



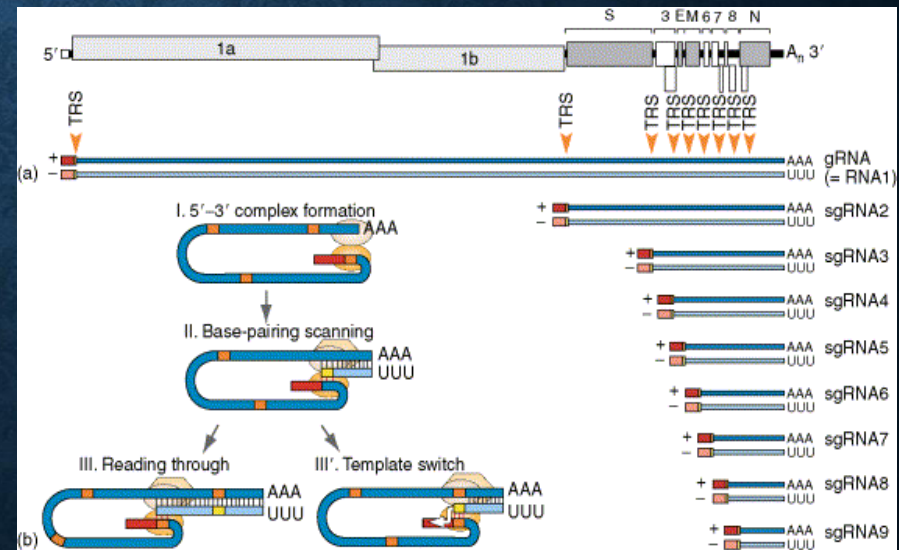
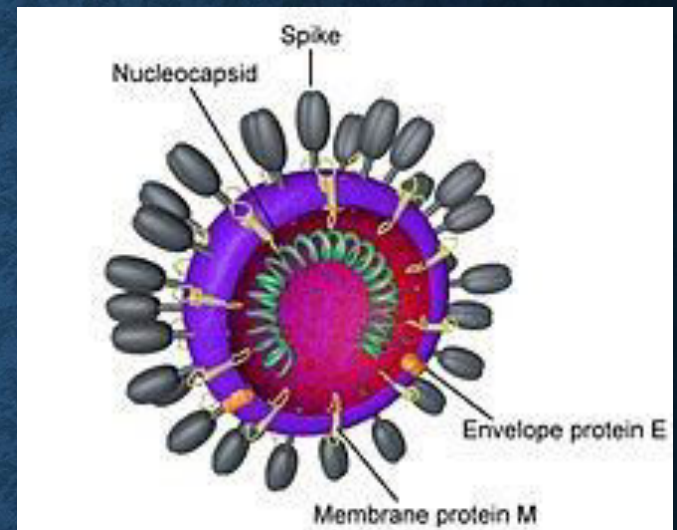
MIDDLE EAST RESPIRATORY SYNDROME CORONAVIRUS MERS-COV

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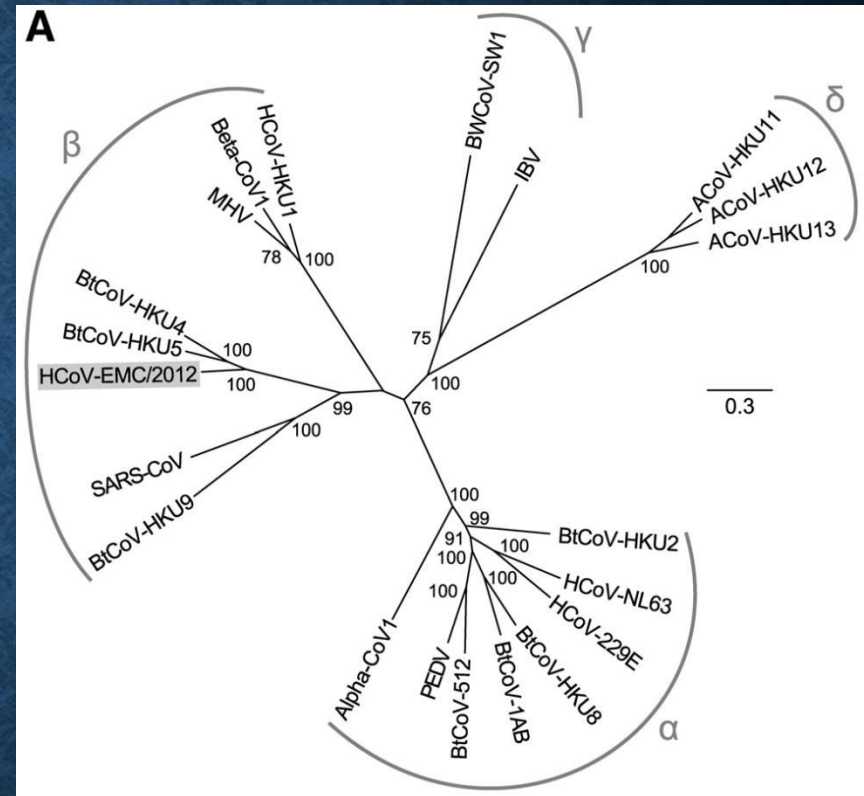
CORONAVIRUSES (COVS)

- infect and cause disease in a wide variety of species
 - bats, birds, cats, dogs, pigs, mice, horses, whales, and humans
 - Until 2003, HCoV-229E and HCoV-OC43
 - In 2002 to 2003, SARSCoV
 - 2004 ,HCoV-NL63
 - 2005 , HCoV-HKU1
- large, enveloped, positive-stranded RNA viruses, large RNA genomes
 - replicate by a similar and unique mechanism
 - high frequency of recombination
 - a **3'-coterminal, nested-set structure** of the mRNAs



CLASSIFICATION

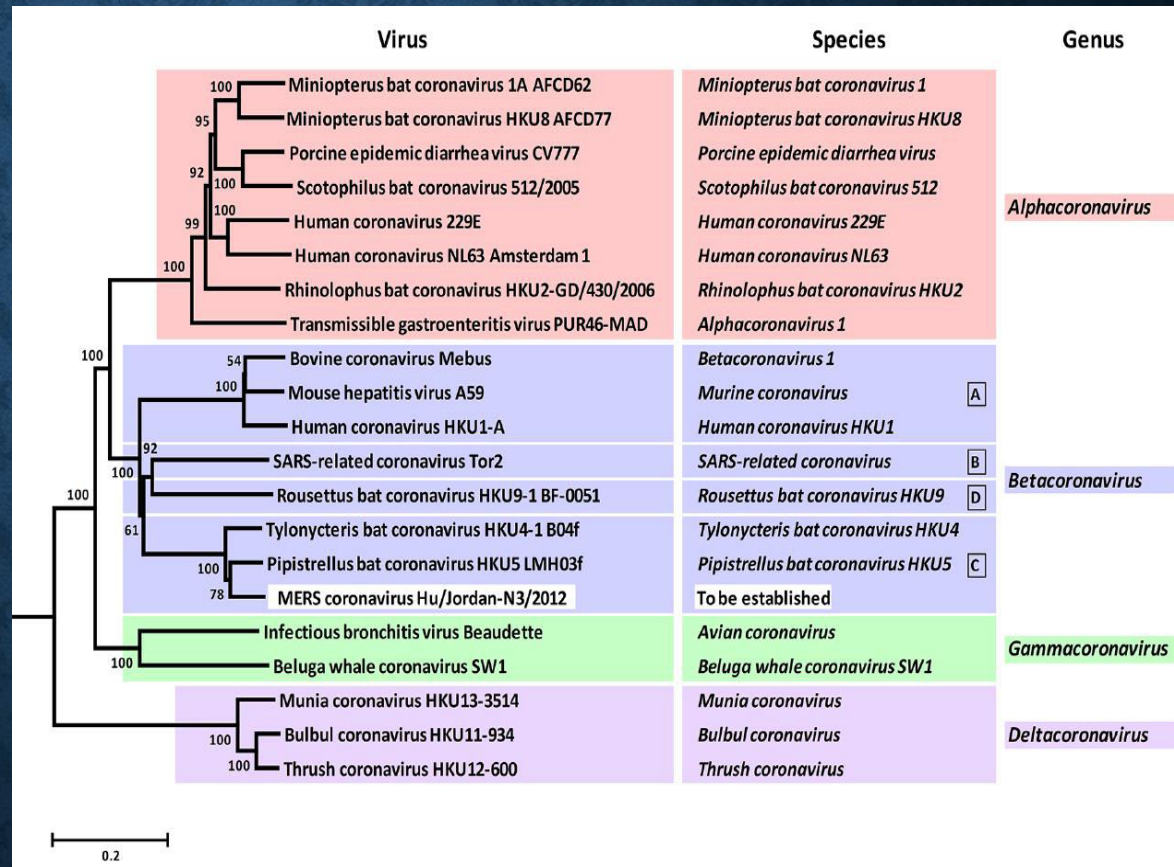
- *Coronavirinae* subfamily:
 - Alphacoronavirus
 - Betacoronavirus
 - Gammacoronavirus
 - Deltacoronavirus
 - ✓ genus α ; HCoV-229E / HCoV-NL63
 - ✓ genus β ; OC43 / HKU1 / SARS-CoV
 - ✓ genus γ & δ ; birds
- “rule”; Most coronaviruses infect only **one animal species** or, at most, a limited number of closely related species.
 - SARS-CoV; an exception to this “rule” to infect a wide range of mammals
 - humans, nonhuman primates, Himalayan palm civets, raccoon dogs, cats, dogs, and rodents



