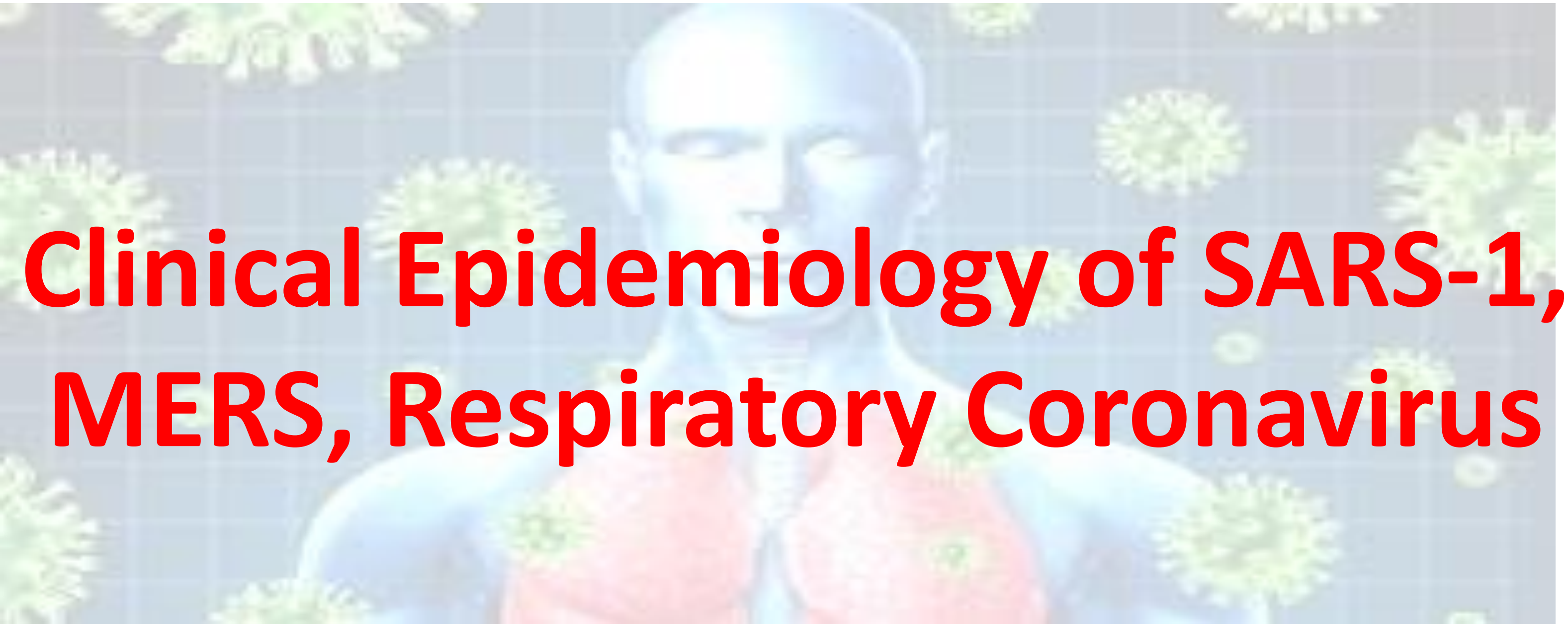

Clinical Epidemiology of SARS-1, MERS, Respiratory Coronavirus

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Outline

-Background and Overview

-Ecology of emerging Respiratory Coronaviruses

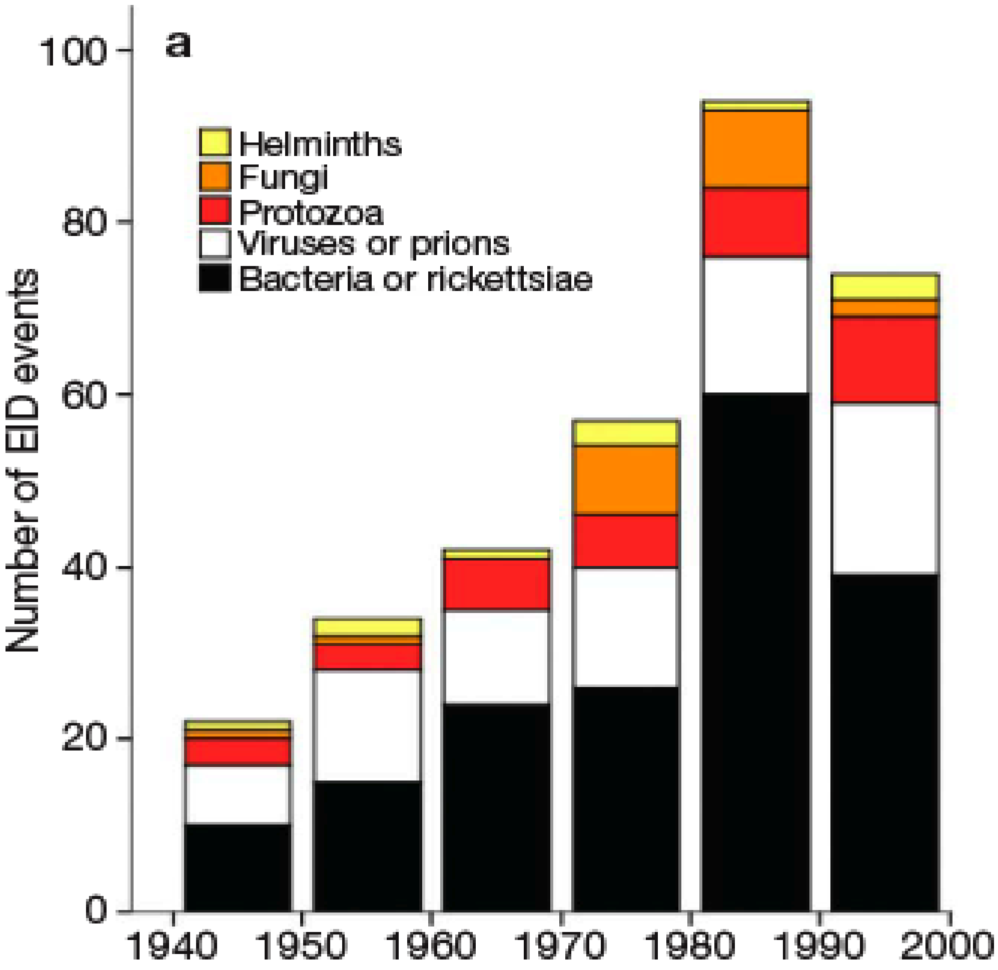
-Emerging Respiratory Coronaviruses; SARS-1, MERS-CoV, SARS-CoV-2

