in the spike protein, including in the receptor binding site. Most of the new candidate vaccines are based upon the spike protein sequence. However, no data are available with respect to the ability of antibodies elicited by vaccines under development to neutralize this variant. Data will be available in the coming weeks.





Continued

Figure 2. England (UK) 14-day age-specific COVID-19 case notification rate with cases per 100 000 population by reporting date as of 16 December 2020

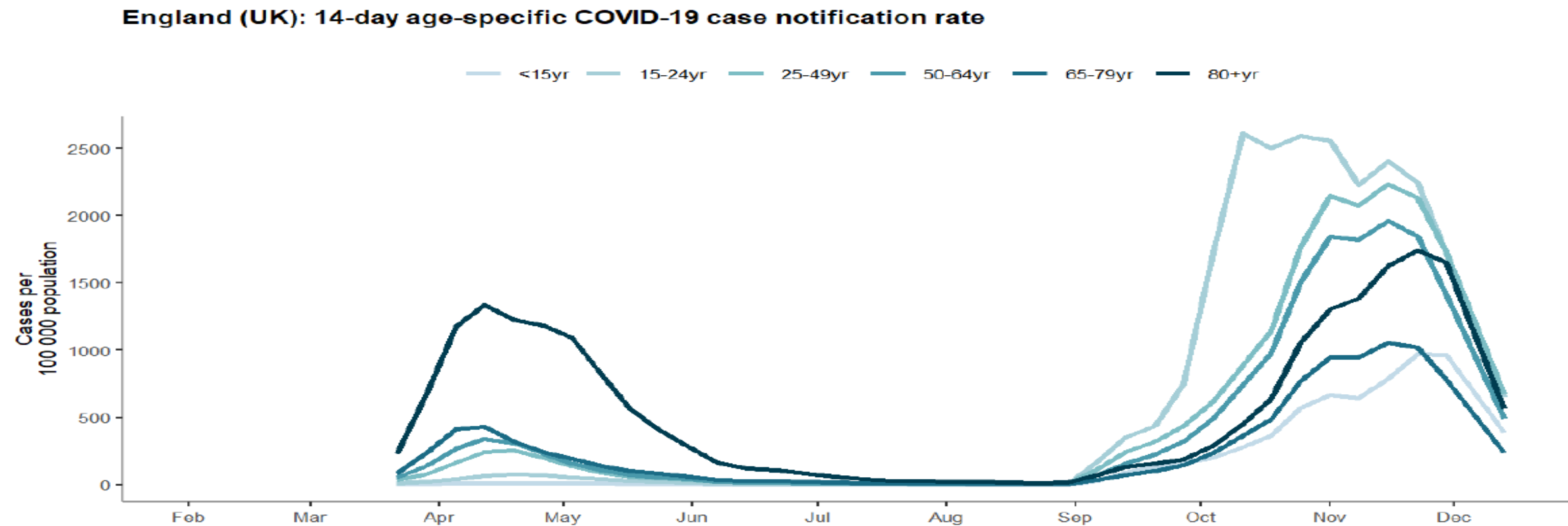
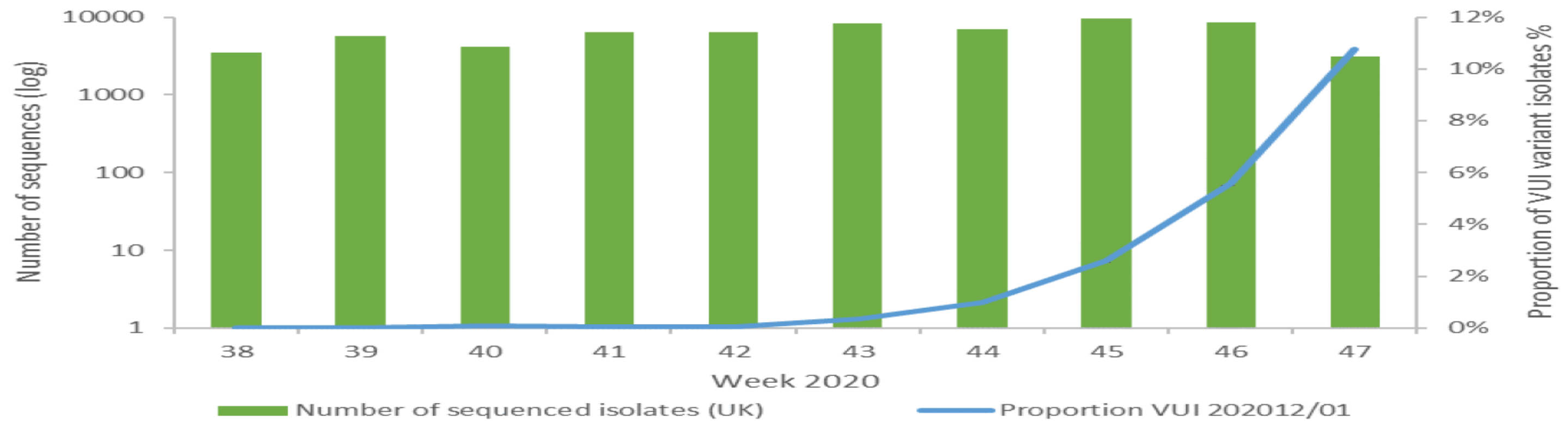


Figure 3. Total number of SARS-CoV-2 sequences from the UK and proportion of VUI 202012/01 variant sequences among all UK sequences in the GISAID EpiCoV database (as of 20 December 2020) by week of sampling, 2020



As of 13 December 2020, 1 108 individuals had been identified with this virus variant in England, with the earliest case identified from 20 September 2020.