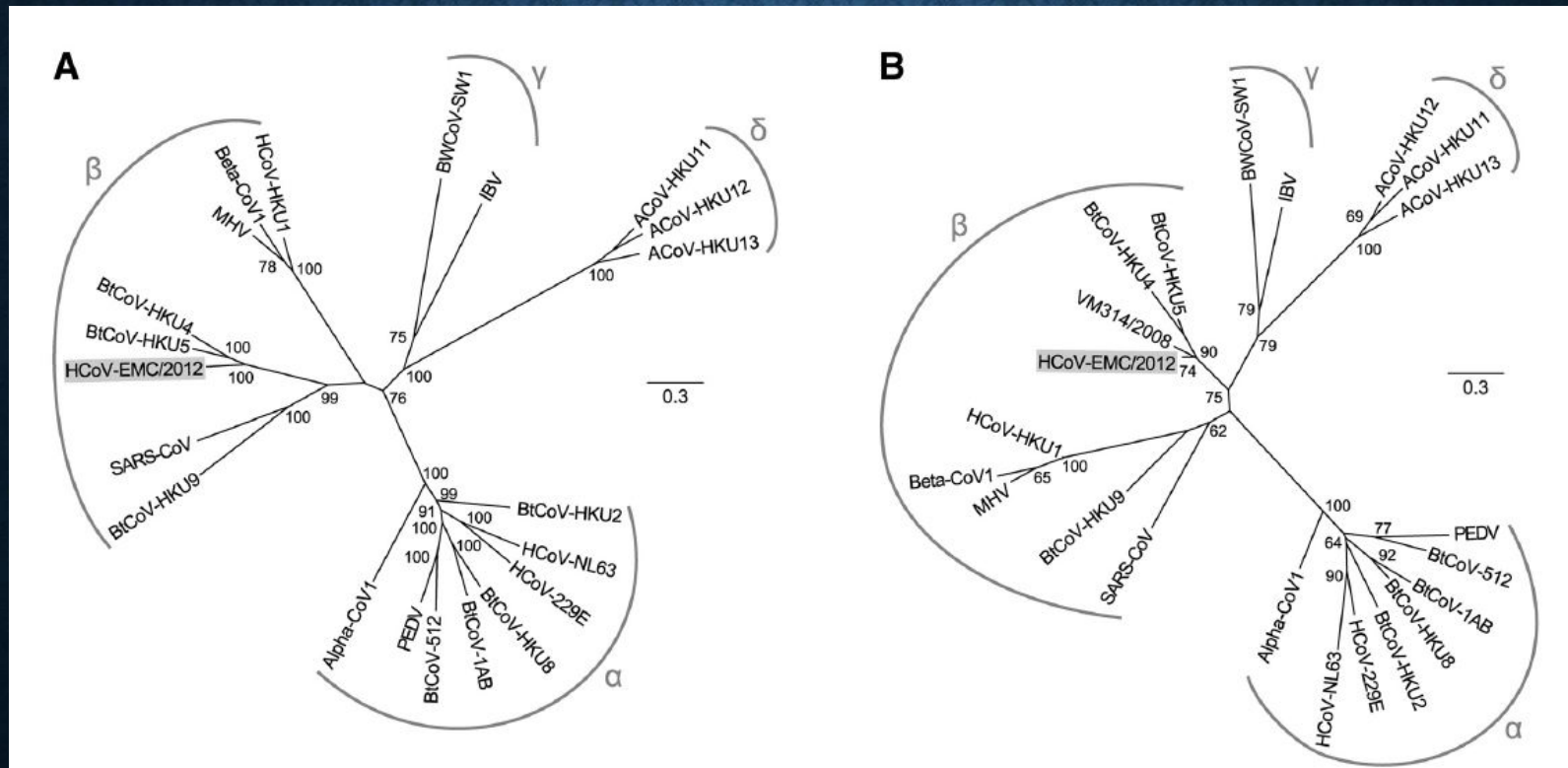
- SARS-CoV diversity based on the nucleocapsid (N) gene
 - Several SARS-like CoVs been detected in bats; 3% to 6% nt diversity with SARS-CoV
 - The group of SARS-CoVs detected in humans and animals in wild animal markets in 2003 and 2004 have $\leq 0.5\%$ nt diversity in the N gene.

MIDDLE EAST RESPIRATORY SYNDROME CORONAVIRUS **MERS-COV**

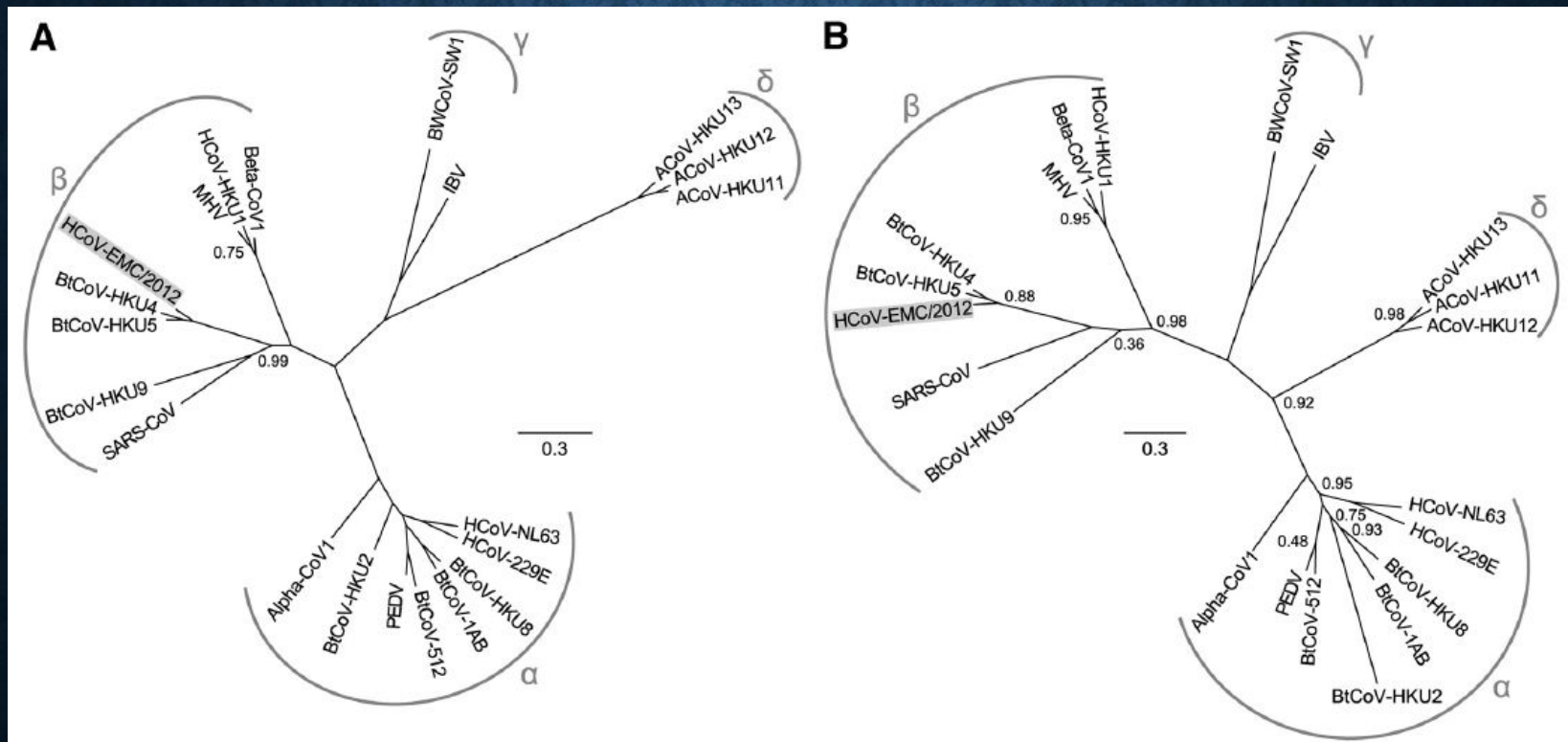
- firstly; HCoV-EMC; “**Erasmus Medical Center**”, the place where the virus characterized in Netherland.
 - isolated from the sputum of a 60-year-old, Saudi Arabia
 - **Viral Genome Sequencing of pan-coronavirus PCR amplicons**
 - HCoV-EMC belonged to the lineage C of genus betacoronavirus; 1st HCoV in **lineage C**
 - HCoV-HKU1 / HCoVOC43; lineage A
 - SARS-CoV; lineage B
 - Lineage D does not contain any human pathogens