-Symptoms and Transmission

-Summary

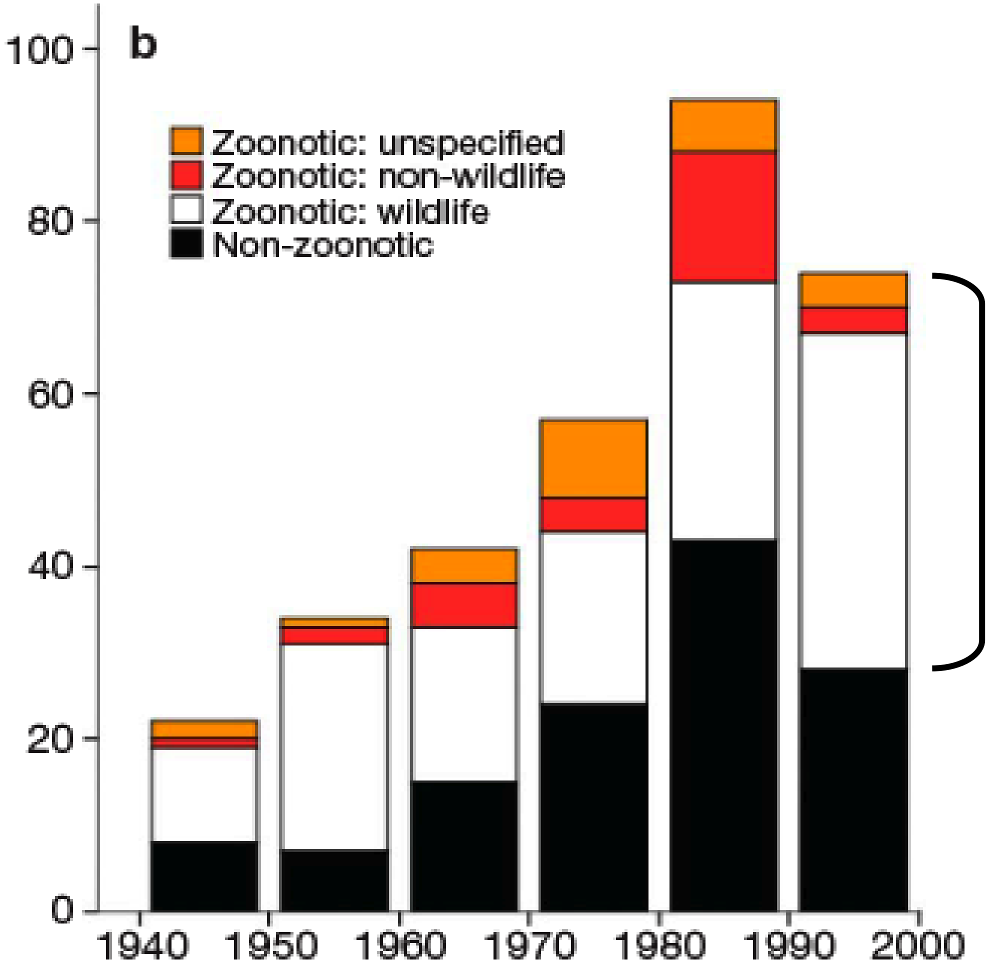
Background and Overview

- Emerging viral disease is a major threat to global health. Because of rapid mutation, adaptation to changing environment several new viral disease and emerging and causing human illness.
- Also, they have polymerase enzyme that helps in viral replication.
- Multiple biological, behavioral, ecological factors contributing to the emergence and reemergence of viral infectious diseases.
- Generally, emerging infections of humans reflect transmission of a virus from a wild or domesticated animal with attendant human disease.
- Most emerged viruses come from zoonotic infectious.
- Detecting new viruses become easy because the technologies that we have recently.



- Out of 335 diseases that have emerged since 1945, 85 are from viruses

- 25% viral



70% are from animals

= Zoonotic viruses: A virus that normally infects animals but can also infect humans

Most from wild animals

Some from captive animals

Respiratory Coronavirus

Ebola Zaire	1995-current	Humans/gorillas	D. R. Congo
Hendra virus	1995-current	Bats/horses/humans	Australia
Nipah virus	1995-current	Bat/pigs/humans	Malaysia
Andes virus	1996	Rodents/humans	South America
Hantaan virus	1997	Rodents/humans	South America
Rift Valley fever virus	1997-current	Goats/humans/mosquito	East Africa/ Saudi Arabia
Sin Nombre virus	1997-1998	Rodents/humans	North America
Marburg virus	1999	humans	D. R. Congo
Crimean Congo hemorrhagic fever virus	1999	humans	Eastern Europe
SARS	2002-2003	Civet cat	China/global
Bird flu H5N1	2002-current	Chickens/birds/humans	China/global
Monkeypox	2003	Monkeys/humans	North America
Swine flu H1N1	2009	Pigs/humans	China/global
MERS	2012-current	Camel/humans	Middle east/global
SARS-COV-2	2019-current	Bats/humans	China/global

There are 2 main reasons for virus emergence in humans

A). Virus mutation.

- RdRp error
- Reassortment
- Recombination

Genetic

B). Change in contact between human and infected vector or host

- Weather
- Bush meat and animal markets
- Farming and land development

Behavioral

Change in contact occurs in 3 main ways

1. Changes in the Weather: eg. Rain, drought, temperature change

- Change in the host’s food supply
- Change in the host’s territory

New contact between host and humans

Change in contact occurs in 3 main ways

2 . Bush meat and live animal markets

- Allows close contact between humans and infected animals that would otherwise not occur

- Can circumvent natural infection barriers that would otherwise not arise. eg. exposure to body fluids

Bush meat

An age old practice in Africa, S. America

Responsible for transmission of:

- Ebola virus
- Monkey pox
- HIV-1 and HIV-2

New contact between virus and humans

Change in contact occurs in 3 main ways

2 . Bush meat and Live animal markets

Allows close proximity of infected animals to other susceptible hosts that would not normally mix

- Widespread in China, Vietnam, HK
- Markets frequently purged following infections in animals and humans
- Responsible for emergence of new viruses:

