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HEALTH CENTRE

SCIENTIFIC RESEARCH MONITORING ON COVID-19

30 AUGUST 2020

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SCIENTIFIC RESEARCH MONITORING ON COVID-19 (ISSUE 210)

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ABU DHABI PUBLIC HEALTH CENTRE

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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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.
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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).

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Treatment

Effect of Convalescent Plasma Therapy on Viral Shedding and Survival in Patients with Coronavirus Disease 2019

Virology

SARS-CoV-2 Whole Genome Amplification and Sequencing for Effective Population-Based Surveillance and Control of Viral Transmission

Virology

Geographical and Temporal Distribution of SARS-CoV-2 Clades in the WHO European Region, January to June 2020

EPIDEMIOLOGY

FROM 21 JAN TO 29 AUG 2020

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

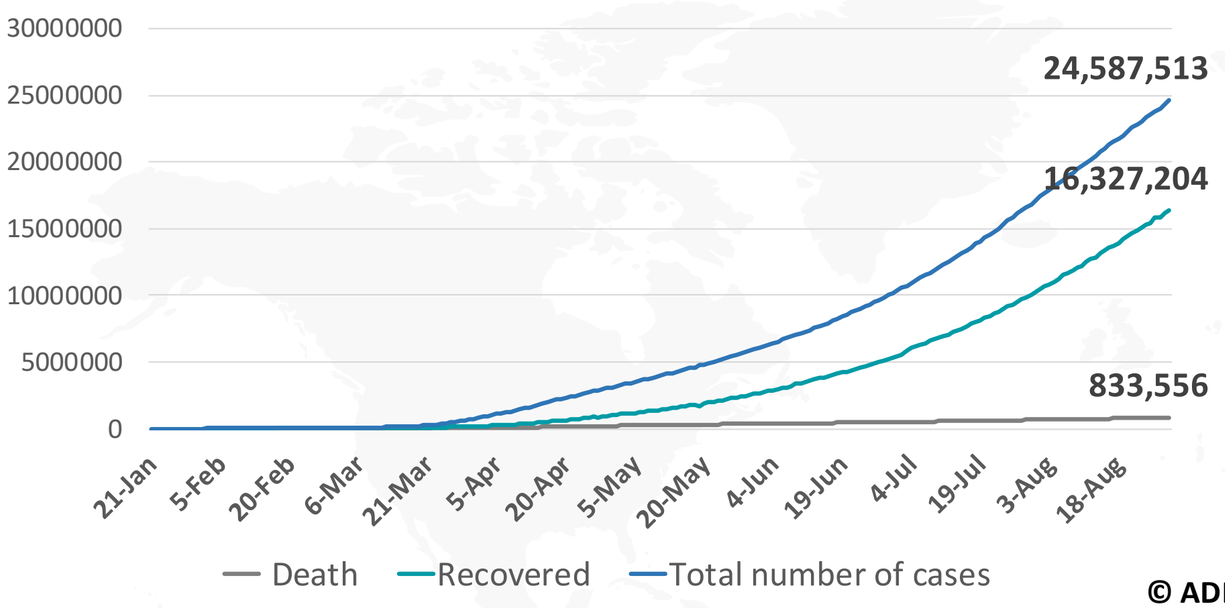


Figure 3: Total Number of Death Due to COVID-19 (china and result of the world)

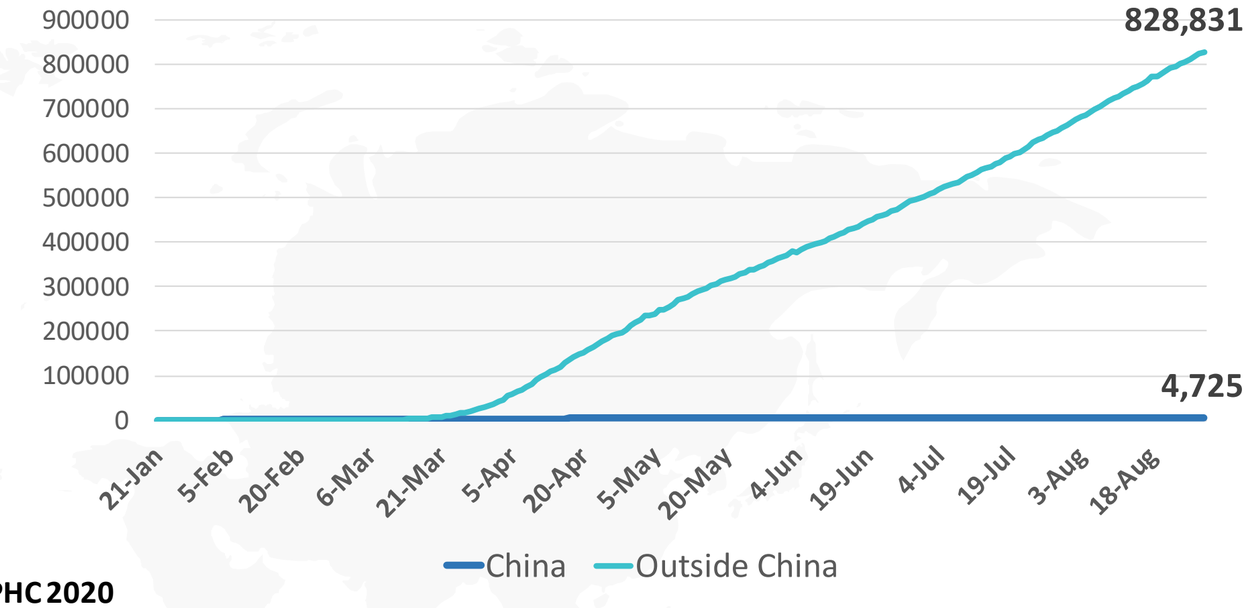


Figure 2: Daily New Infected COVID-19 Cases (China and rest of the world)

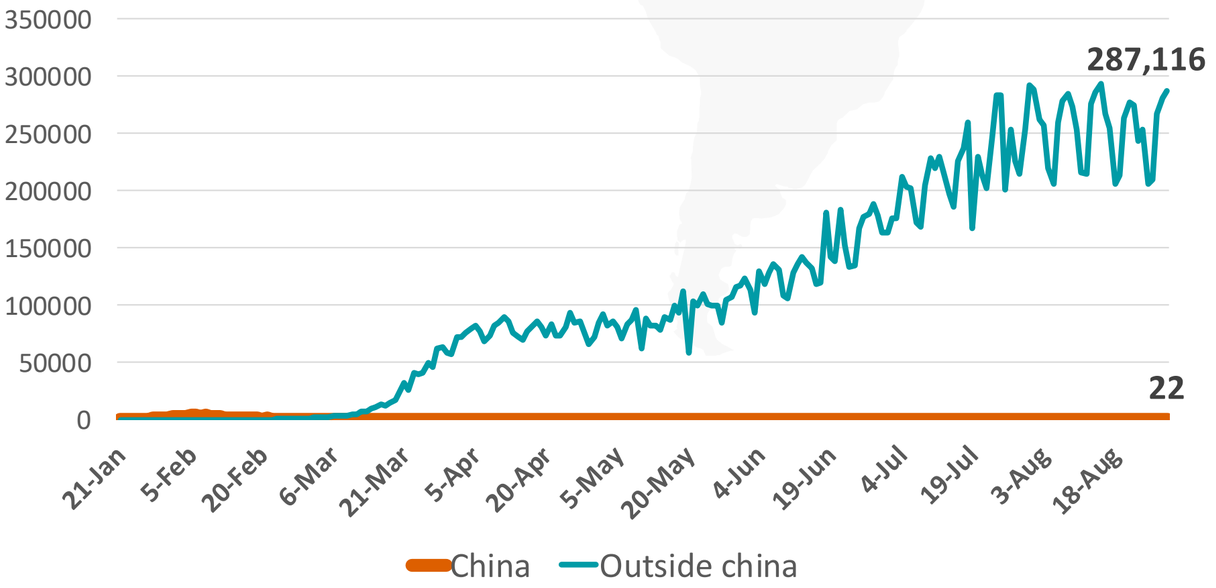
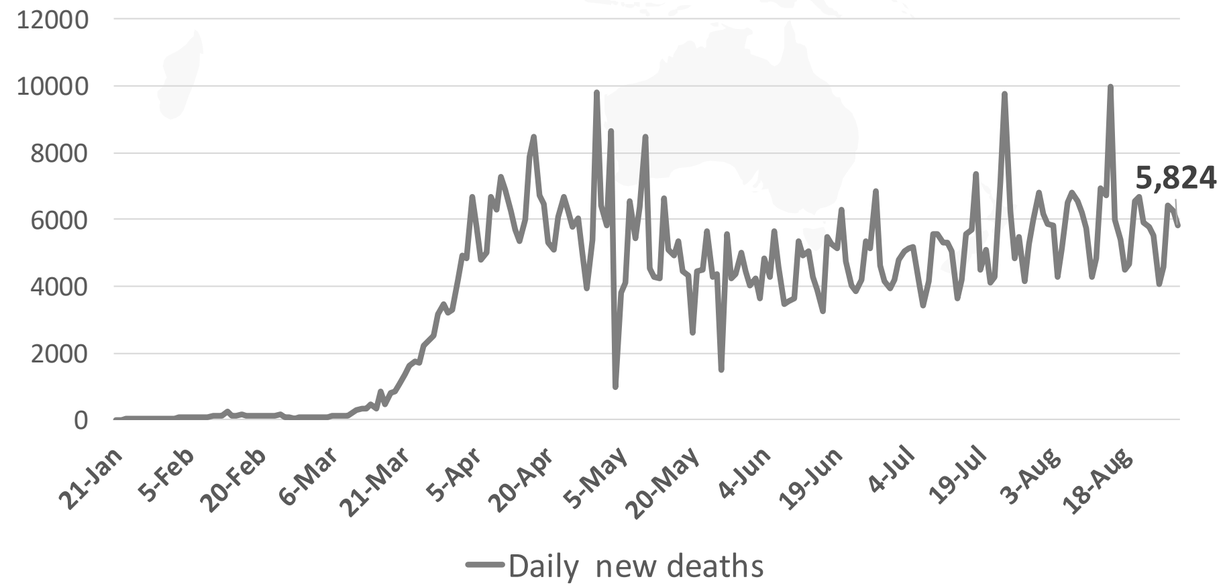