PHYLOGENETIC TREES FOR HCoV-EMC/2012 AND SELECTED OTHER CORONAVIRUSES. UNROOTED MAXIMUM LIKELIHOOD PHYLOGENIES INFERRED FROM THE NUCLEOTIDE SEQUENCES OF FULL-LENGTH ORF1AB (A) OR A 332-NT FRAGMENT FROM THE RDRP-ENCODING DOMAIN OF ORF1B (B)



PHYLOGENIES BASED ON CORONAVIRUS-WIDE CONSERVED PROTEIN DOMAINS IN REPLICASE PP1AB (A) OR ON THE CONSERVED PARTS OF STRUCTURAL PROTEINS S2, E, M, AND N (B)



COUNTRIES WITH LAB-CONFIRMED MERS CASES

Countries in or near the Arabian Peninsula with Cases

- Saudi Arabia
- United Arab Emirates (UAE)
- Qatar
- Oman
- Jordan
- Kuwait
- Yemen
- Lebanon
- Iran

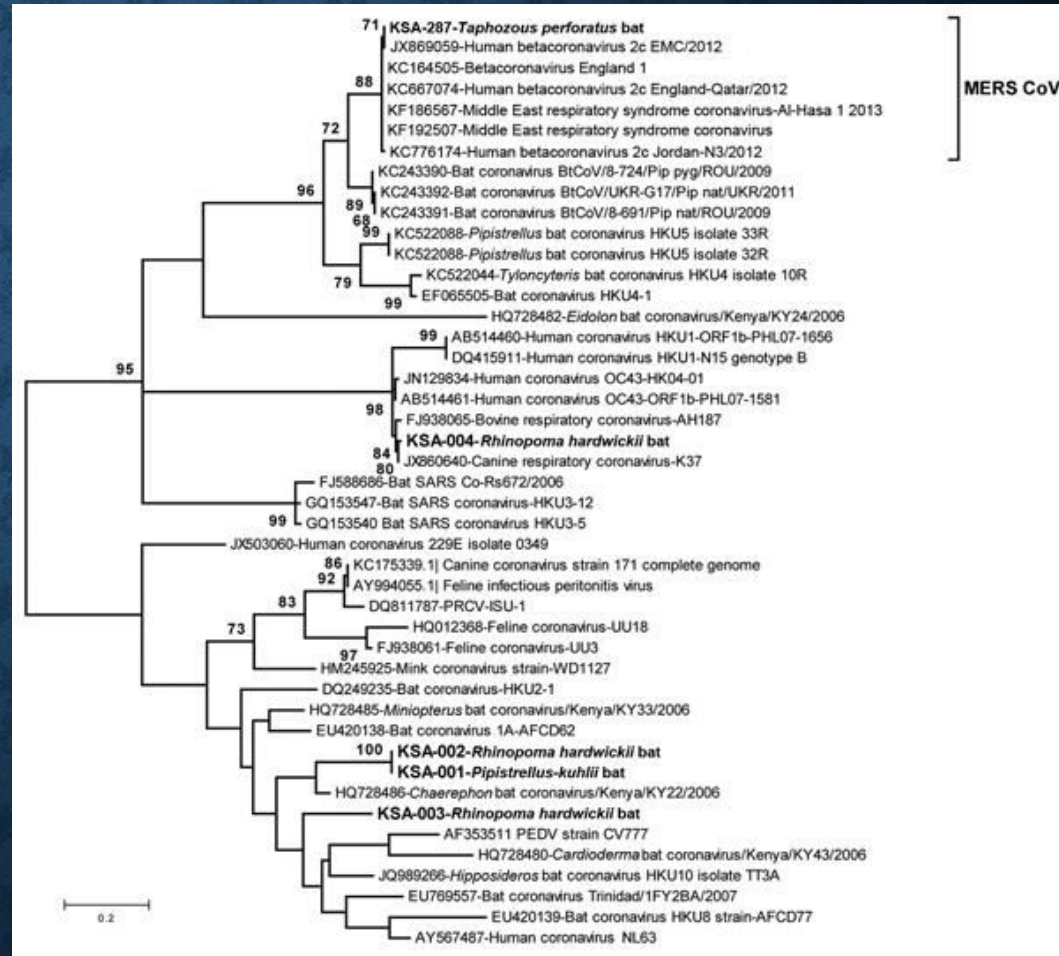
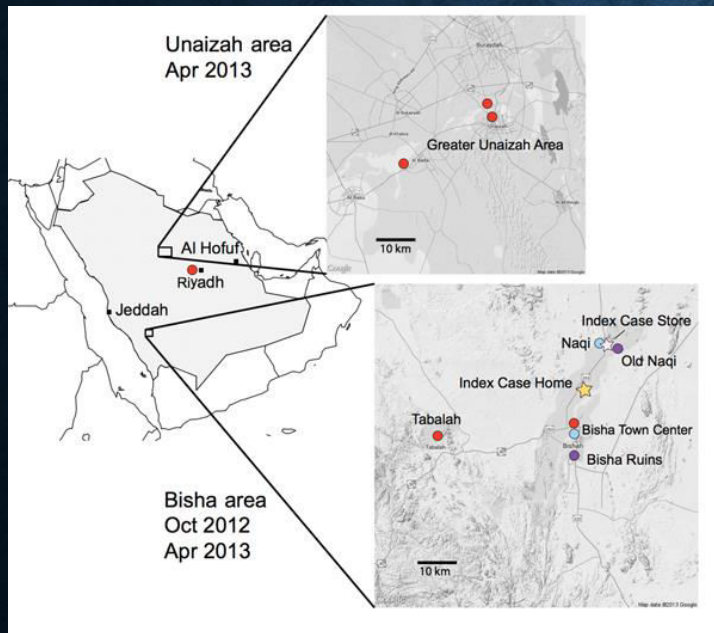
Countries with Travel-associated Cases

- United Kingdom (UK)
- France
- Tunisia
- Italy
- Malaysia
- Philippines
- Greece
- Egypt
- United States of America (USA)
- Netherlands
- Algeria
- Austria
- Turkey

Two patients were transferred to Germany for care.