H5N1 bird flu

SARS-1
MERS-CoV
SARS-CoV-2

New contact between virus and humans

SARS-1 outbreak: 2002-2003

Disease originated in animal markets in China November 2002, civet cats suspected

Disease contained in China, then suddenly became pandemic

8,500 cases and >900 deaths worldwide

Disease surveillance able to trace infected and halt the outbreak

One key individual stayed at HK Metropole hotel, room 911

Passed the virus onto 14 other people

SARS-1outbreak: 2002-2003

HK room 911 guest passed SARS to 14 residents during his stay

5 of these further transmitted SARS to others

9 of these were dead end hosts – no further spread

- HK room 911 guest passed SARS to 24 of 112 passengers on plane to China
- This single individual caused SARS spread to 17 countries in 4 weeks
- SARS eventually spread to 37 countries, due mostly to air travel

Interesting features of SARS transmission:

Airborne

Carried in sewage

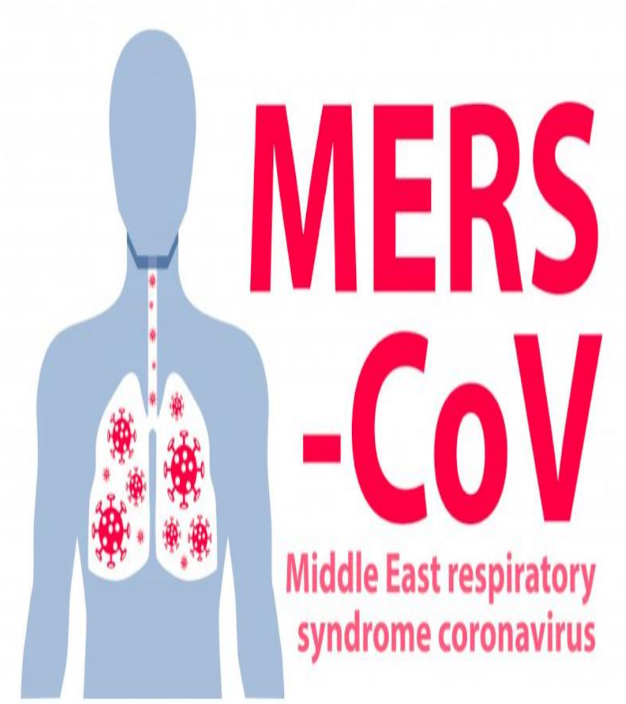
Highly stable

MERS-CoV

MERS-CoV is a novel positive-sense, single-stranded RNA virus of the genus Betacoronavirus.

Initially called as the novel coronavirus 2012 or simply novel coronavirus, it was first reported in 2012 in Saudi Arabia after genome sequencing of a virus isolated from sputum samples from a person who fell ill in a 2012 outbreak of a new flu.

It appears that some people became infected after contact with camels.



The symptoms of MERS-CoV

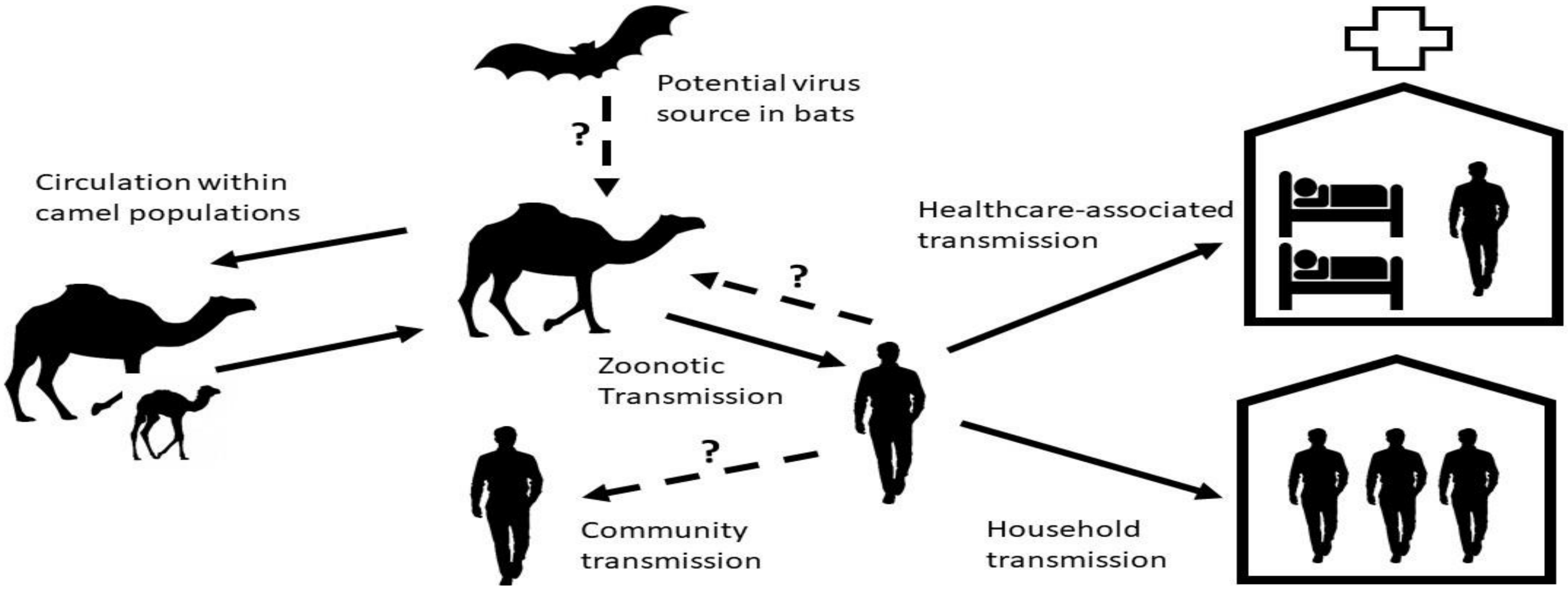
The clinical spectrum of MERS-CoV infection ranges from symptoms or mild respiratory symptoms to severe acute respiratory disease and death.