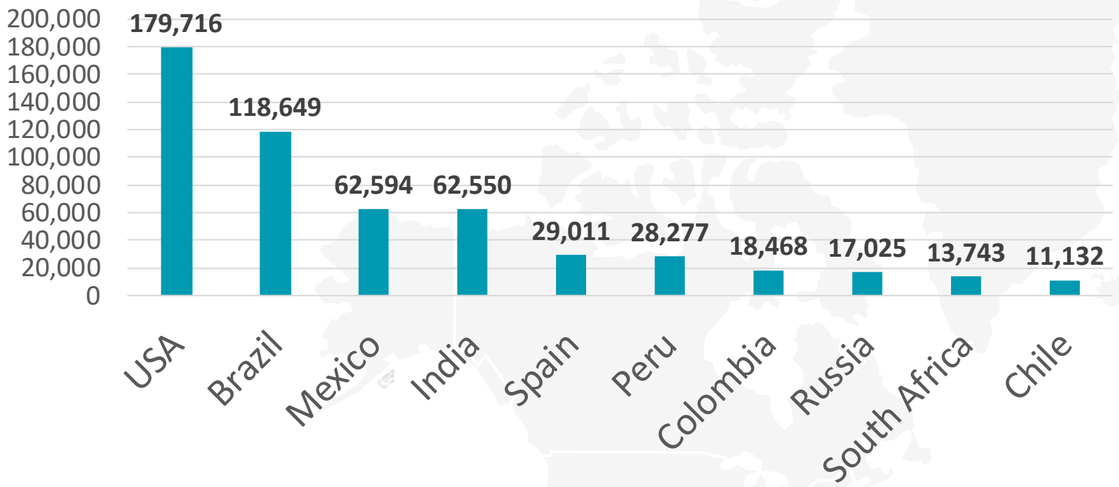
Figure 4: Global Daily New Deaths Due to COVID-19 (china and rest of the world)



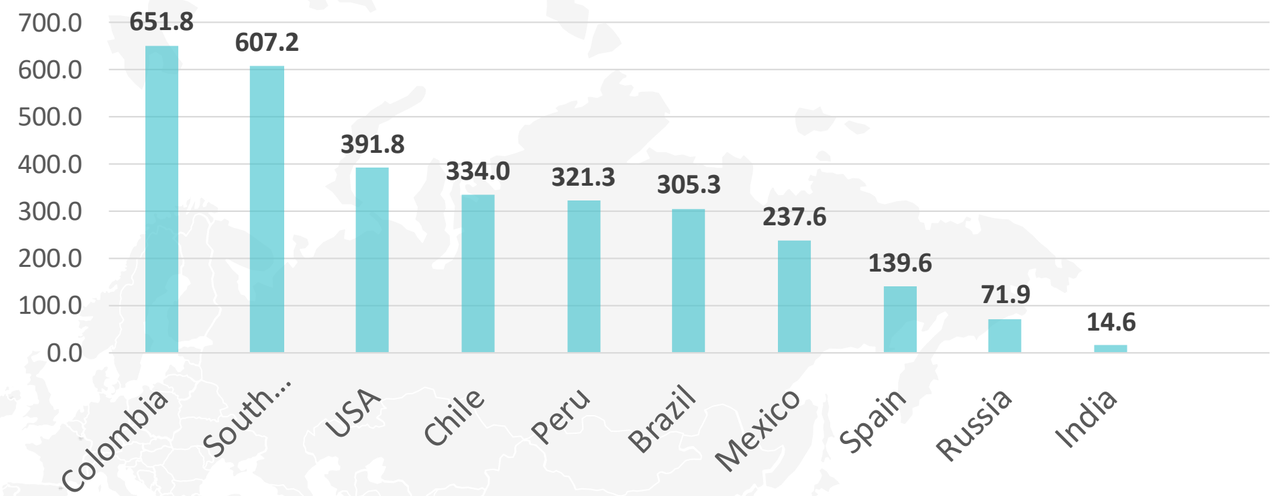
Graphs published by Abu Dhabi Public Health Center 2020 | Data resources: WHO

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

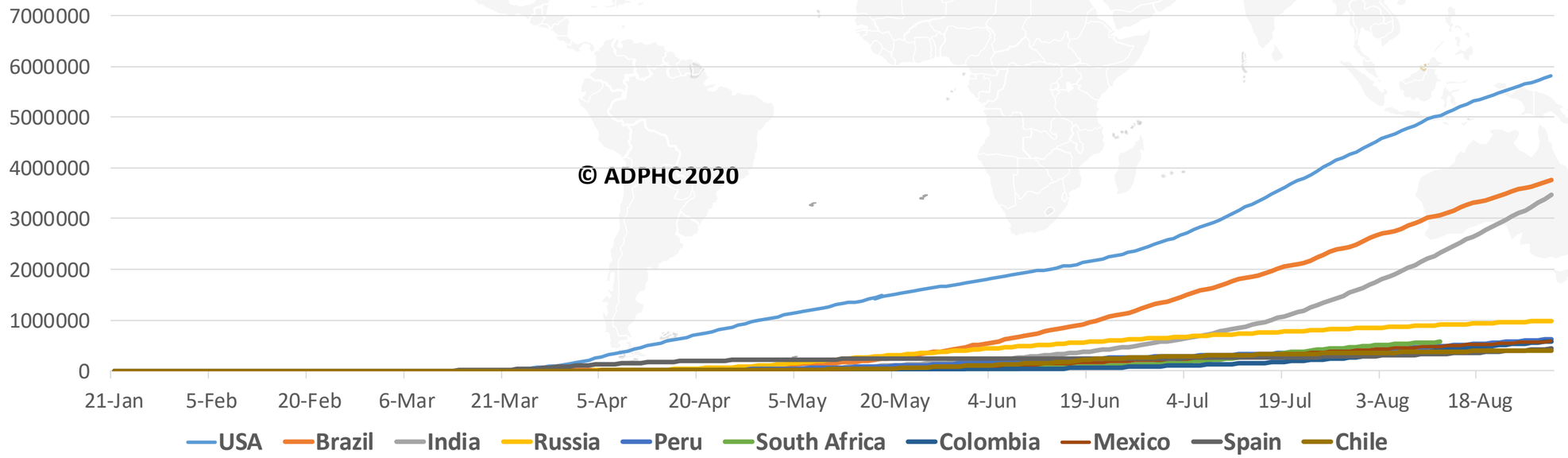
TOTAL DEATHS



DEATHS PER MILLION



TOTAL INFECTED CASES



USA	5,811,519
Brazil	3,761,391
India	3,463,972
Russia	985,346
Peru	621,997
South Africa	620,132
Colombia	582,022
Mexico	579,914
Spain	439,286
Chile	405,972

Graphs published by Abu Dhabi Public Health Center 2020 | Data resources: WHO

EPIDEMIOLOGY

FROM 21 JAN TO 29 AUG 2020

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

Daily Tests

72,250.3 Average Tests

730.5 per 100k population

0.5% Positive Rate

Daily Cases

387.3 Average Cases

3.9 per 100k population

Daily Recovered

256.3 Average Recovered

2.6 per 100k population

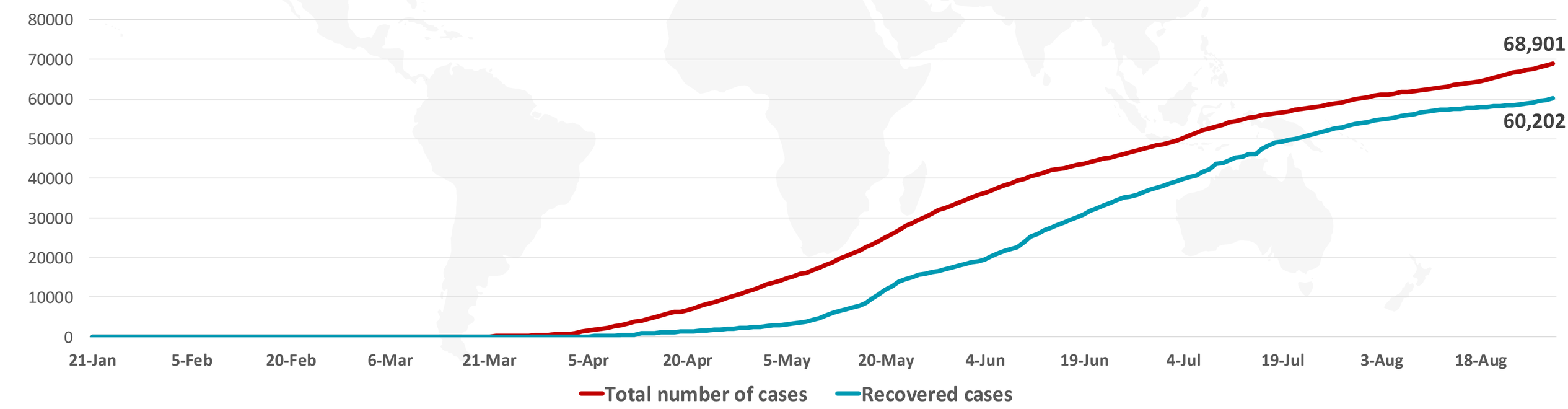
Daily Deaths

1.0 Average Deaths

0.0 per 100k population

0.3% Case Fatality Rate

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



Graphs published by Abu Dhabi Public Health Center 2020 | Data resources: FCSA, WHO,