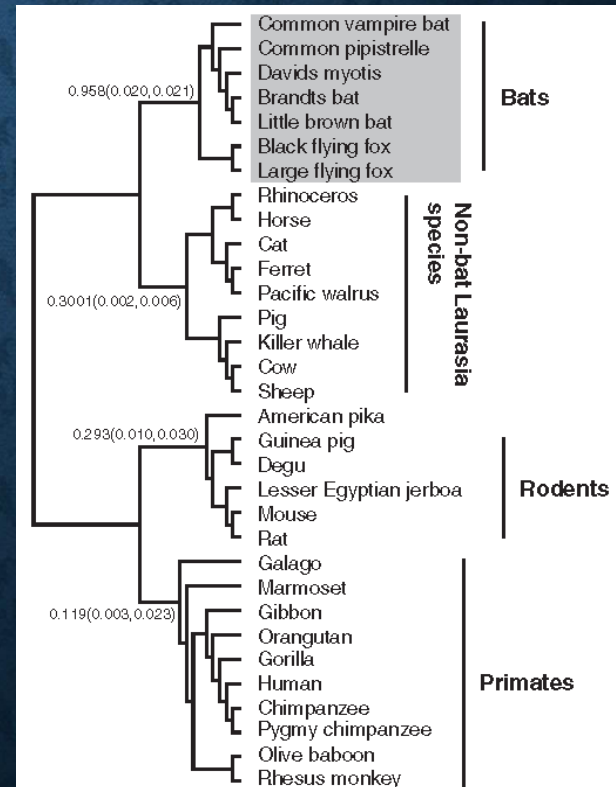
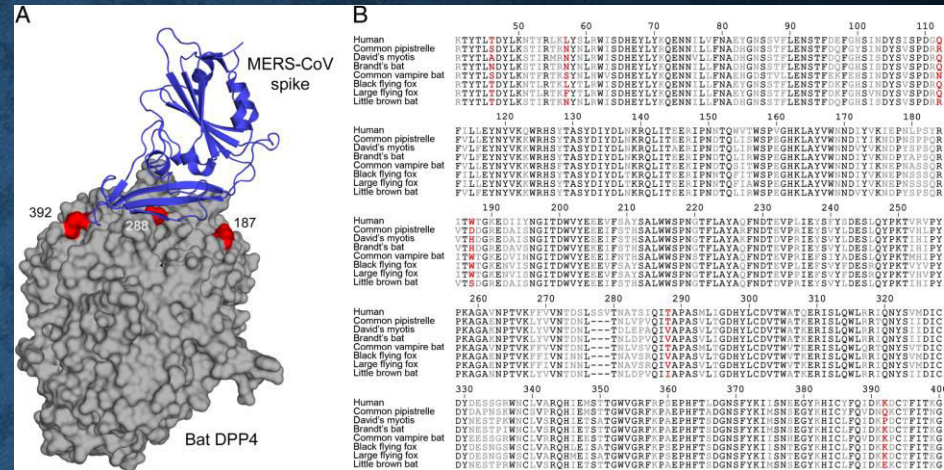
MERS VIRUS DISCOVERED IN BAT NEAR SITE OF OUTBREAK IN SAUDI ARABIA

- Molecular investigation indicated that bats in Saudi Arabia are infected
- with several alphacoronaviruses and betacoronaviruses.
- Virus from 1 bat showed 100% nucleotide identity to virus from the human index case-patient.
- Bats might play a role in human infection.



ORIGIN OF MERS CORONAVIRUS

- newly emerged MERSCoV not only has a bat origin, but also evolved over an extended time period in bat populations before making the leap to infect humans
- Bat DPP4** genes have adapted significantly as they evolved, suggesting a long-term arms race between the bat and the virus.
- Evolutionary footprints in receptor-encoding genes of hosts and their binding domains during long battles with the hosts
 - jumping species boundaries to infect humans, perhaps through an intermediate host**



MERS CORONAVIRUS CAN BE TRANSMITTED FROM CAMEL TO HUMANS

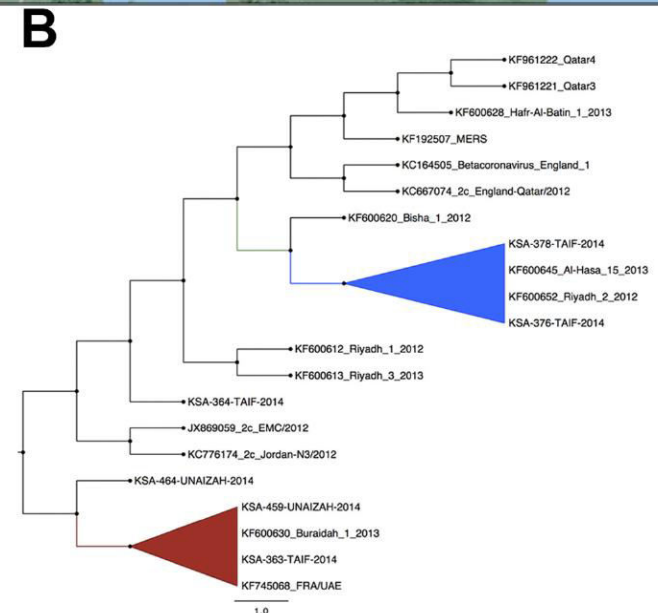
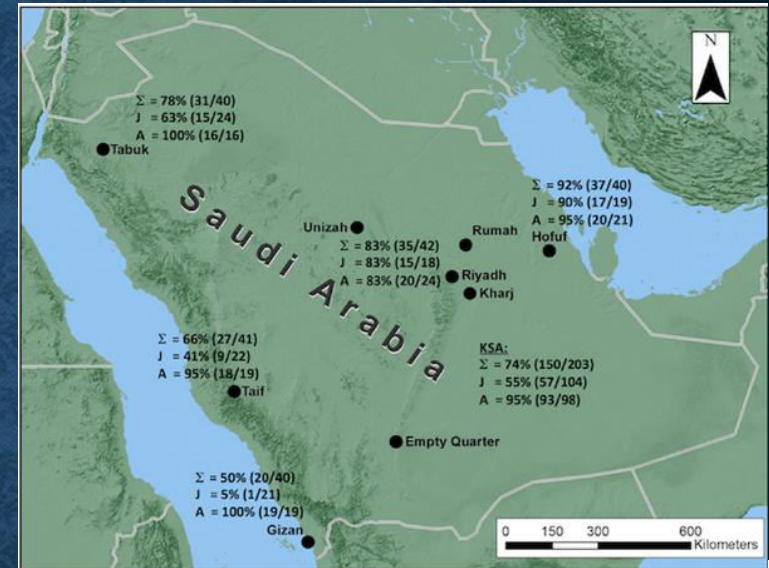
- **Viruses in humans and camels from one region are identical**
 - This indicates transmission between animals and man
 - Virus RNA differs from region to region
- **Transmission pathway through nose and eyes**
 - Virus levels high in the nasal mucosa and conjunctiva of camels
 - Transmission through these contact sites, especially through nasal discharge
- **MERS and SARS coronaviruses are relatives**
 - SARS coronavirus probably passing from bats to humans
 - MERS coronavirus is being constantly transmitted from camels to humans



MERS coronavirus is transmitted not only between animals but also from camels to humans.

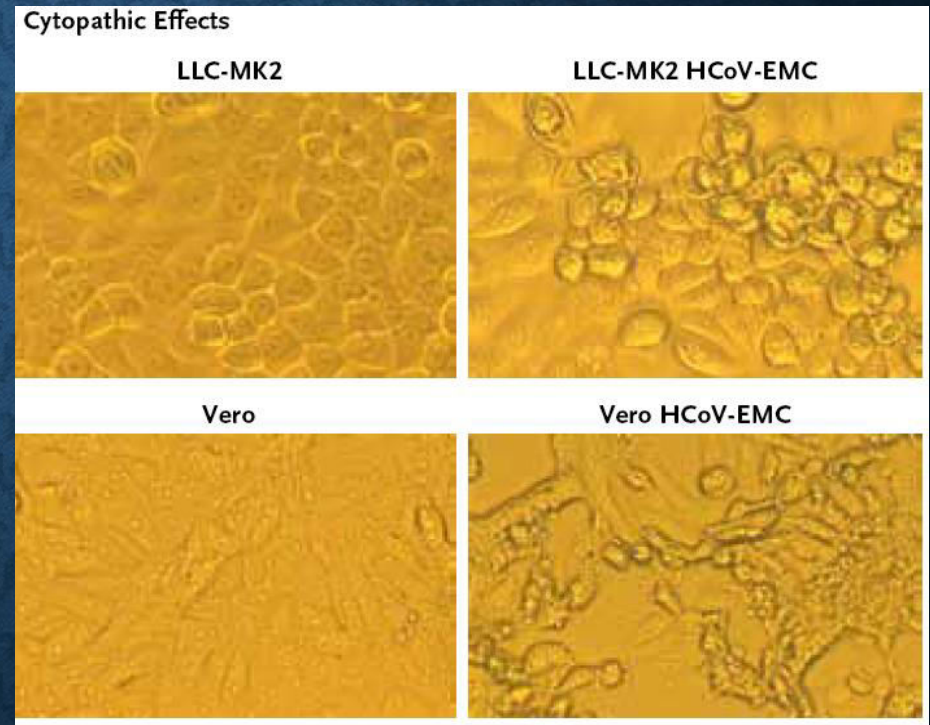
MERS VIRUS WIDESPREAD IN SAUDI ARABIAN CAMELS: CORONAVIRUS HAS BEEN INFECTING THE ANIMALS FOR AT LEAST 20 YEARS

- **Blood samples from dromedary camels taken from 1992 through 2010**
 - **infection in camels typically occurs in early life**
 - **Overall, 74%** of camels sampled
 - **Adult camels** were more likely to have antibodies to the virus (**>80%**)
 - **juveniles** were more likely to have **active virus**.
 - age two or younger the prevalence ranged from **90% in the east** to **5% in the southwest**
 - people get the virus from camels the most likely source is young camels
- **Active virus in nasal swabs in 35% of young camels and 15% of adult camels countrywide**
 - **Less frequently found in rectal swabs and not in blood**
 - **virus most likely is spread by respiratory secretions**



