Clinical Epidemiology of SARS-1, MERS, Respiratory Coronavirus

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Background and Overview

Ecology of emerging Respiratory Coronaviruses

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

Symptoms and Transmission

Summary
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
<table>
<thead>
<tr>
<th>Virus/Agent</th>
<th>Year(s)</th>
<th>Hosts</th>
<th>Location(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ebola Zaire</td>
<td>1995-current</td>
<td>Humans/gorillas</td>
<td>D. R. Congo</td>
</tr>
<tr>
<td>Hendra virus</td>
<td>1995-current</td>
<td>Bats/horses/humans</td>
<td>Australia</td>
</tr>
<tr>
<td>Nipah virus</td>
<td>1995-current</td>
<td>Bat/pigs/humans</td>
<td>Malaysia</td>
</tr>
<tr>
<td>Andes virus</td>
<td>1996</td>
<td>Rodents/humans</td>
<td>South America</td>
</tr>
<tr>
<td>Hantaan virus</td>
<td>1997</td>
<td>Rodents/humans</td>
<td>South America</td>
</tr>
<tr>
<td>Rift Valley fever virus</td>
<td>1997-current</td>
<td>Goats/humans/mosquito</td>
<td>East Africa/ Saudi Arabia</td>
</tr>
<tr>
<td>Marburg virus</td>
<td>1999</td>
<td>humans</td>
<td>D. R. Congo</td>
</tr>
<tr>
<td>Crimean Congo hemorrhagic fever virus</td>
<td>1999</td>
<td>humans</td>
<td>Eastern Europe</td>
</tr>
<tr>
<td>SARS</td>
<td>2002-2003</td>
<td>Civet cat</td>
<td>China/global</td>
</tr>
<tr>
<td>Bird flu H5N1</td>
<td>2002-current</td>
<td>Chickens/birds/humans</td>
<td>China/global</td>
</tr>
<tr>
<td>Monkeypox</td>
<td>2003</td>
<td>Monkeys/humans</td>
<td>North America</td>
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<tr>
<td>Swine flu H1N1</td>
<td>2009</td>
<td>Pigs/humans</td>
<td>China/global</td>
</tr>
<tr>
<td>MERS</td>
<td>2012-current</td>
<td>Camel/humans</td>
<td>Middle east/global</td>
</tr>
<tr>
<td>SARS-COV-2</td>
<td>2019-current</td>
<td>Bats/humans</td>
<td>China/global</td>
</tr>
</tbody>
</table>
There are 2 main reasons for virus emergence in humans

   • RdRp error
   • Reassortment
   • Recombination
   \[ \text{Genetic} \]

B). Change in contact between human and infected vector or host
   • Weather
   • Bush meat and animal markets
   • Farming and land development
   \[ \text{Behavioral} \]
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

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
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
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 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 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 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
MERS SITUATION UPDATE | FEBRUARY 2022

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

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

- Age and fatality distribution of primary and secondary cases of MERS reported from Saudi Arabia June 2012 - February 2022
- Cases of MERS in healthcare workers reported from Saudi Arabia, January 2013 – February 2022
- Summary of MERS cases in the Eastern Mediterranean Region by month and outcome in 2022
- 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
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 – phase 1/2 clinical trials.
  - INO-4700 MERS-CoV-Phase 1 trial.
  - MVA-MERS (Modified Vaccinia virus Ankara) contains the full-length spike gene of MERS-CoV.
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

- Cross-species transmission
- Animals in live wet markets
- Zoonotic transmission
- Intermediate Host?
- SARS-CoV-2
- Cross-species transmission
- Livestock
- Wild animals
- Mobility
- Mass Gathering
- Community contact
- Hospitalized individuals
- COVID-19
- Health-care workers
- Other patients
• 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.
Amplicon and Metagenomic Analysis of Middle East Respiratory Syndrome (MERS) Coronavirus and the Microbiome in Patients with Severe MERS

Waleed Aljabr 1,*, Ahod Al-Amri 1, Basma Abbas 2, Alaa Karkashan 2, Saad Alamri 2, Mohammed Almannakani 2, Athba Al-Qahtani 2

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3Department of Biological Sciences, College of Science, University of Jeddah, Jeddah, Kingdom of Saudi Arabia
4Pathology and Clinical Laboratory Medicine, King Fahad Medical City, Riyadh, Kingdom of Saudi Arabia

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

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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,*, Muhammad Alruwaili 1,*, Nadine Randle 1,*, Stuart Armstrong 1,*, Catherine Hartley 1,*, Sam Haldenby 1,*, Xiaofeng Dong 1,*, Isabel Garcia 1,*, Parul Sharma 1,*, Daniel P. Casey 2,*, Michael Beattie 3,*, Andrew D. Paint 3,*, Richard Vipond 3,*, J. Kenneth Hill 3,*, Malcolm Smith 3,*,

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 1, Majed F. Alghoribi 2, Waleed Aljabr 1, Hadel Alsaran 1,
Characterisation of SARS-CoV-2 and MERS-CoV and variants in humans and animal models for medical countermeasure development
Thanks

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