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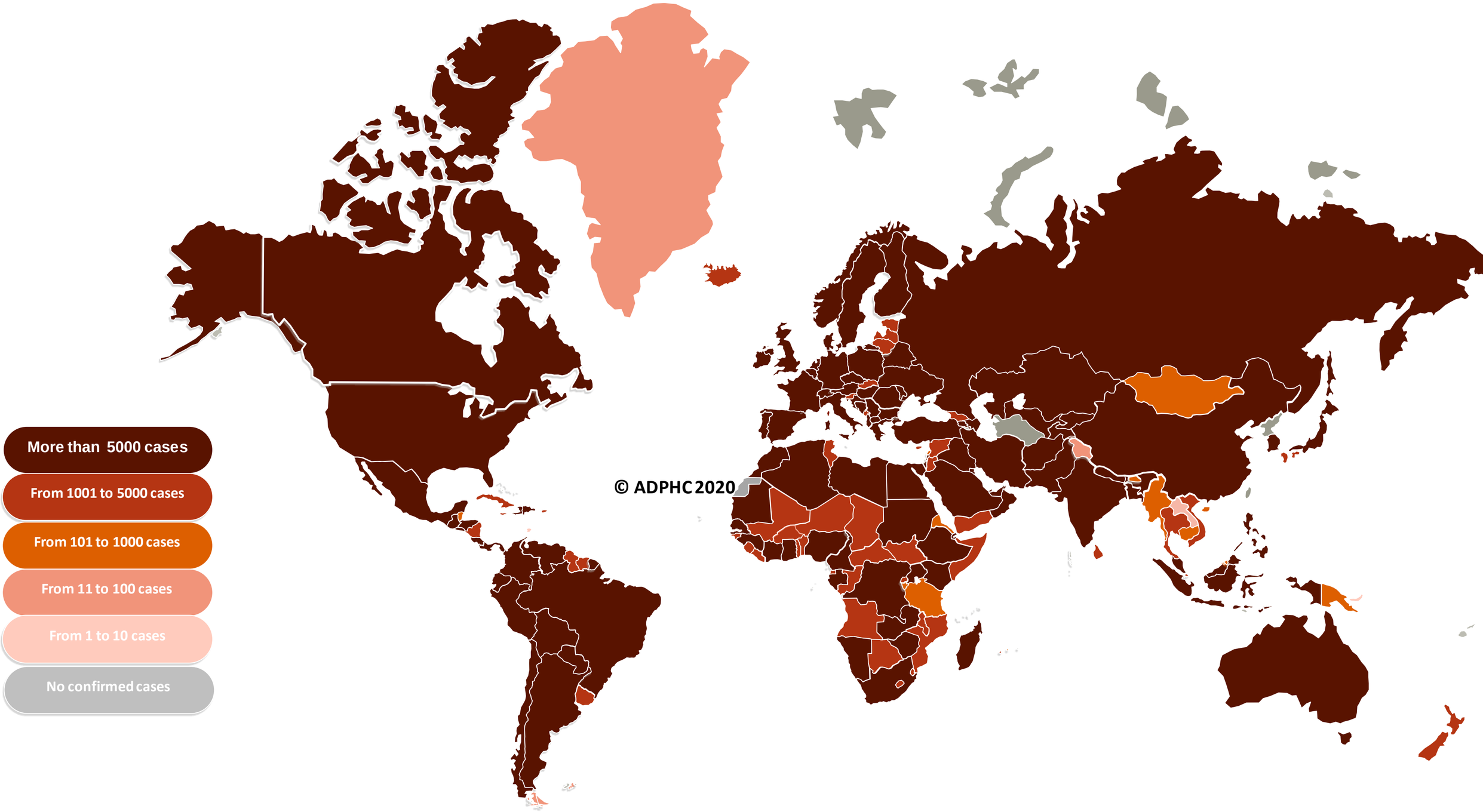
Figure 7A : Global Distribution of COVID-19 Cases



Graphs published by Abu Dhabi Public Health Center 2020 | Data resources: WHO

EPIDEMIOLOGY

Date: 29 AUG 2020

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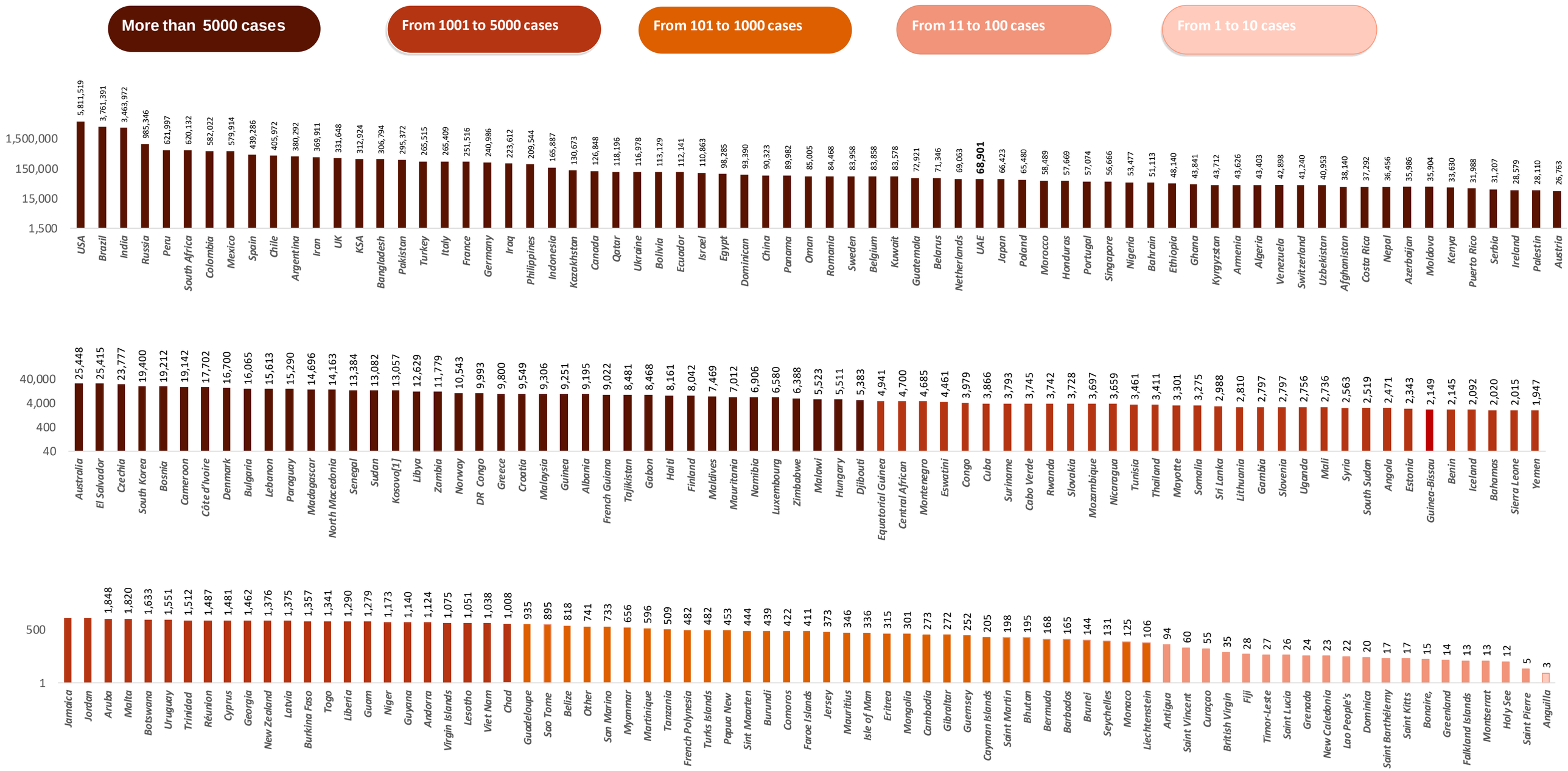
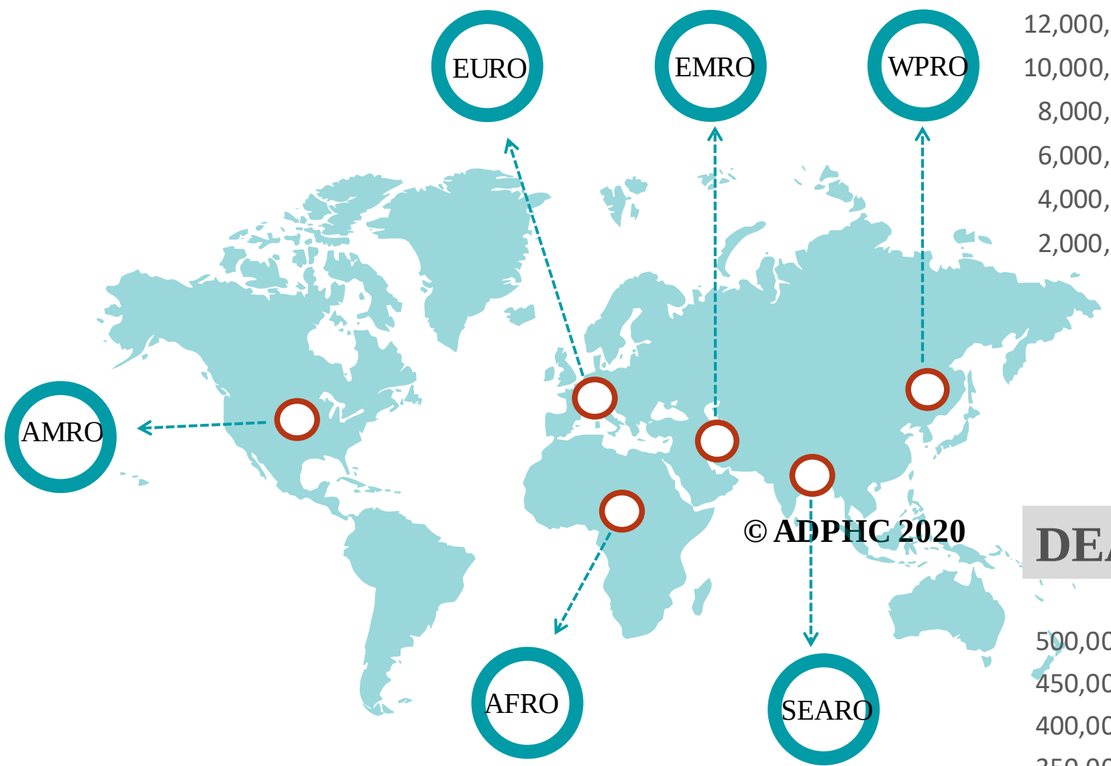
Figure 7B: Bar Chart Illustrates the Global Distribution of COVID19 Cases