-Fever
-Shortness of Breath
-Cough
-Vomiting
-Diarrhea
-Sore Throat
-Pneumonia

MERS-CoV Transmission

The Virus spread:

-Close contact with infected persons
-Sharing household items
-Infected person’s respiratory secretions
-Infected camel or their product



Primary and Secondary Transmission

- Primary transmission does not result from contact with a human MERS case
  - Zoonotic transmission from camels
    - No current evidence of other sources
- Secondary transmission results from contact with a human MERS case
  - healthcare-associated, household-associated

- Human to human transmission follows zoonotic transmission
- Humans are considered terminal or transient hosts only
- Human to human transmission can occur within households, but transmission potential is considered limited in community settings
- Healthcare-associated outbreaks have provided most of the context for investigation of risk factors for human to human transmission

Environmental transmission

- MERS-CoV has been isolated from bed sheets, bedrails, IV fluid hangers and X-ray devices
  - suggesting the potential for environmental transmission
- RNA has also been identified in air samples from hospital rooms of MERS patients
- No epidemiologic evidence to definitively implicate fomite or aerosol transmission

Viral shedding in humans

- RNA and live virus found in URT and LRT
- Higher RNA levels in LRT
- More severely ill have lower Ct values and longer duration of shedding

Bin SY, et al. *Clinical Infectious Diseases* 2015

Alabdely et al. *EID* 2019

MERS SITUATION UPDATE | FEBRUARY 2022

World Health Organization
REGIONAL OFFICE FOR THE Eastern Mediterranean

Highlights

- At the end of February 2022, a total of 2585 laboratory-confirmed cases of Middle East respiratory syndrome (MERS), including 890 associated deaths (case-fatality ratio of 34.4%) were reported globally. The majority of these cases were reported from Saudi Arabia (2184 cases) including 812 related deaths (CFR 37.2%).
- No new cases were reported during the month of February 2022.
- The demographic and epidemiological characteristics of reported cases, when compared to the same corresponding period between 2016 and 2022, do not show any significant difference or change.
- The age group 50–59 years continues to be at the highest risk for acquiring infection as primary cases. The age group 30–39 years is most at risk as secondary cases. The number of deaths is higher in the age group 50–59 years as primary cases and 70–79 years as secondary cases.

SUMMARY

2585
Laboratory-confirmed cases reported since April 2012

890
Deaths reported since April 2012

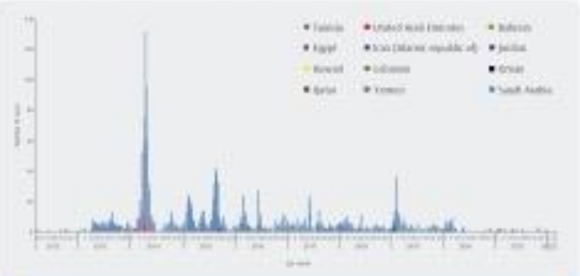
12
Countries reported cases since April 2012 in the Eastern Mediterranean Region

27
Countries reported cases globally

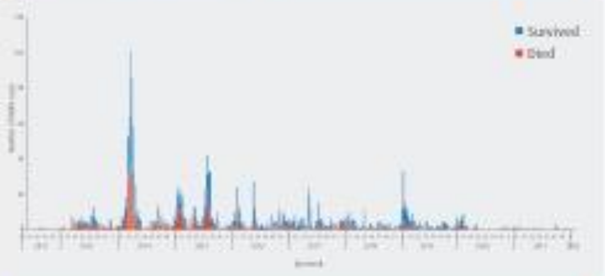
Number of MERS cases in the Easter Mediterranean Region by month and outcome in 2022

2022	Survived	Died
January	0	0
February	0	0
Total	0	0

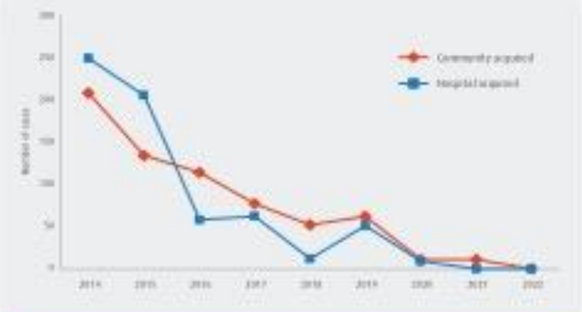
Distribution of MERS reported cases from Eastern Mediterranean Region by week of onset, June 2012 – February 2022



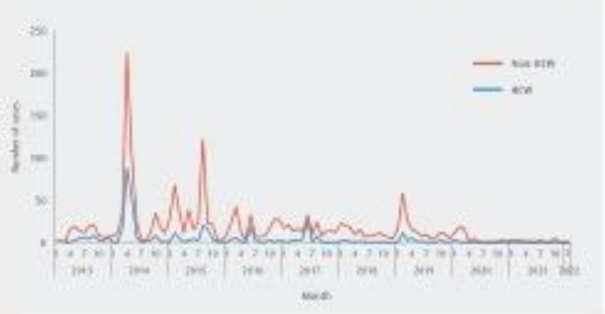
MERS cases per week of onset in Saudi Arabia, June 2012 – February 2022



Community versus hospital acquired MERS cases in Eastern Mediterranean Region, January 2014 – February 2022



Cases of MERS in healthcare workers reported from Saudi Arabia, January 2013 – February 2022



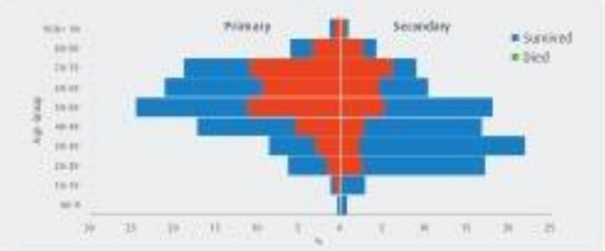
Epidemiological characteristics of MERS cases reported globally between September 2016 – February 2017 and September 2021 – February 2022

Characteristic	Sep 16 - Feb 17	Sep 17 - Feb 18	Sep 18 - Feb 19	Sep 19 - Feb 20	Sep 20 - Feb 21	Sep 21 - Feb 22
Number	120	96	131	76	10	7
Median age in years	58	59	50	58	52	58
Gender (% male)	77	76	79	82	100	100
% of Primary Cases	78	77	39	32	78	100
% of Secondary cases	19	23	61	13	0	0
(%) of Unknown Contact History	3	0	1	56	22	0
% of HCW	4	4	11	7	0	0
% Fatal	34	41	39	38	50	29

Characteristics of MERS cases reported from Saudi Arabia, June 2012 - February 2022