Continued

- Given that there is currently a lack of evidence to indicate the extent to which the new virus variant is spread outside the UK, **timely efforts to prevent and control its spread are needed, and include the following:**
 - Public health authorities and laboratories are urged to analyze and sequence virus isolates in a timely manner to identify cases of the new variant. People with an epidemiological link to cases with the new variant or travel history to areas known to be affected **should be identified immediately to test, isolate and follow up their contacts in order to stop the spread of the new variant.**
 - If cases infected with this new SARS-CoV-2 variant or other new SARS-CoV-2 variants of potential concern are identified, countries should notify.
 - **The importance of strict adherence to non-pharmaceutical interventions** according to national policies needs to be communicated to the public, and in particular guidance on **the avoidance of non-essential travel and social activities should be stressed.**
 - Laboratories should review the PCR performance and drop-out of the S-gene. PCR could be used as an indicator for cases with the new variant for further sequencing and investigation.
 - Suspected cases of COVID-19 reinfection should be followed up, closely accompanied by sequencing respective virus isolates from these cases. Similarly, cases with treatment failures using convalescent plasma or monoclonal antibodies should be further studied.
 - With the implementation of vaccination, close monitoring of COVID-19-vaccinated individuals needs to be ensured to **identify possible vaccination failure** and breakthrough infections. Virus isolates from these cases should be sequenced and characterized genetically and antigenically.



Article 2

Published

New and Emerging Respiratory Virus Threats Advisory Group of the UK

December 18 , 2020 [NERVTAG MoM](#)

- Details of the Minutes of Meeting :
- New and Emerging Respiratory Virus Threats Advisory Group had a meeting on 18 of December Concluded that there are currently insufficient data to draw any conclusion on:
 - Underlying mechanism of increased transmissibility (e.g. increased viral load, tissue distribution of virus replication, serial interval etc)
 - The age distribution of cases
 - Disease severity: 4 deaths in around 1000 cases have been identified but further.
- The committee has moderate confidence that VUI-202012/01 demonstrates a substantial increase in transmissibility compared to other variants.



Article 3

Published

Preliminary genomic characterisation of an emergent SARS-CoV-2 lineage in the UK defined by a novel set of spike mutations

December 20, 2020, virological.org

- Recently a distinct phylogenetic cluster (named lineage B.1.1.7) was detected within the COG-UK surveillance dataset. This cluster has been growing rapidly over the past 4 weeks and since been observed in other UK locations, indicating further spread.
- Several aspects of this cluster are noteworthy for epidemiological and biological reasons and we report preliminary findings below. In summary:
 - The B.1.1.7 lineage accounts for an increasing proportion of cases in parts of England. The number of B.1.1.7 cases, and the number of regions reporting B.1.1.7 infections, are growing.
 - B.1.1.7 has an unusually large number of genetic changes, particularly in the spike protein.
 - Three of these mutations have potential biological effects that have been described previously to varying extents:
 - Mutation N501Y is one of six key contact residues within the receptor-binding domain (RBD) and has been identified as increasing binding affinity to human and murine ACE2.
 - The spike deletion 69-70del has been described in the context of evasion to the human immune response but has also occurred a number of times in association with other RBD changes.
 - Mutation P681H is immediately adjacent to the furin cleavage site, a known location of biological significance.
- The rapid growth of this lineage indicates the need for enhanced genomic and epidemiological surveillance worldwide and laboratory investigations of antigenicity and infectivity.





Article 4

GISAID COMMENTS

Published

[GISAID Database](#)

- GISAID EpiCov database which is an initiative data sharing of SARS-cov2 genetic mutation and strains have Commented on recent spike protein mutations:
- As seen on many occasions before, mutations are naturally expected for viruses and are most often simply neutral regional markers useful for contact tracing. The mutations seen have rarely affected viral fitness and almost never affected clinical outcome but the detailed effects of these mutations remain to be determined fully. Mutations in the spike protein have relevance for potential effects on both host receptor as well as antibody binding with possible consequences for infectivity, transmission potential and antibody and vaccine escape. Actual effects need to be measured and verified experimentally.
- As has become evident, these few spike mutations and some deletions are found in multiple genomic contexts (different clades in different countries) that may be an early indication for some potential advantage for these viruses but needs to be verified and does not necessarily mean change in clinical severity or transmission efficiency.



THANK YOU

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