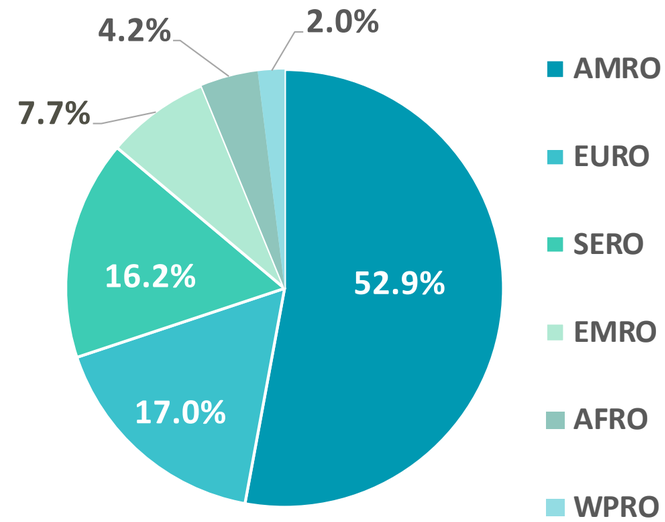
Other*:includes cases and deaths reported under the international conveyance(Diamond Princess)

Graphs published by Abu Dhabi Public Health Center 2020 | Data resources: WHO

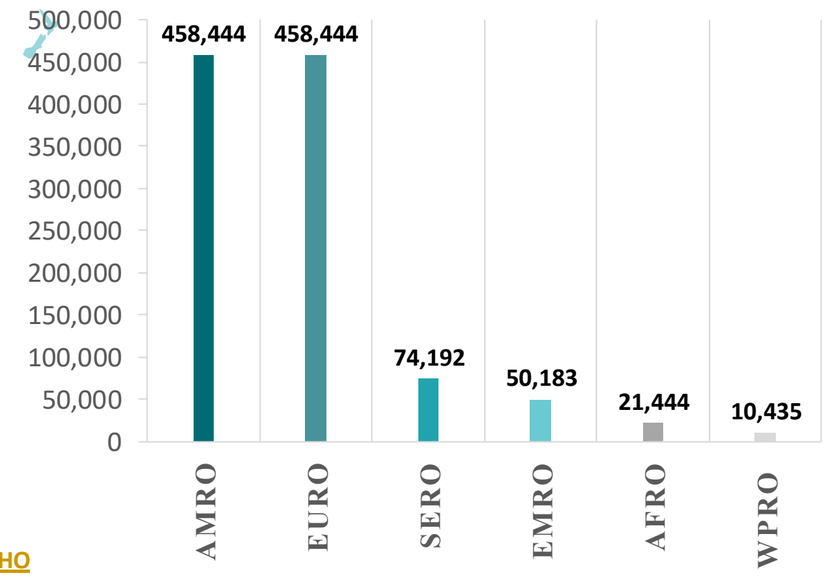
Figure 8: Global Distribution of COVID-19 Cases per Region