Type of case	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	Grand Total
Missing		1	15	102	103	68	52	56	7	4	0	408
Primary	3	16	164	52	75	78	54	57	11	11	0	533
Secondary	2	83	266	222	60	98	35	75	9	0	0	850
Unknown		28	219	78	11	5	1	16	33	2	0	393
Grand Total	5	158	662	454	249	235	142	204	60	17	0	2184

Age and fatality distribution of primary and secondary cases of MERS reported from Saudi Arabia June 2012 – February 2022



The aim of this situation update is to provide the epidemiological status of MERS in the Region in order to aid better planning, coordination and response. The information in this document has been reported to WHO by ministries of Health.
For further information, contact: Tel + 20-2-22765[illegible], Fax + 20-2-2765[illegible] E-mail: [illegible]

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www.emro.who.int

Document number: WHO-EM/CSR/502/E

MERS-CoV Vaccine & Treatment

Treatments:

-There is no specific antiviral treatment recommended for MERS-CoV infection.

Vaccine:

-10 years have passed since MERS-CoV discovered in 2012.
-No vaccines have been approved for human.

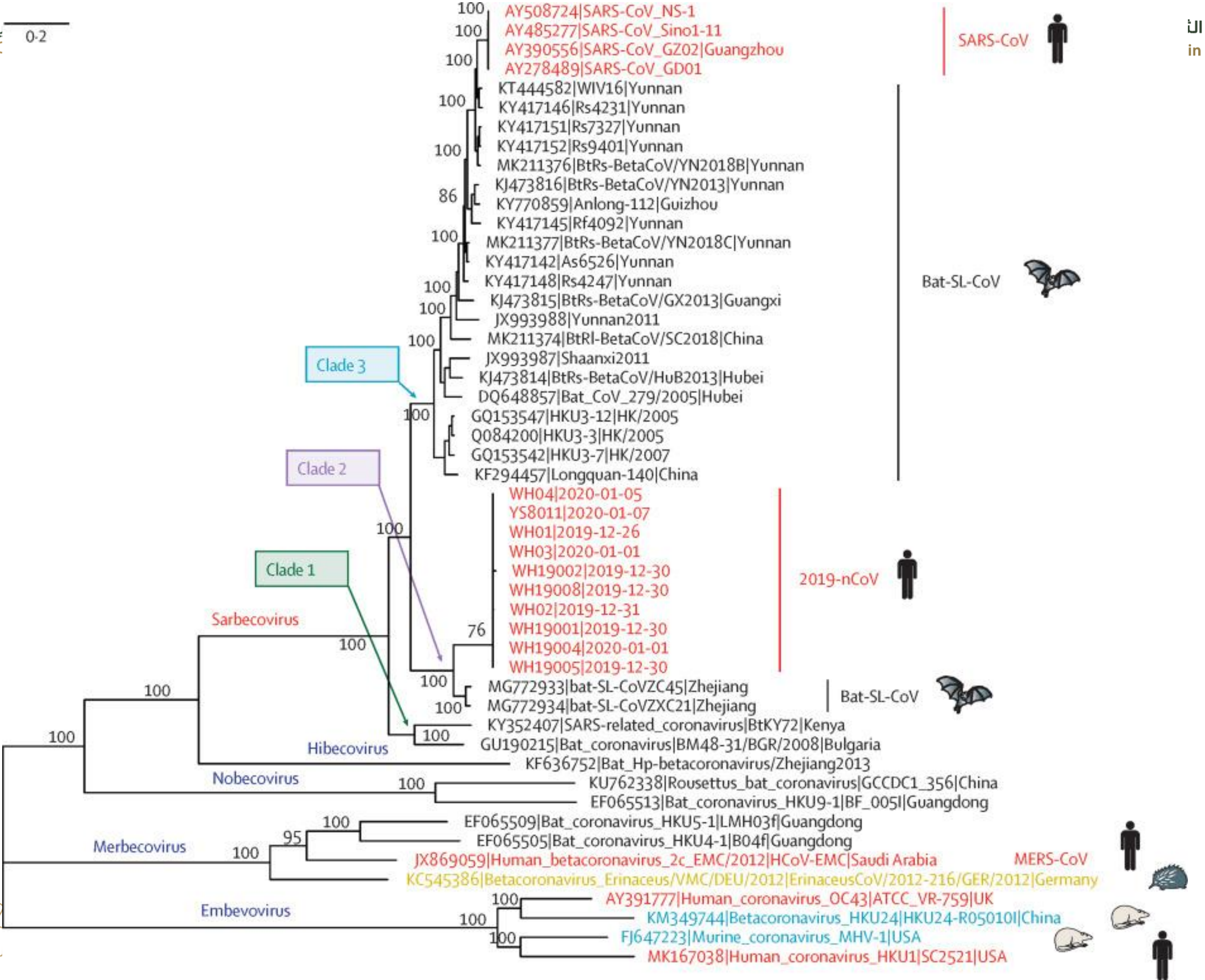
- There is vaccine available for camels
- VTP-500 (ChAdOx1)
- BVRS-GamVac-Comi –phase1/2 clinical trials.
- INO-4700 MERS-CoV-Phase 1 trial.
- MVA-MERS (Modified Vaccinia virus Ankara) contains the full-length spike gene of MERS-CoV.

SARS-CoV-2

- The earliest reported symptoms occurred 1 December 2019, in a person who did not have any exposure to the Huanan Seafood Wholesale Market or to the remaining 40 affected people.
- Of the following 40 confirmed cases of 2019-nCoV infection, two-thirds were found to have a link with the market, which also sold live animals. Of cases that began before 1 January 2020, 55% were linked to the market.
- The market sold fish, chickens, pheasants, bats, marmots, venomous snakes, spotted deer, and other wild animals.

Globally, 23 March 2022, there have been 472,816,657 confirmed cases of COVID-19, including 6,099,380 deaths, reported to WHO.