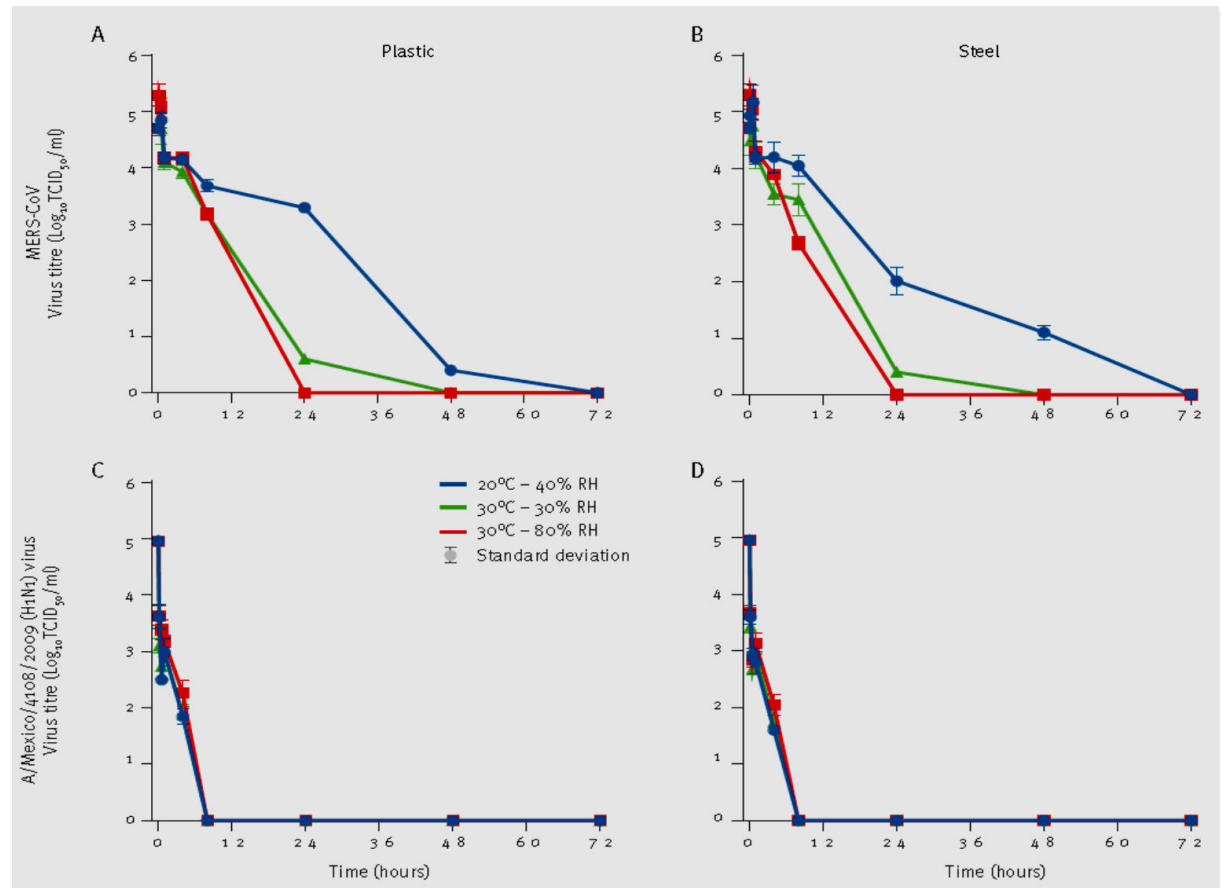
OTHER CHARACTERISTIC OF MERS-COV

- **MERS-CoV** was isolated and propagated relatively easily in Vero B4 and LLC-MK2 cells
 - **SARS-CoV and HCoV-NL63**
 - **Cell Culture:** In certain circumstances, but not routine diagnosis, laboratories with the appropriate experience and containment facilities, may attempt to isolate the virus in cell culture.



STABILITY OF MERS-COV IN ENVIRONMENT

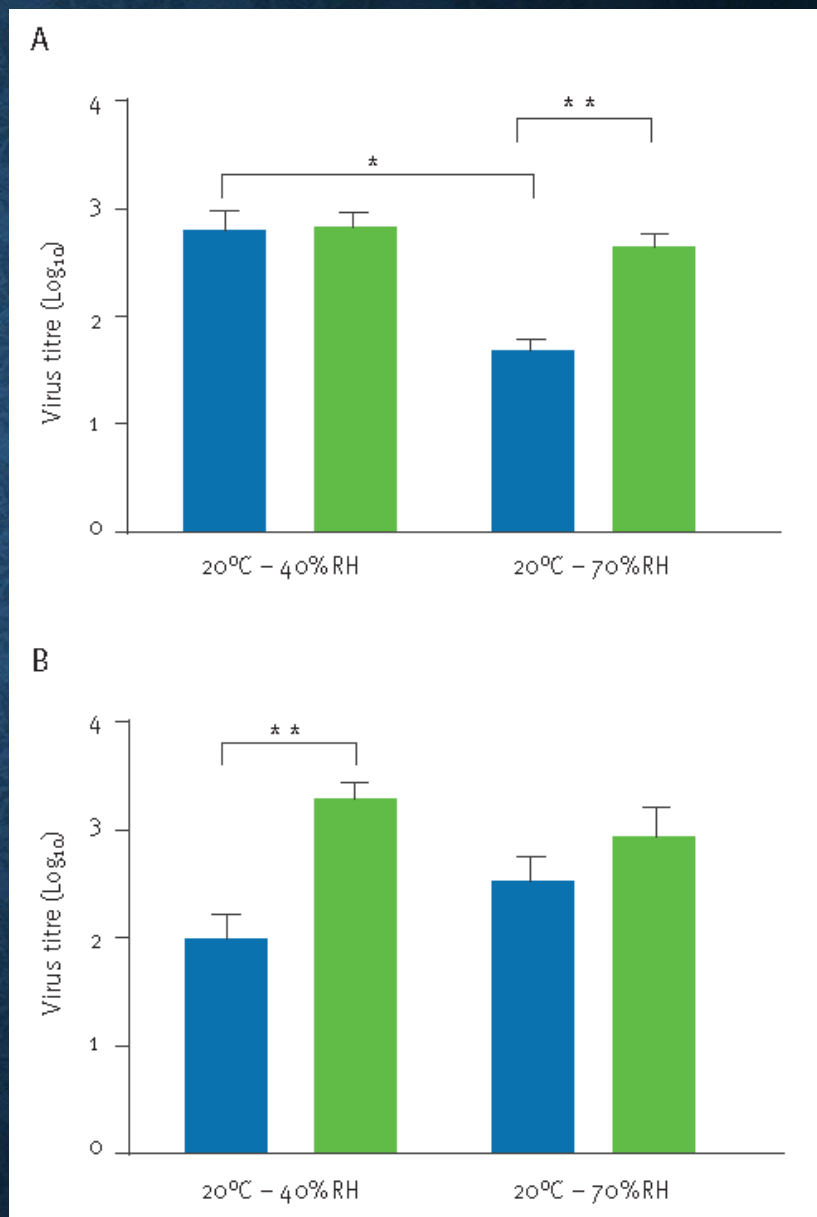
**compared to
A(H1N1)09pdm
MERS-CoV remains
viable for a longer
duration in the
environment**



After four hours no viable A(H1N1)09pdm virus was detected in comparison to 8, 24 or 48 hours for MERS-CoV depending on environmental conditions

STABILITY OF MERS-COV IN ENVIRONMENT

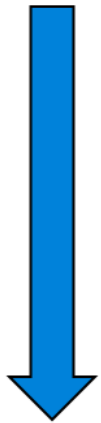
- MERS-CoV was very stable in aerosol form at 20°C – 40% RH.
- The decrease in viability at 20°C – 70% RH (89%) was comparable to that of A(H1N1)09pdm
- MERS-CoV and SARS-CoV share relatively similar stability characteristics
 - SARS-CoV has been reported to stay viable for up to five days at 22 to 25°C and 40 to 50% RH and increase in temperature and humidity resulted in a rapid loss of viability
- The prolonged survival of MERS-CoV compared to A(H1N1)09pdm on surfaces increases the likelihood of contact and fomite transmission.
 - decrease in viability observed at high temperature suggests that direct contact transmission, and not fomite transmission, in the Arabian Peninsula would be the most likely route of zoonotic and human to human transmission in outdoor settings