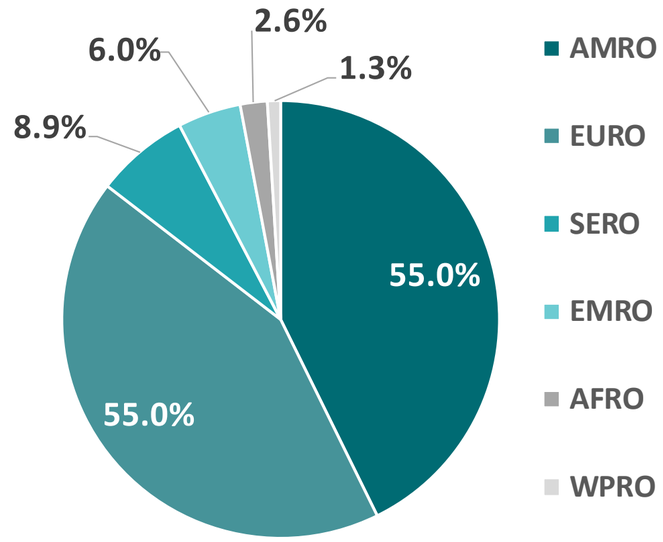


INFECTED



DEATHS

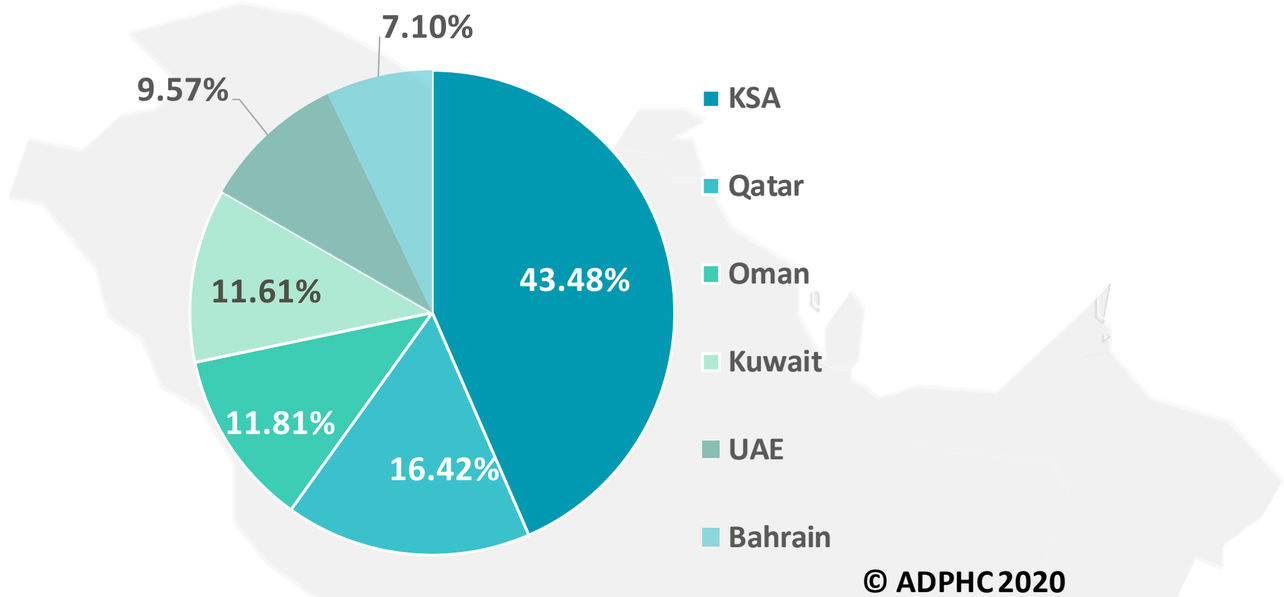


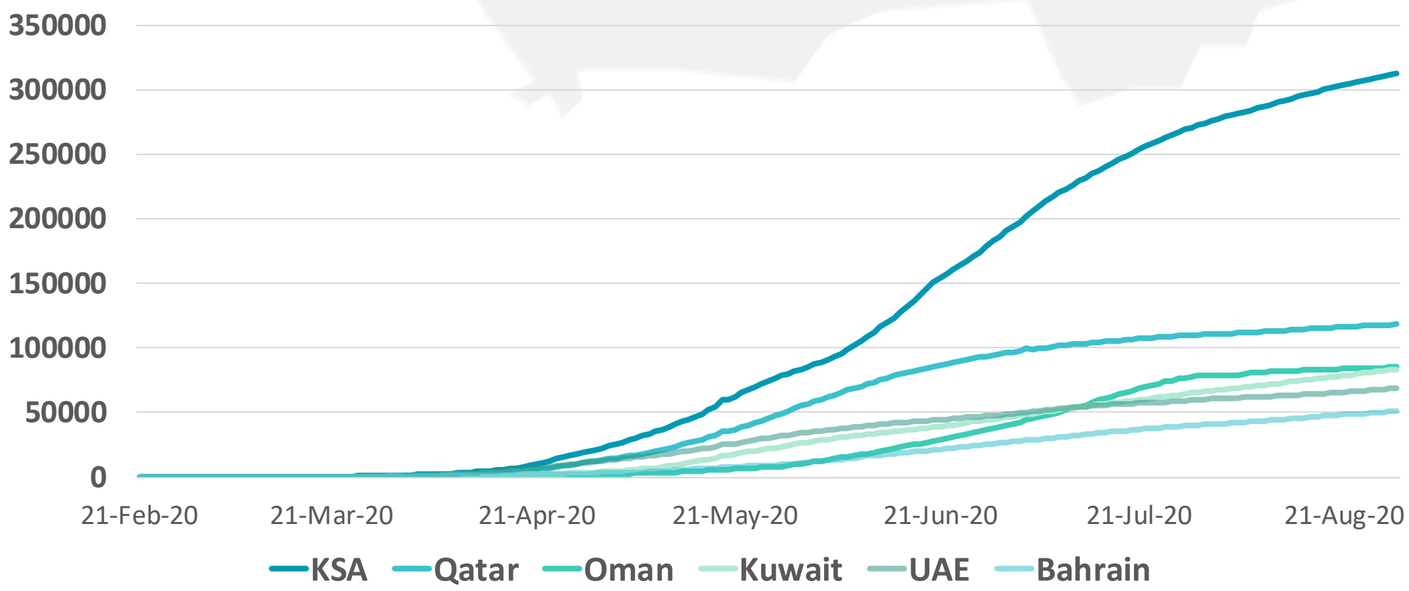


Graphs published by Abu Dhabi Public Health Center 2020 | Data resources: WHO

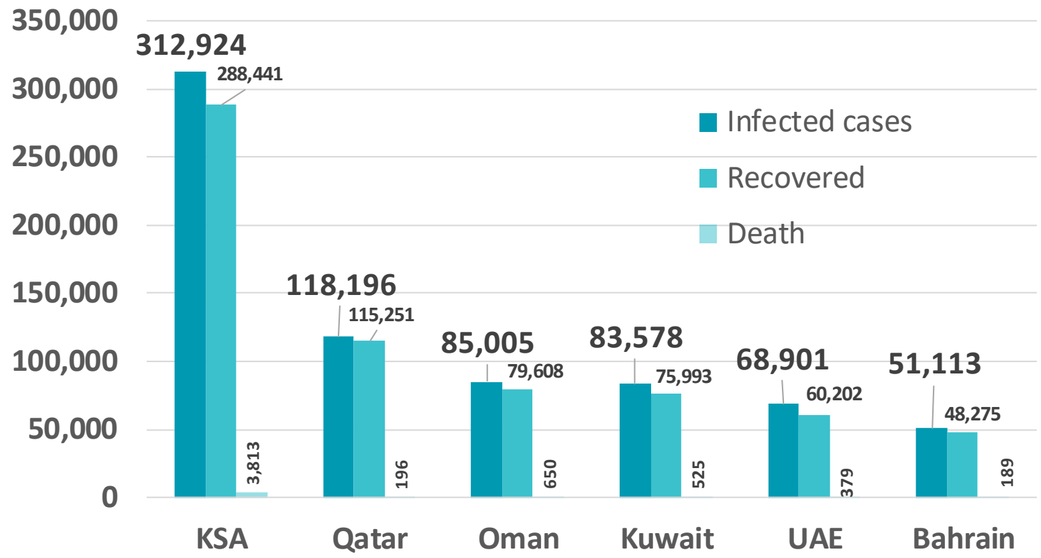
Figure 9: Comparative Analysis of the Distribution of COVID-19 Cases in GCC Countries

TOTAL NUMBER OF INFECTED CASES

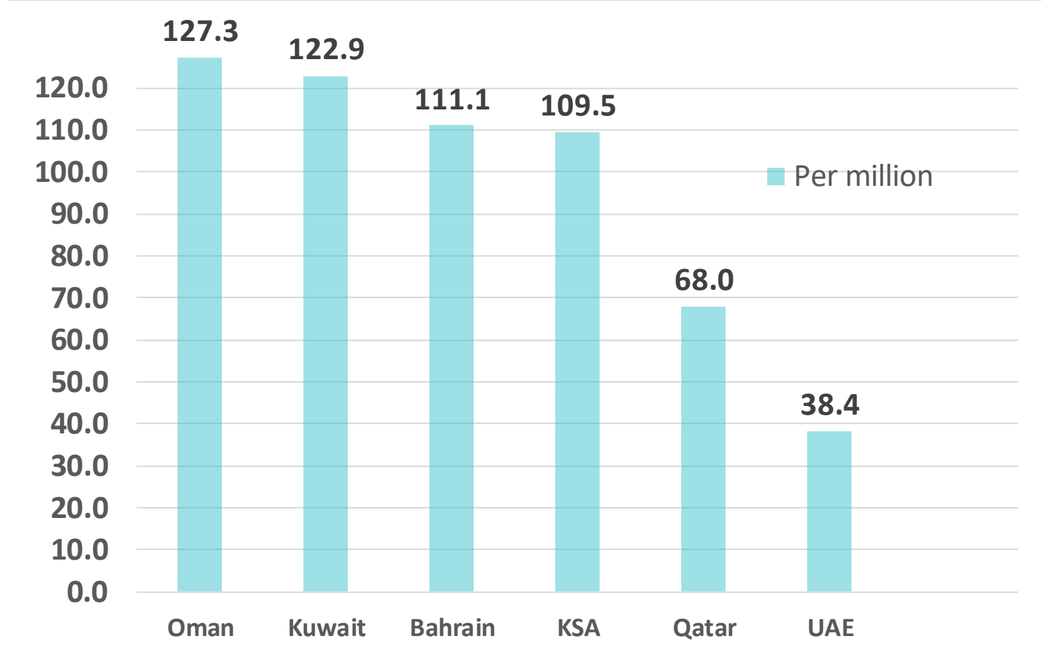




TOTAL NUMBER OF INFECTED, RECOVERED AND DEATHS



DEATHS PER MILLION



Graphs published by Abu Dhabi Public Health Center 2020 | Data resources: WHO

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

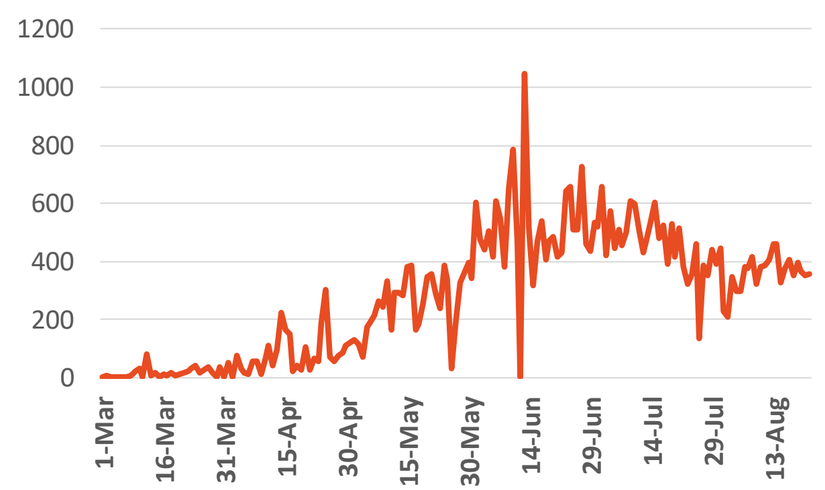
UAE

Source : National Emergency Crisis and Disaster Management Authority

KSA

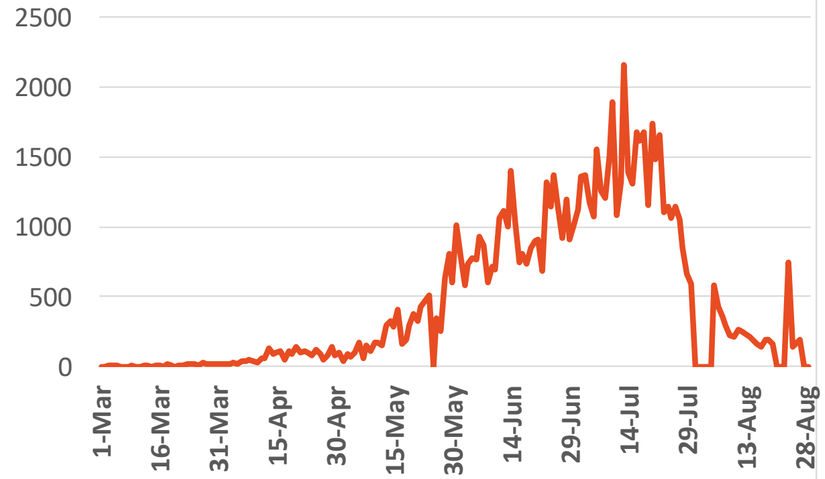
Source : KSA ministry of health

Bahrain



Source :WHO

Oman

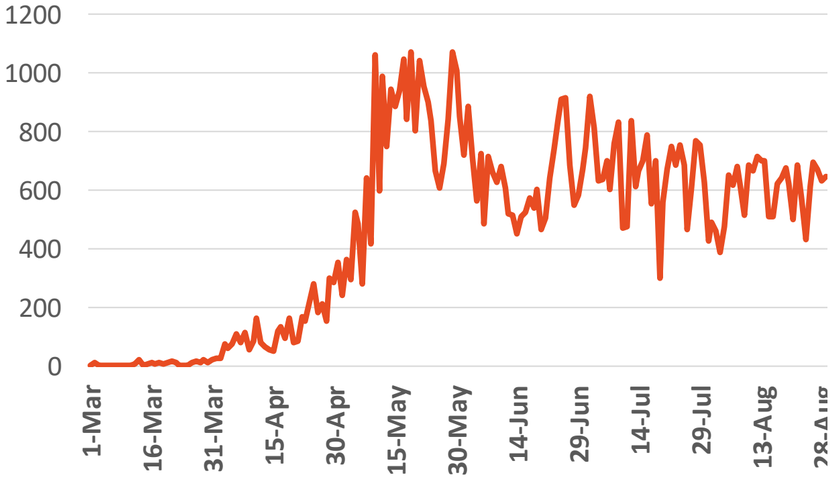


Source :Oman ministry of health

*No announced statistic data from 31 July to 4 August, 21 to 23 August & from 28 to 30 August

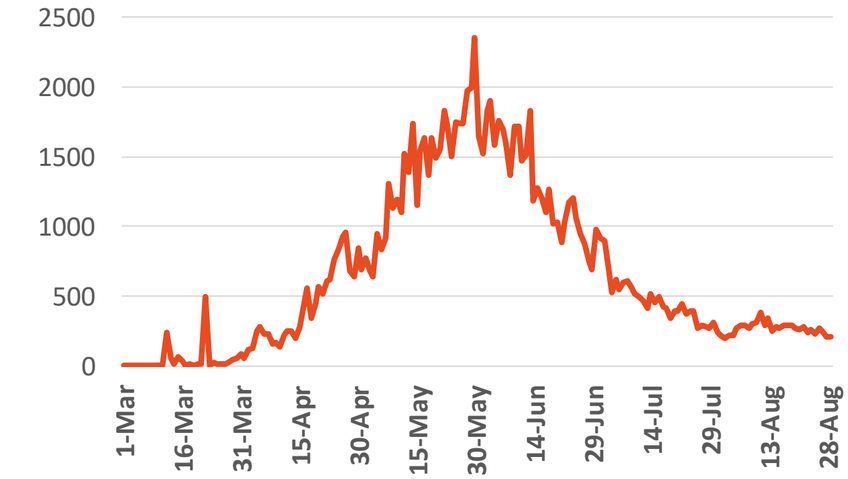
*No announced statistic data on weekends and official holidays.