SARS-CoV-2


0·2
AY508724|SARS-CoV_NS-1
AY485277|SARS-CoV_Sino1-11
AY390556|SARS-CoV_GZ02|Guangzhou
AY278489|SARS-CoV_GD01
SARS-CoV
KT444582|WIV16|Yunnan
KY417146|Rs4231|Yunnan
KY417151|Rs7327|Yunnan
KY417152|Rs9401|Yunnan
MK211376|BtRs-BetaCoV/YN2018B|Yunnan
KJ473816|BtRs-BetaCoV/YN2013|Yunnan
KY770859|Anlong-112|Guizhou
KY417145|Rf4092|Yunnan
MK211377|BtRs-BetaCoV/YN2018C|Yunnan
KY417142|As6526|Yunnan
KY417148|Rs4247|Yunnan
KJ473815|BtRs-BetaCoV/GX2013|Guangxi
JX993988|Yunnan2011
MK211374|BtRl-BetaCoV/SC2018|China
JX993987|Shaanxi2011
KJ473814|BtRs-BetaCoV/HuB2013|Hubei
DQ648857|Bat_CoV_279/2005|Hubei
GQ153547|HKU3-12|HK/2005
Q084200|HKU3-3|HK/2005
GQ153542|HKU3-7|HK/2007
KF294457|Longquan-140|China
Bat-SL-CoV
Clade 3
Clade 2
Clade 1
WH04|2020-01-05
YS8011|2020-01-07
WH01|2019-12-26
WH03|2020-01-01
WH19002|2019-12-30
WH19008|2019-12-30
WH02|2019-12-31
WH19001|2019-12-30
WH19004|2020-01-01
WH19005|2019-12-30
2019-nCoV
MG772933|bat-SL-CoVZC45|Zhejiang
MG772934|bat-SL-CoVZXC21|Zhejiang
Bat-SL-CoV
KY352407|SARS-related_coronavirus|BtKY72|Kenya
GU190215|Bat_coronavirus|BM48-31/BGR/2008|Bulgaria
KF636752|Bat_Hp-betacoronavirus/Zhejiang2013
KU762338|Rousettus_bat_coronavirus|GCCDC1_356|China
EF065513|Bat_coronavirus_HKU9-1|BF_005I|Guangdong
EF065509|Bat_coronavirus_HKU5-1|LMH03f|Guangdong
EF065505|Bat_coronavirus_HKU4-1|B04f|Guangdong
JX869059|Human_betacoronavirus_2c_EMC/2012|HCoV-EMC|Saudi Arabia
MERS-CoV
KC545386|Betacoronavirus_Erinaceus/VMC/DEU/2012|ErinaceusCoV/2012-216/GER/2012|Germany
AY391777|Human_coronavirus_OC43|ATCC_VR-759|UK
KM349744|Betacoronavirus_HKU24|HKU24-R05010I|China
FJ647223|Murine_coronavirus_MHV-1|USA
MK167038|Human_coronavirus_HKU1|SC2521|USA
Sarbecovirus
Hibecovirus
Nobecovirus
Merbecovirus
Embevovirus
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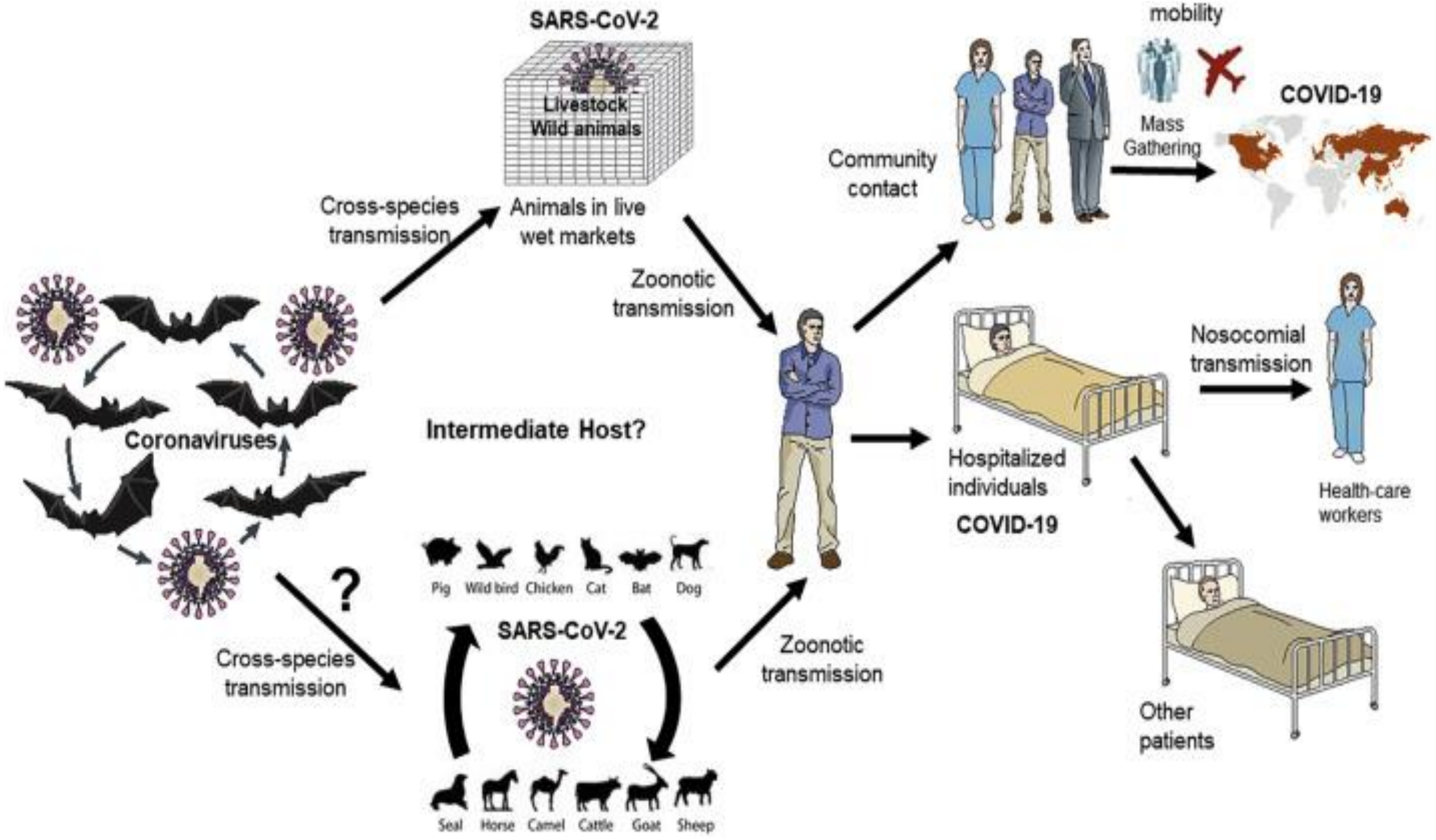
SARS-CoV-2