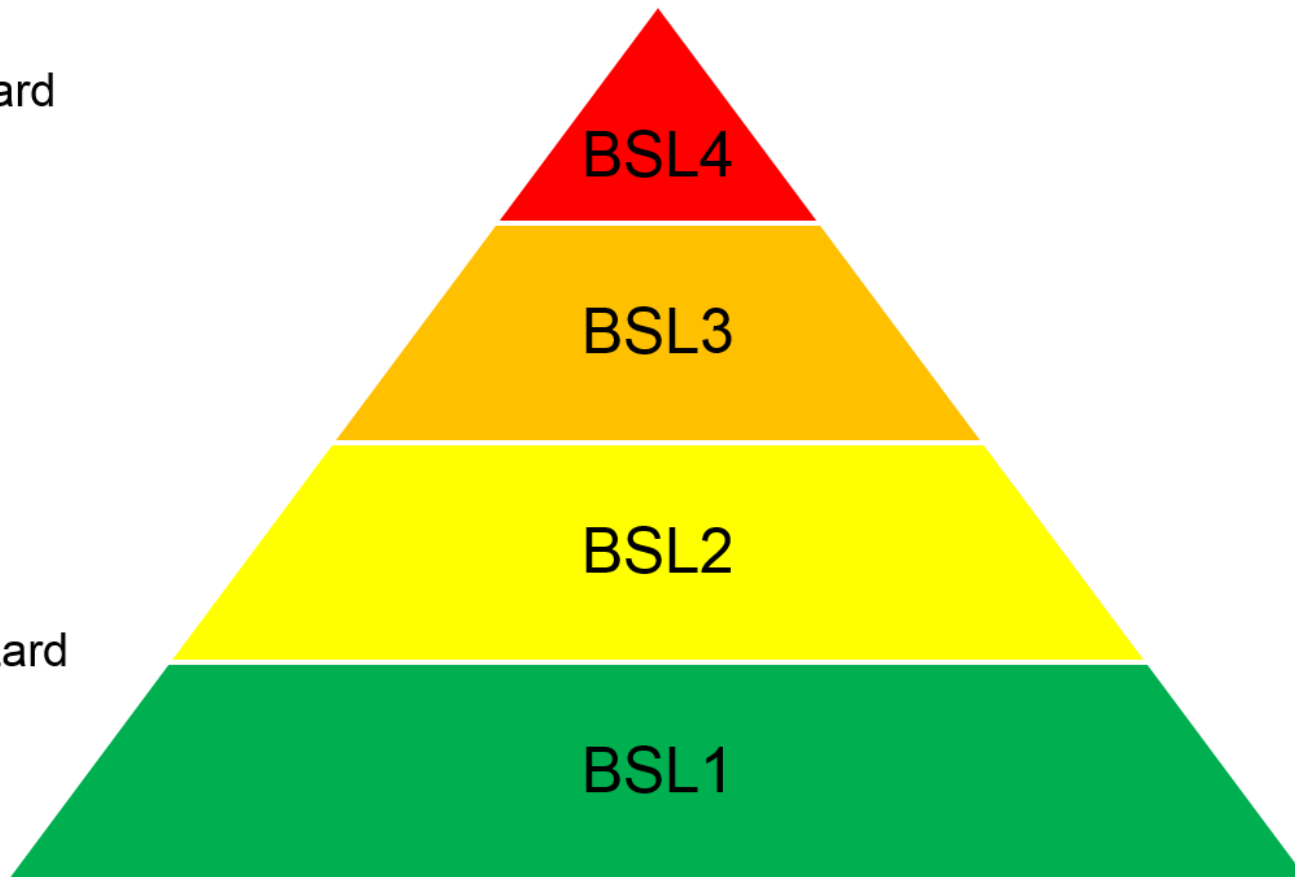
LABORATORY CLASSIFICATION

Containment levels for work will depend on potential exposure to different groups of biological agents.

High hazard



Low hazard



LABORATORY BIORISK MANAGEMENT FOR LABORATORIES

- WHO recommends that all diagnostic laboratory work and PCR analysis on clinical specimens taken from patients who are suspected or confirmed to be infected with MERS coronavirus should be conducted according to practices and procedures described for basic laboratory —
Biosafety Level 2 (BSL2)
- Routine laboratory procedures that require **BSL-2** include:
 - ✓ Diagnostic testing of serum, blood (including haematology and clinical chemistry), respiratory tract specimens, or other specimens;
 - ✓ Manipulations involving neutralized or inactivated (lysed, fixed, or otherwise treated) virus particles and/or incomplete, non-infectious portions of the viral genome.
 - ✓ The reason for working with these types of specimens in a BSL-2 facility is to protect the specimen from contamination and accordingly the quality of the specimen;
 - ✓ Routine examination of mycotic and bacterial cultures developed from respiratory tract specimens.

BSL2

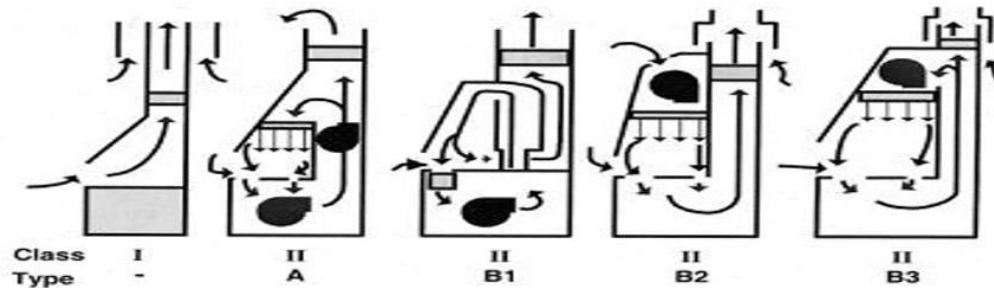
- **PROHIBITED**; Eating, drinking, smoking, applying cosmetics, and handling contact lenses in the laboratory working areas.
- **Personal Protective Equipment (PPE)**
 - masks, respirators, lab coats, etc.
- All manipulations of potentially infectious materials should be performed in appropriately maintained and validated **biological safety cabinets**
 - Use of Class II BSCs should be considered to protect work surface materials as well as personnel and the environment.
- **Appropriate disinfectants**
- **Contaminated waste**

CLASS II BSC

The Class II BSC was designed not only to provide personnel protection but also to protect work surface materials from contaminated room air.

Class II BSCs, of which there are four types:

- Class II type A1
- Class II type A2
- Class II type B1
- Class II type B2



BSC	FACE VELOCITY (m/s)	AIRFLOW (%)		EXHAUST SYSTEM
		RECIRCULATED	EXHAUSTED	
Class Ia	0.36	0	100	Hard duct
Class IIA1	0.38–0.51	70	30	Exhaust to room or thimble connection
Class IIA2 vented to the outside ^a	0.51	70	30	Exhaust to room or thimble connection
Class IIB1 ^a	0.51	30	70	Hard duct
Class IIB2 ^a	0.51	0	100	Hard duct

SPECIMEN COLLECTION AND SHIPMENT

- **Lower respiratory tract specimens ; the highest virus titer**
 - **tracheal aspirates and BAL**
- **Upper respiratory tract specimens recommended**
 - **especially when lower respiratory tract specimens cannot be collected**
- **Paired serum samples** pending the availability of serological assays
 - **collected at least 21 days apart, with the first being collected during the first week of illness**
- **Specimens testing for the novel coronavirus should preferably be tested to exclude the presence of known respiratory pathogens.**
- **Specimens**
 - **should reach the laboratory as soon as possible after collection.**
 - **The importance of proper handling during transportation**
 - **When there is likely to be a delay in the laboratory receiving respiratory tract specimens or serum, it is strongly advised to¹⁹ freeze them on dry ice.**