Kuwait



Source : Kuwait ministry of health

Qatar



Source : Qatar ministry of health

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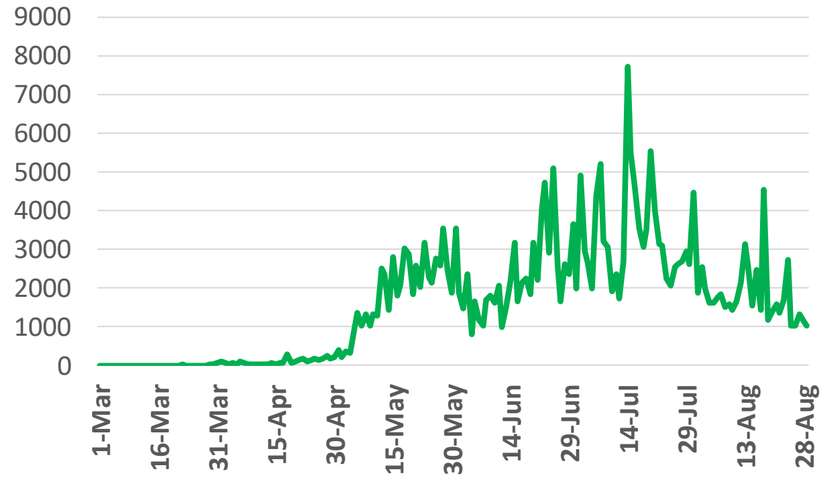
Figure 11: Comparative Analysis of the Distribution of COVID-19 Newly Recovered Cases in GCC Countries

UAE

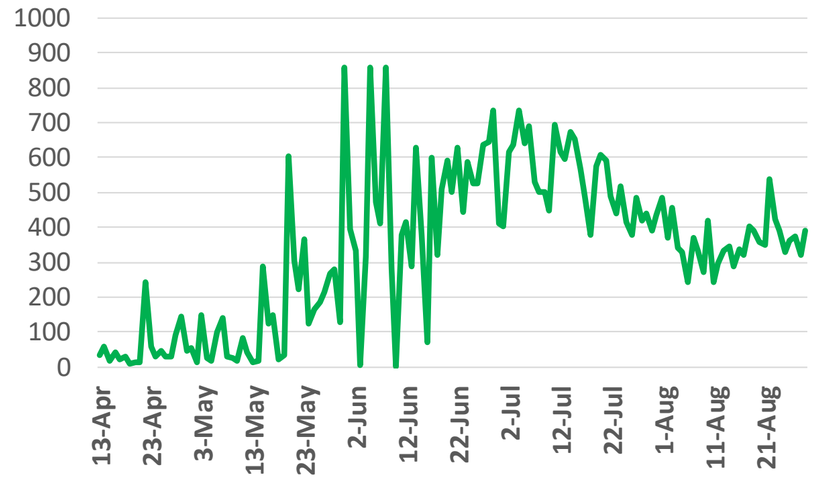
Source : National Emergency Crisis and Disaster Management Authority

KSA



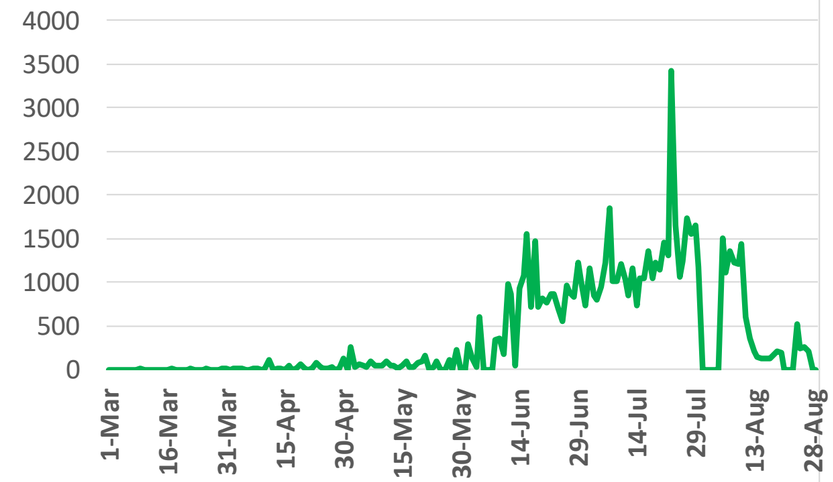
Source : KSA ministry of health

Bahrain



Source : GCCStat

Oman



Source :Oman ministry of health

*No announced statistic data from 31 July to 4 August, 21 to 23 August & from 28 to 30 August

*No announced statistic data on weekends and official holidays.

Kuwait

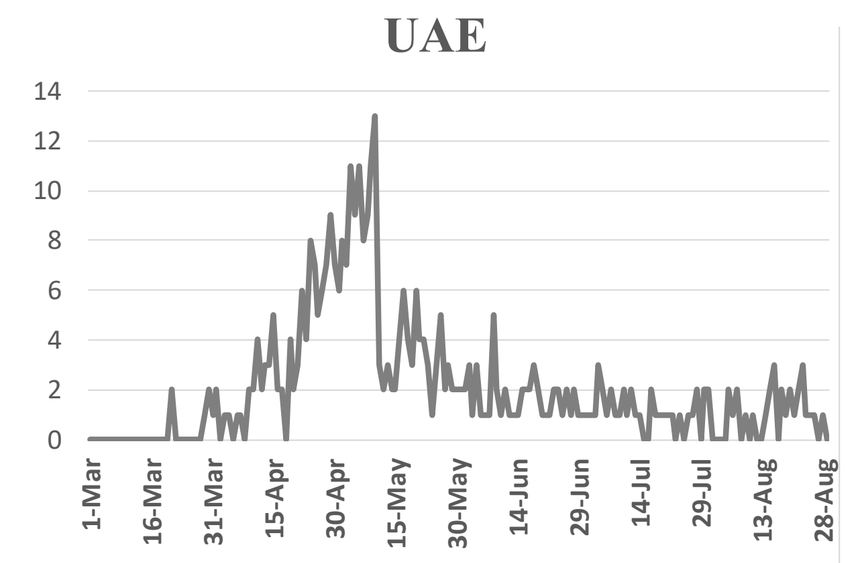
Source : Kuwait ministry of health

Qatar

Source : Qatar ministry of health

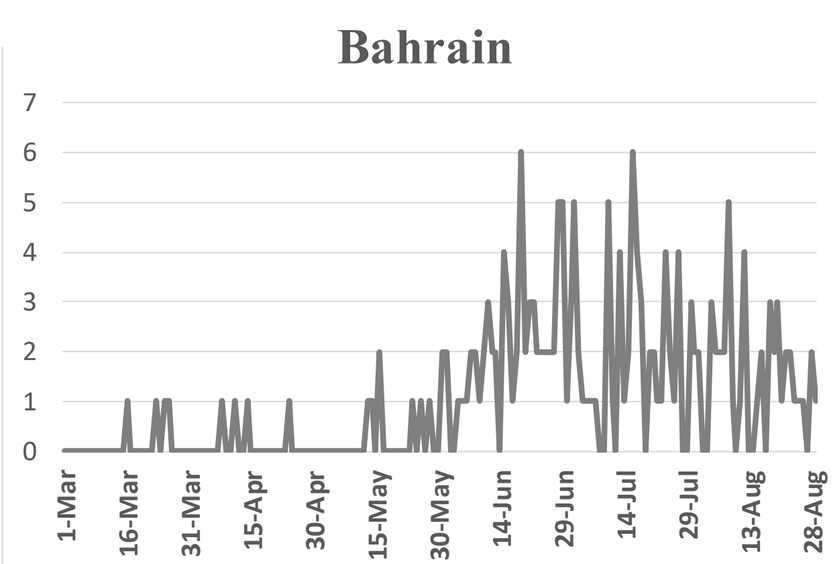
Graphs published by Abu Dhabi Public Health Center 2020 | Data resources: WHO