SARS-CoV-2
Livestock
Wild animals
Cross-species transmission
Animals in live wet markets
Zoonotic transmission
Community contact
mobility
Mass Gathering
COVID-19
Coronaviruses
Intermediate Host?
Hospitalized individuals
COVID-19
Nosocomial transmission
Health-care workers
Other patients
?
Cross-species transmission
Pig
Wild bird
Chicken
Cat
Bat
Dog
SARS-CoV-2
Zoonotic transmission
Seal
Horse
Camel
Cattle
Goat
Sheep

SARS-CoV, MERS-CoV and SARS-CoV-2

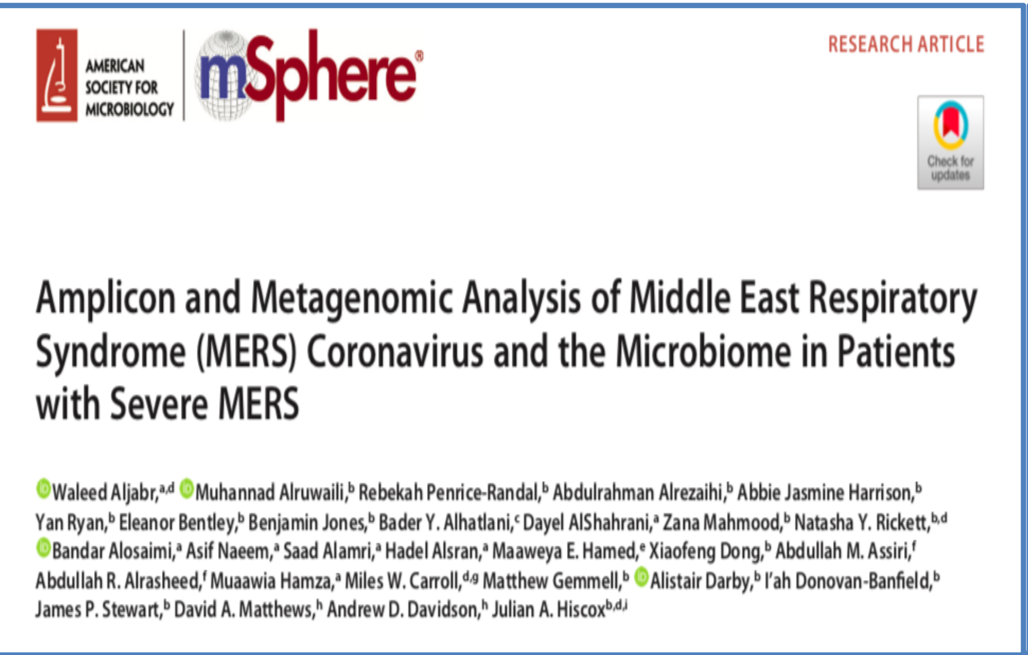
- Similarities of clinical features between SARS-CoV- 2 and previous betacoronavirus infections have been noted. In this cohort, most patients presented with fever, dry cough, dyspnoea, and bilateral ground-glass opacities on chest CT scans.

- These features of SARS-CoV-2 infection bear some resemblance to SARS-CoV and MERS-CoV infections. However, few patients with 2019-nCoV infection had prominent upper respiratory tract signs and symptoms (eg, rhinorrhoea, sneezing, or sore throat), indicating that the target cells might be located in the lower airway.

- Furthermore, SARS-CoV-2 patients rarely developed intestinal signs and symptoms (eg, diarrhoea), whereas about 20–25% of patients.

Identification of New Coronavirus

- Field and epidemiologic studies lead to the initial genetic characterization of the virus.
- A description of the clinical and epidemiologic features of infected persons.
- Characterization of viral transmission within different populations.
- Assessments of population susceptibility through serological surveys.



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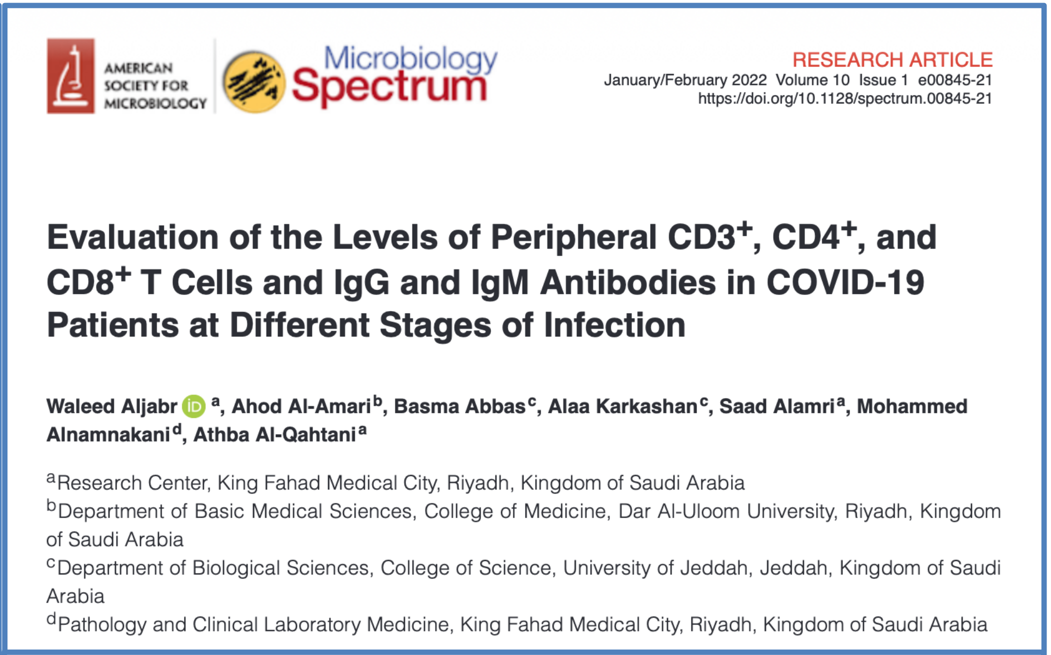
RESEARCH ARTICLE

Check for updates

Amplicon and Metagenomic Analysis of Middle East Respiratory Syndrome (MERS) Coronavirus and the Microbiome in Patients with Severe MERS