Types of specimens for testing for the presence of MERS-CoV

Specimen type	Transport medium	Transport to laboratory	Dangerous goods shipping category	Comment
Naturally produced sputum*	no	On ice. If a delay in testing of > 24 hours consider freezing with dry ice	Biological substance, Category B	Need to ensure the material is from the lower respiratory tract
Bronchoalveolar lavage	no	On ice. If a delay in testing of > 24 hours consider freezing with dry ice	As above	There may be some dilution of virus but still a worthwhile specimen
Tracheal aspirate	no	On ice. If a delay in testing of > 24 hours consider freezing with dry ice	As above	
Nasopharyngeal aspirate	no	On ice. If a delay in testing of > 24 hours consider freezing with dry ice	As above	
Combined nose/throat swab	Virus transport medium	On ice.	As above	Virus has been detected in this type of specimen
Nasopharyngeal swab	Virus transport medium	On ice.	As above	
Tissue from biopsy or autopsy including from lung	Virus transport medium or saline	On ice. If a delay in testing of > 24 hours consider freezing with dry ice	As above	
Serum for serology or virus detection: always collect paired samples if possible. Acute – first week of illness	no	On ice or frozen	As above	
Convalescent - ideally 3 to 4 weeks later				
Whole blood	EDTA anticoagulant	On ice	As above	For virus detection, particularly in the first week of illness

- **Category A**

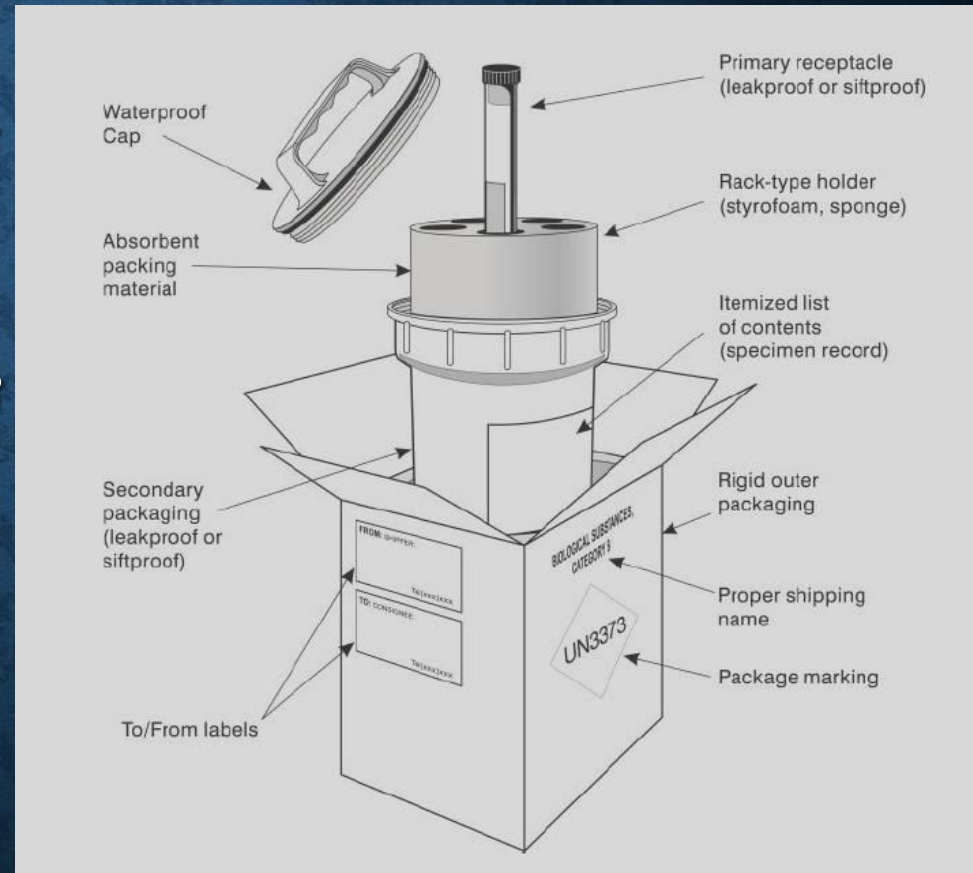
- "suspected category A infectious substance"**



INFECTIOUS SUBSTANCES IN CATEGORY B

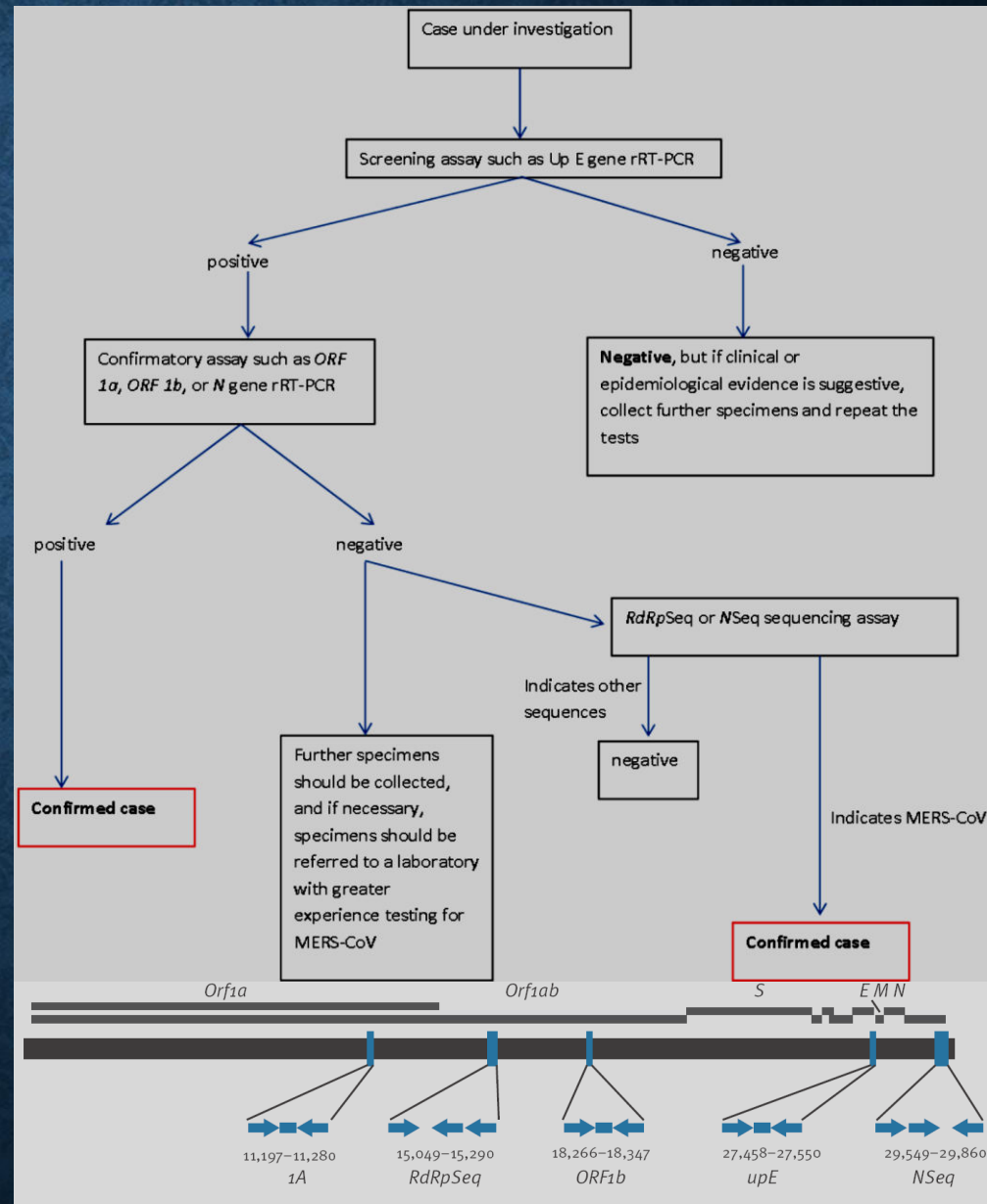
Category B

- *An infectious substance which does not meet the criteria for inclusion in Category A.*
- *Infectious substances in Category B shall be assigned to **UN 3373**.*
- ***NOTE: The proper shipping name of UN 3373 is “BIOLOGICAL SUBSTANCE, CATEGORY B”.***



LABORATORY TESTING METHODS AND ALGORITHM

- **Routine confirmation of cases;** be based on detection of viral RNA by real-time RT-PCR and sequencing.
- **Detection:** RT-PCR assays that are specific for the novel coronavirus
 - **Up-stream E protein gene (*upE*), ORF 1b gene and ORF 1a gene**
 - *upE* target ; highly sensitive,
 - ORF 1a assay ; equal sensitivity
 - ORF 1b assay ;
 - less sensitive than the ORF 1a assay but may be more specific
- **Sequencing:** sequencing to aid confirmation
 - **RNA-dependent RNA polymerase (*RdRp*) and nucleocapsid (*N*) protein genes**
 - sequencing of an amplicon is useful for discordant results with two assays
 - provide valuable information to help understand the origins of the virus
 - sequencing of nucleic acid from as many positive specimens as possible is recommended



RT-PCR false-negative results importance of serological testing

- A number of factors could result in false-negative results, including:
 - ✓ poor quality of specimen, such as a respiratory tract specimen containing primarily oropharyngeal material
 - ✓ the specimen was collected late or very early in the illness
 - ✓ the specimen was not handled and shipped appropriately
 - ✓ technical reasons inherent in the test, e.g., virus mutation or PCR inhibition
- When the clinical presentation and epidemiology suggest an infection with novel coronavirus despite negative PCR results, serological testing may be useful to confirm infection.
 - This highlights the importance of collecting paired serum samples from cases under investigation.