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

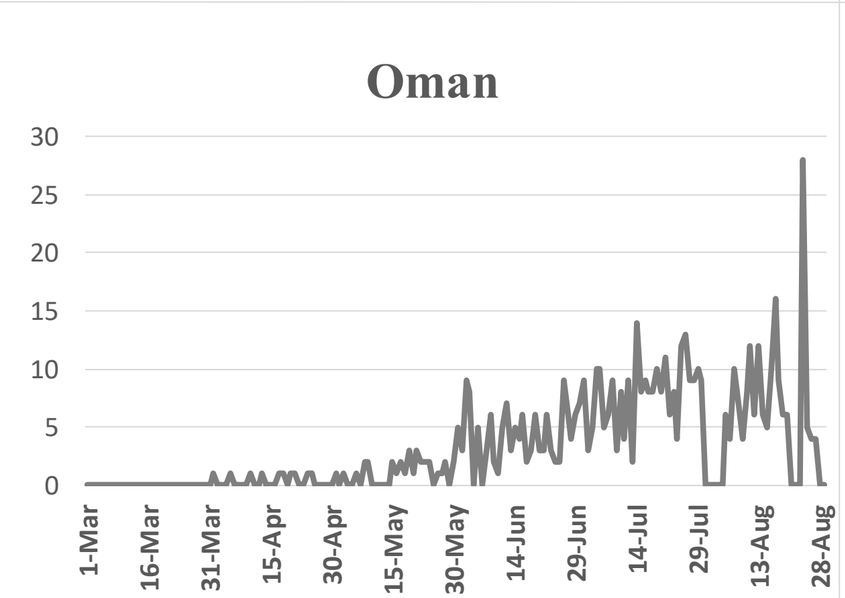


Source : National Emergency Crisis and Disaster Management Authority

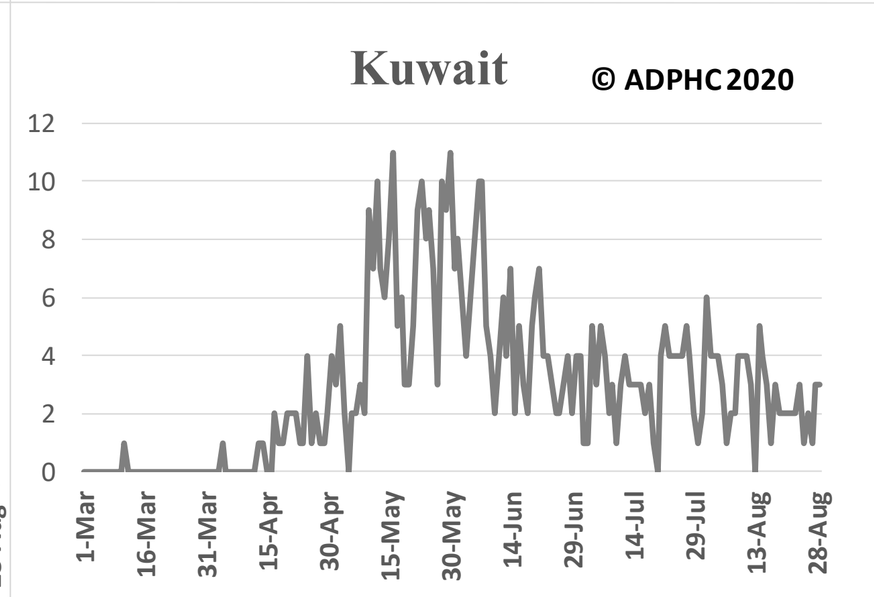
Source : KSA ministry of health



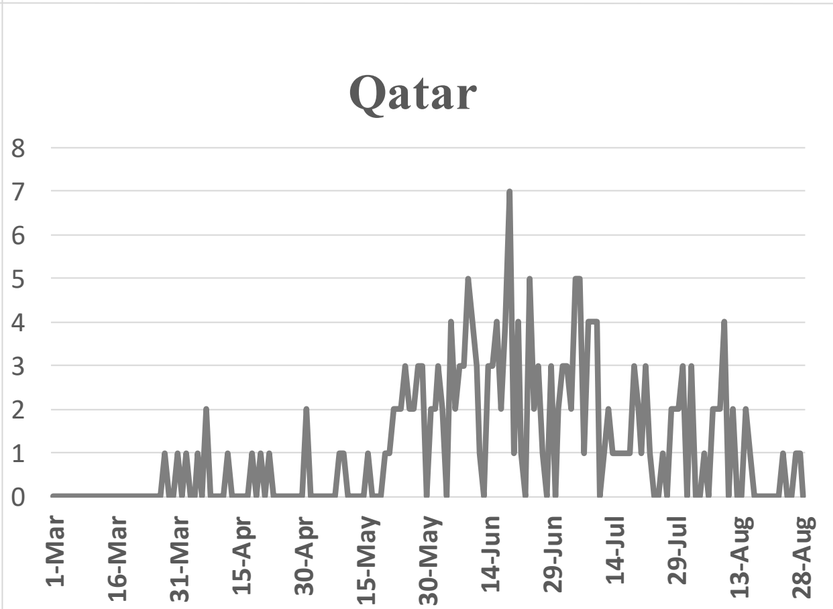
Source :WHO



Source :Oman ministry of health



Source : Kuwait ministry of health



Source : Qatar ministry of health

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*No announced statistic data on weekends and official holidays.

Graphs published by Abu Dhabi Public Health Center 2020 | Data resources: WHO

TREATMENT

Article 1

Published 01 July 2020 OXFROD ACADMIC

Effect of Convalescent Plasma Therapy on Viral Shedding and Survival in Patients With Coronavirus Disease 2019

This retrospective, observational study compared and analyzed the treatment efficacy in COVID-19 patients who received or did not receive convalescent plasma.

Methodology

- This study was conducted in 21 individuals. Six patients were in the convalescent plasma group (treatment), and 15 patients were in the non–convalescent plasma group (control).
- The primary endpoint was death or recovery (discharge)
- The secondary endpoint was SARS-COV-2 viral clearance.

Results

- Six patients in the treatment group had achieved viral clearance.
- Both groups (plasma vs control) had one recovered patient. While the rest of the patients died.
- Five patients in the treatment group and three in the control group had undetectable SARS-CoV-2 before they die.

Conclusion

- Convalescent plasma helps to stop viral shedding and extend survival in patients with COVID-19 and respiratory failure.
  - The failure to reduce the mortality rate may be attributed to the late transfusion of convalescent plasma.
  - Convalescent plasma treatment should be given to patients with COVD-19 at the right phase or severity of illness.
  - It will be improper to use it for patients with mild symptoms and patients with end-stage COVID-19.
- Future large-scale studies are needed to investigate whether an early-phase infusion of convalescent plasma inappropriate recipients can prevent clinical deterioration and improve the survival rate.

Article 2

Published

SARS-CoV-2 Whole Genome Amplification and Sequencing for Effective Population-Based Surveillance and Control of Viral Transmission

27 July 2020 CLINCHEM

Authors

Divinlal Harilal, Sathishkumar Ramaswamy, Tom Loney, Hanan Al Suwaidi, Hamda Khansaheb, Abdulmajeed Alkhaja, Rupa Varghese, Zulfa Deesi, Norbert Nowotny, Alawi Alsheikh-Ali, Ahmad Abou Tayoun

With the continued spread of SARS-CoV-2 around the globe and the emergence of the second wave of COVID-19, the need for tracing and identifying the source of virus in the community is gaining more significance. Currently, whole genome transcriptome-based sequencing (WGS) is considered the best approach to identify viral clades (genotypes) in a population which is crucial for developing public health policy decisions (Fig. 1). However, the technique is expensive and requires a lot of data space that becomes problematic when population-wide studies are conducted, especially in resource-poor environments. In this study from the **Mohammed Bin Rashid University of Medicine and Health Sciences (MBRU), UAE,** the authors demonstrate the superiority of an alternative protocol that uses targeted whole genome amplification of SARS-CoV-2, followed by sequencing (amplification of the viral genome and not the host genome)(Fig. 2), rather than the transcriptome-based sequencing approach currently being used on viral RNA isolated from nasal swabs (Fig. 1).

Results & Conclusions

The study reveals that prior enrichment of whole-genome viral sequences via reverse transcriptase-PCR (using 26 overlapping primer sets covering most of the viral genome) led to more than 99% of the sequencing reads being successfully mapped to the viral genome compared to an average of 0.63% of the reads without enrichment. This resulted in a more sensitive and in-depth coverage of the viral genome using substantially less sequencing data, enabling higher scalability and sizable **cost reductions ($87/sample at 400x depth vs $403/sample at 50x depth)**. They go on to show that free software from the internet could be used to analyze this data and determine the probable origin of the viral strains through phylogenetic analysis. However, as with any sequencing data, caution is advised with result interpretation as the sequencing data should be combined with other epidemiological information (such as travel history) to avoid inaccurate conclusions.

Implications

Use of the alternative protocol developed in this paper can lead to substantially lower costs of successfully sequencing and identifying the genomes of SARS-CoV-2 isolates from patients and identifying whether they were introduced from outside the country or are they community derived, thus cost-effectively influencing public policy decisions.