Waleed Aljabr,[a,d] Muhannad Alruwaili,[b] Rebekah Penrice-Randal,[b] Abdulrahman Alrezaihi,[b] Abbie Jasmine Harrison,[b] Yan Ryan,[b] Eleanor Bentley,[b] Benjamin Jones,[b] Bader Y. Alhatlani,[c] Dayel AlShahrani,[a] Zana Mahmood,[b] Natasha Y. Rickett,[b,d] Bandar Alosaimi,[a] Asif Naeem,[a] Saad Alamri,[a] Hadel Alsran,[a] Maaweya E. Hamed,[e] Xiaofeng Dong,[b] Abdullah M. Assiri,[f] Abdullah R. Alrasheed,[f] Muaawia Hamza,[a] Miles W. Carroll,[d,g] Matthew Gemmell,[b] Alistair Darby,[b] I'ah Donovan-Banfield,[b] James P. Stewart,[b] David A. Matthews,[h] Andrew D. Davidson,[h] Julian A. Hiscox[b,d,i]



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RESEARCH ARTICLE
January/February 2022 Volume 10 Issue 1 e00845-21
https://doi.org/10.1128/spectrum.00845-21

Evaluation of the Levels of Peripheral $CD3^+$, $CD4^+$, and $CD8^+$ T Cells and IgG and IgM Antibodies in COVID-19 Patients at Different Stages of Infection

Waleed Aljabr[a], Ahod Al-Amari[b], Basma Abbas[c], Alaa Karkashan[c], Saad Alamri[a], Mohammed Alnamnakani[d], Athba Al-Qahtani[a]

[a]Research Center, King Fahad Medical City, Riyadh, Kingdom of Saudi Arabia
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[c]Department of Biological Sciences, College of Science, University of Jeddah, Jeddah, Kingdom of Saudi Arabia
[d]Pathology and Clinical Laboratory Medicine, King Fahad Medical City, Riyadh, Kingdom of Saudi Arabia

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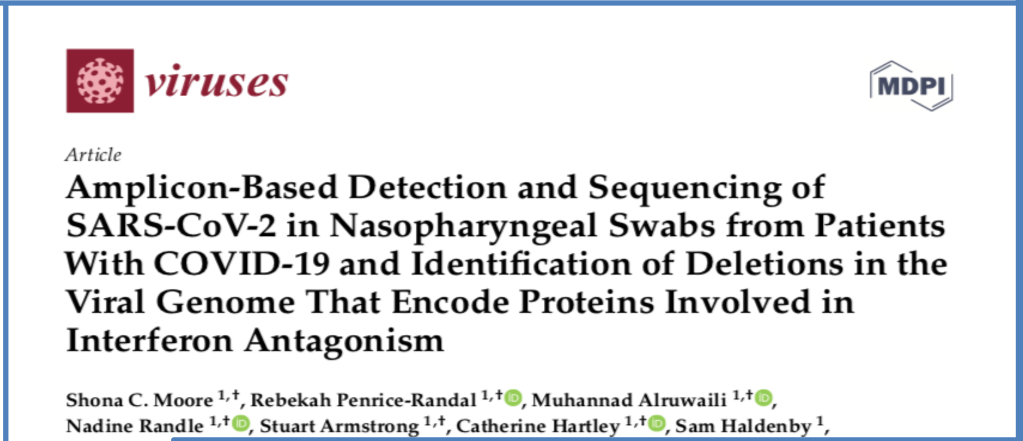

viruses | MDPI

Article

Amplicon-Based Detection and Sequencing of SARS-CoV-2 in Nasopharyngeal Swabs from Patients With COVID-19 and Identification of Deletions in the Viral Genome That Encode Proteins Involved in Interferon Antagonism

Shona C. Moore[1,†], Rebekah Penrice-Randal[1,†], Muhannad Alruwaili[1,†], Nadine Randle[1,†], Stuart Armstrong[1,†], Catherine Hartley[1,†], Sam Haldenby[1],
Xiaofeng D
Isabel Garc
Parul Sharn
Daniel P. C
Michael Be
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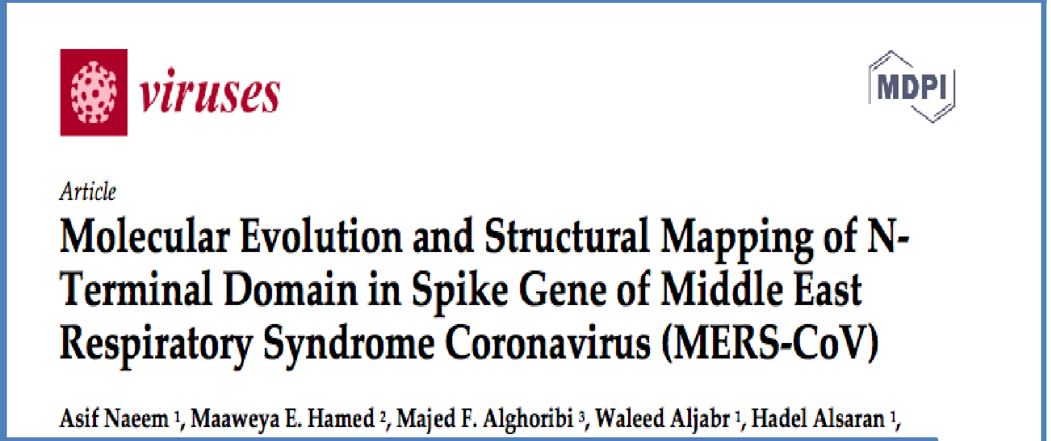
Richard Vip
J. Kenneth
Malcolm Se



viruses | MDPI

Article

Molecular Evolution and Structural Mapping of N-Terminal Domain in Spike Gene of Middle East Respiratory Syndrome Coronavirus (MERS-CoV)

Asif Naeem[1], Maaweya E. Hamed[2], Majed F. Alghoribi[3], Waleed Aljabr[1], Hadel Alsaran[1],

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Short Communication

Unique challenges to control the spread of COVID-19 in the Middle East

Check for updates

Zulqarnain Baloch[a,1], Zhongren Ma[a,1], Yunpeng Ji[a,b], Mohsen Ghanbari[c,d], Qiuwei Pan[a,b], Waleed Aljabr[e,*]

nc Riyadh

Characterisation of SARS-CoV-2 and MERS-CoV and variants in humans and animal models for medical countermeasure development

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