INTERPRETATION OF LABORATORY RESULTS

- positive PCR assays for at least two different specific targets on the novel coronavirus genome

OR

- one positive PCR assay for a specific target on the novel coronavirus genome and an additional different PCR product sequenced, confirming identity to known sequences of the new virus

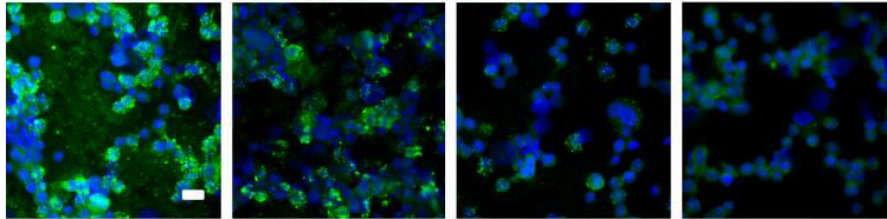
SEROLOGICAL TESTING RECOMMENDATIONS

- **No official recommendations are currently available regarding serological**
- **Currently recommended a two-step diagnostic approach:**
 - **Step 1. Conventional immunofluorescence assay (cIFA)**
 - **Substrate (glass slides): MERS-CoV infected and uninfected Vero cells**
 - **Diagnostic parameters: Immunoglobulin G (Ig)G and IgM in patient serum**
 - **Step 2.**
 - **A) Recombinant IFA (rIFA) using spike protein**
 - **Substrate (glass slides): Transfected Vero cells expressing recombinant spike protein of MERS-CoV. Remark: For differential rIFA prototype humanpathogenic CoV (HCoV-NL63, -229E, -OC43, -HKU-1, SARS-CoV) should be included.**
 - **Diagnostic parameters: Immunoglobulin G (Ig)G and IgM in patient serum**
 - **B) Confirmation by virus plaque reduction neutralization test (PRNT)**
 - **Testing material: Heat-inactivated serum/ dilutions starting at 1:20 until 1:640**
 - **Diagnostic parameter: MERS-CoV neutralizing Ig in patient serum**

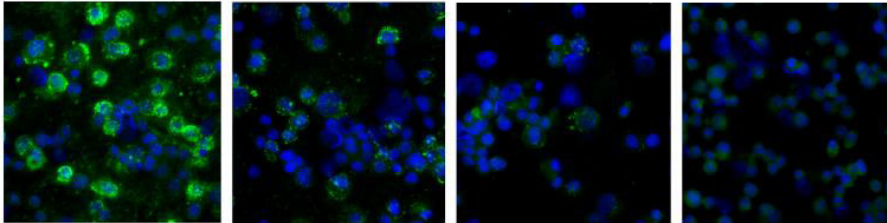
SEROLOGICAL TESTING

Reactivity with hCoV-EMC/2012

1:40 1:100 1:400 1:1600

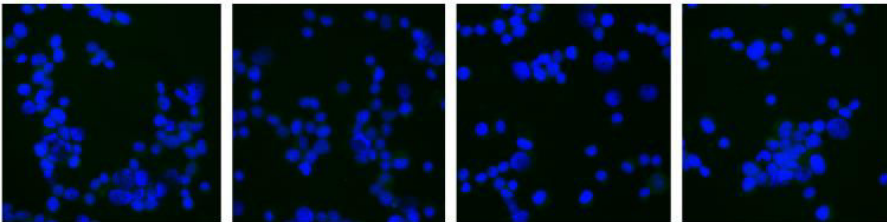


Serum 25/10/12



Serum 23/11/12

Cross-reactivity test with SARS-CoV

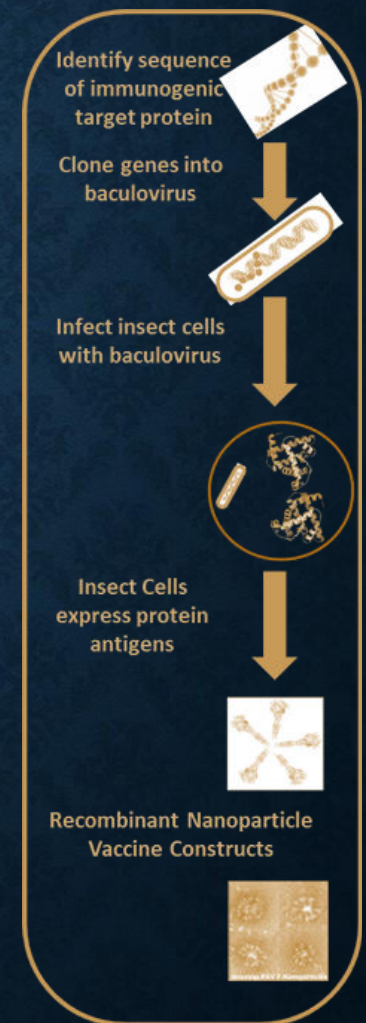


Serum 23/11/12

- The use of IFA is only to be applied in individuals with symptoms according to WHO case definition and a history of proven exposure to a laboratory-confirmed case of MERS-CoV during the infectious period.
 - IFA seroconversions usually began to show from **day 10** of symptoms onward
 - while **virus RNA could not be detected** by RT-PCR in respiratory secretions starting from day 15 onward
- MERS-CoV provides a fine granular cytoplasmatic fluorescence pattern sparing the nucleus.
- IFA will **generate false-positive results** due to cross-reactivity between anti-HCoV antibodies. **such as OC43 and HKU1?**
 - impossible to discriminate cross-reactive antibodies by IFA

MERS-COV VACCINE CANDIDATE

- **Novavax** on **June , 2013** announced that it had successfully produced a vaccine candidate designed to provide protection against the recently emerging MERS-CoV.
- The vaccine candidate was made using **Novavax** nanoparticle vaccine technology, is based on the major **surface spike (S) protein**.
- **Novavax** believes that MERS-CoV vaccine candidate may provide a path forward for a vaccine for this emerging threat.



REFERENCES

- [Abdulaziz N. , et al. 2014. Middle East Respiratory Syndrome Coronavirus Infection in Dromedary Camels in Saudi Arabia. *mBio*.](#)
- [Chantal BEM Reusken , et al. 2013;.Middle East respiratory syndrome coronavirus neutralising serum antibodies in dromedary camels: a comparative serological study. *The Lancet Infectious Diseases*, 13 \(10\)](#)
- [Corman VM, et al. 2012. Detection of a novel human coronavirus by real-time reverse-transcription polymerase chain reaction. *Euro Surveill* 17: pii=20285.](#)
- [Corman VM, et al. 2012. Assays for laboratory confirmation of novel human coronavirus \(hCoV-EMC\) infections. *Euro Surveill* 17\(49\):pii=20334.](#)
- [CWA15793 Laboratory Biorisk Management, 2011](#)
- [Jie Cui, et al. 2013. Adaptive evolution of bat dipeptidyl peptidase 4 \(dpp4\): implications for the origin and emergence of Middle East respiratory syndrome coronavirus. *Virology Journal*, October 2013](#)
- [Ndapewa Laudika Ithete, et al. Close Relative of Human Middle East Respiratory Syndrome Coronavirus in Bat, South Africa. *Emerging Infectious Diseases*, 2013; 19 \(10\)](#)
- [Van Boheemen S, et al. 2012. Genomic characterization of a newly discovered coronavirus associated with acute respiratory distress syndrome in humans. *mBio* 3\(6\): e00473-12. doi:10.1128/mBio.00473-12.](#)
- [WHO Laboratory Biosafety Manual, 3rd edition, 2004](#)
- [WHO Guidance on regulations for the Transport of Infectious Substances 2013-2014 \(Applicable as from 1 January 2013\)](#)
- [WHO Laboratory testing for novel coronavirus , Interim recommendations , 21 December 2012](#)
- [Ziad A. et al. 2013. Middle East Respiratory Syndrome Coronavirus in Bats, Saudi Arabia. *Emerging Infectious Diseases*, 2013; 19 \(11\).](#)