Article 2

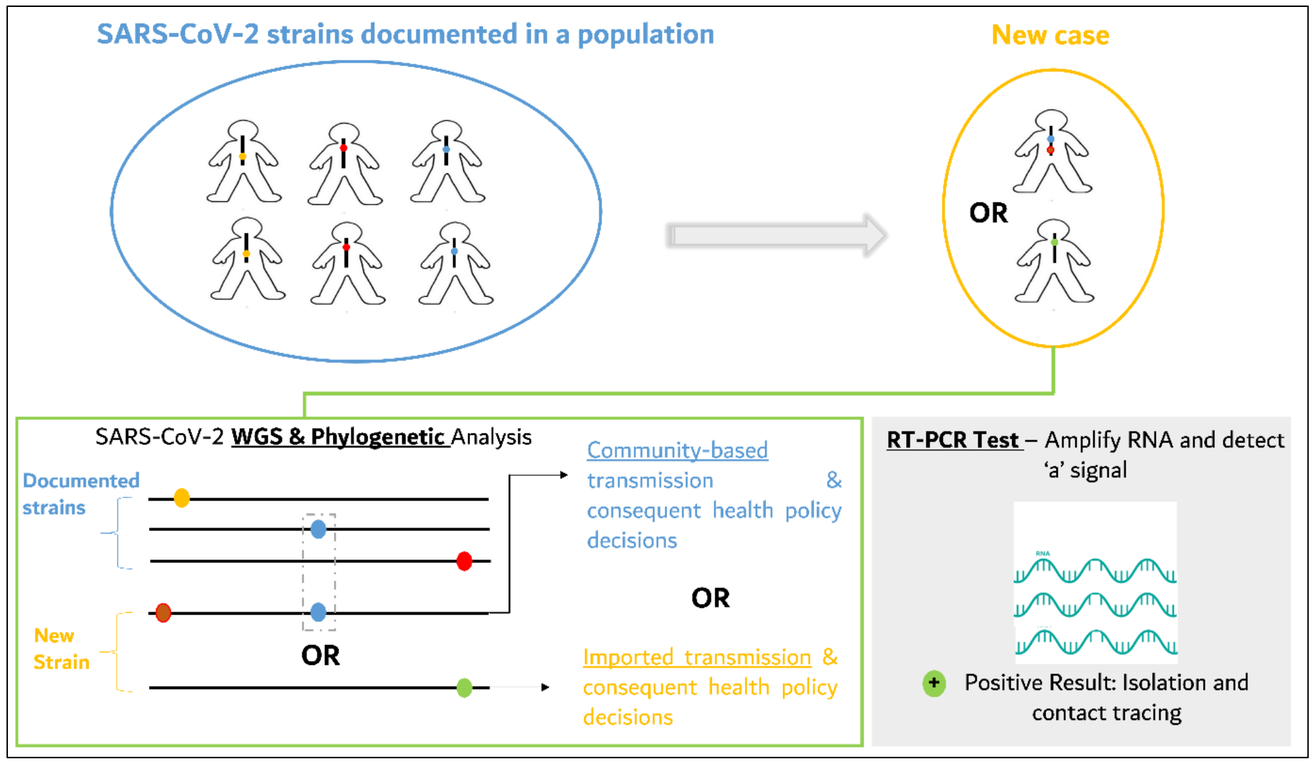
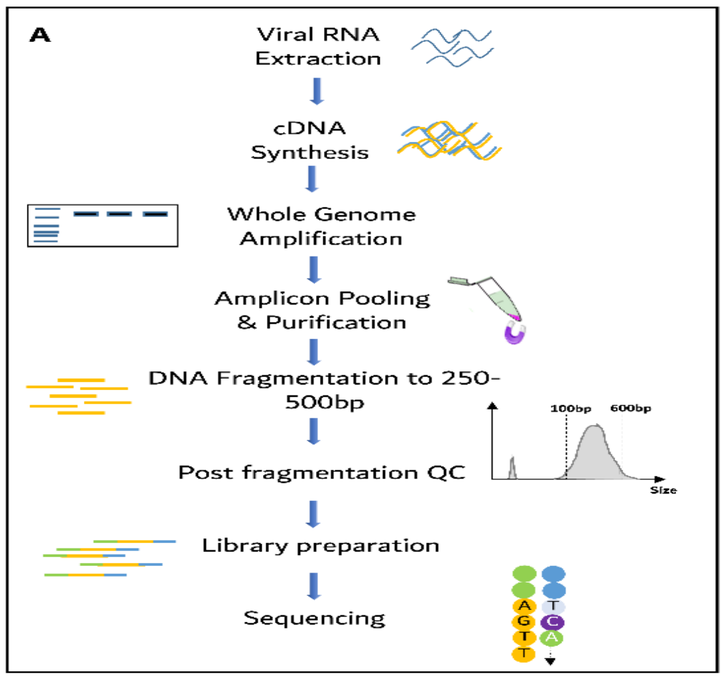
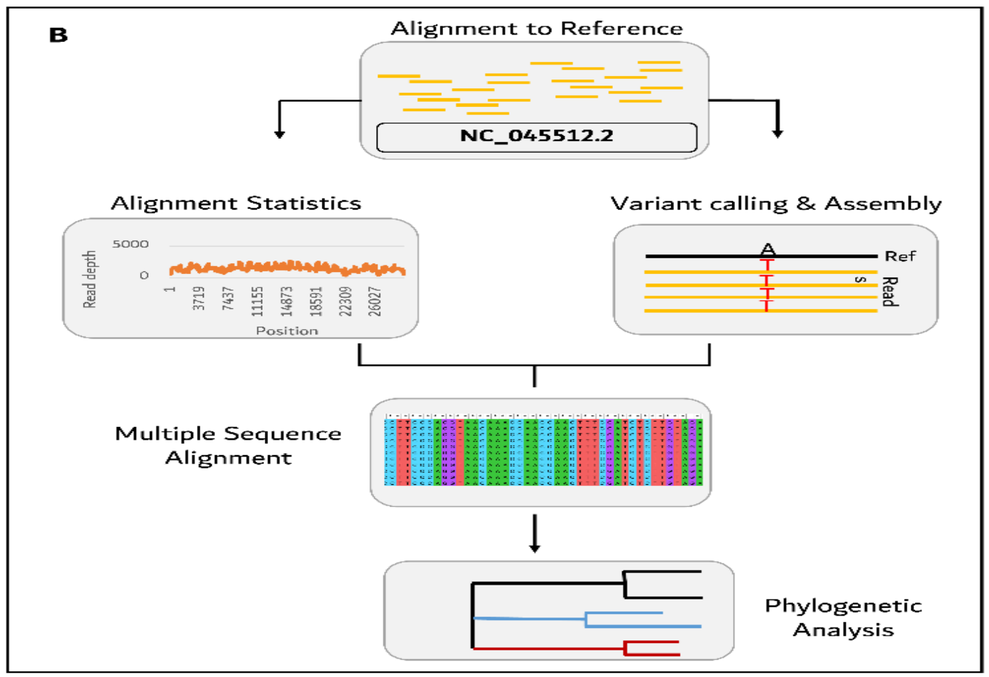


Figure 1. SARS-CoV-2 whole genome sequencing-based surveillance. A schematic illustrating how SARS-CoV-2 whole genome sequencing (cWGS) can be used as a surveillance tool to uncover community-based versus international/travel-related introductions. Mutations are represented by colored dots or circles on SARS-CoV-2 genomes (black bars) within each patient with COVID-19. A population of viral genomes in a community can be used as a reference set (circled blue) for future analysis when new cases (circled orange) emerge. Two scenarios are represented for the new case: the first represents community transmission while the second represents external introduction. The strain representing community transmission has two mutations, one of which (blue) has been identified in a strain from a previous patient in this community, while the second is a new mutation (brick red), arising as part of the virus evolution. The strain with a single novel mutation (green) not seen previously in this population represents a new introduction.





The Alternative Approach Demonstrated

Figure 2. Whole genome amplification, sequencing, and phylogenetic analysis of SARS-CoV-2 genome. A) Wet bench steps describing SARS-CoV-2 genome enrichment and sequencing. B) Bioinformatics and computational steps for sequence alignment, variant calling, SARS-CoV-2 genome assembly, multiple sequence alignment and phylogenetic analysis. All steps are described in detail in Methods.

Article 3

Published August 13, 2020 Euro Surveillance

Geographical and temporal distribution of SARS-CoV-2 clades in the WHO European Region, January to June 2020

This study analyzed thousands of SARS-CoV-2 genomes that were reported in the WHO European Region (January to July 2020) to determine their geographical spread with time (i.e., surveillance) in the European continent. To accomplish this task, they compared viral sequences deposited into three SARS-CoV-2 sequence repositories: Nextstrain, GISAID, and Rambaut et al. (cov-lineages.org) to determine how similar the repositories were in revealing the spread of different viral genetic strains, termed "clades" in various European countries with time. The first two repositories type viruses observed worldwide, while the last one analyzes "outbreaks" of viruses in communities at the micro-level. As of July 10, 2020, >63,000 whole-genome sequences were deposited in GISAIDS of which ~ 39,000 were from 35 countries present in the WHO European region which were analyzed in this study. The difficulty in analyzing SARS-CoV-2 sequences is that different naming schemes (nomenclatures) have emerged in the three databases. Thus, the spread of the different clades was monitored to determine if similarities could be observed between the databases so that their surveillance potential could be assessed.

Results & Conclusions

The three databases had different names for the viral strains. Clade 19B of Nextstrain was the same as clade S of GISAID, 19A ~ L/O/V, 20A ~ G, 20C ~ GH, and 20B ~ GR. Nextstrain and GISAID were observed to be more similar in their trend predictions than cov-lineages. Clade 19B/S started the epidemic and evolved into 19A/LOV, showing the **D614G mutation in spike protein that increased virus transmissibility but not pathogenicity in the populations. This was,** followed by a rapid increase in clade 20B/R between March to May with max in June, while 20C/GH appeared in April (Nextstrain) or May (GISAID) and then declined rapidly.

They conclude that "Overall, the GISAID and Nextstrain nomenclatures provide similar pictures of the situation and may provide useful systems for genomic situation reporting globally. The cov-lineages.org nomenclature provides information at a finer scale and has the potential to provide early warning of expanding lineages that may represent regional outbreaks or later become dominant because of some selective advantage such as vaccine escape or increased transmissibility.

Implications

The authors identify key surveillance objectives for the use of SARS-CoV-2 sequence data at the European level to: 1) Investigate transmission dynamics and appearance of novel genetic variants, 2) Determine relationship of clades to each other and their correlation with transmissibility and severity to guide public policy decisions, 3) Understand impact of public policy on virus population, 4) Assess impact of mutations on molecular testing & serological tests. Once drugs and vaccines become available, the goals will include: 5) Assessment of the impact of mutations on drugs and 6) Risk of vaccine escape by modeling changes in viral antigenic epitopes.

THANK YOU

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