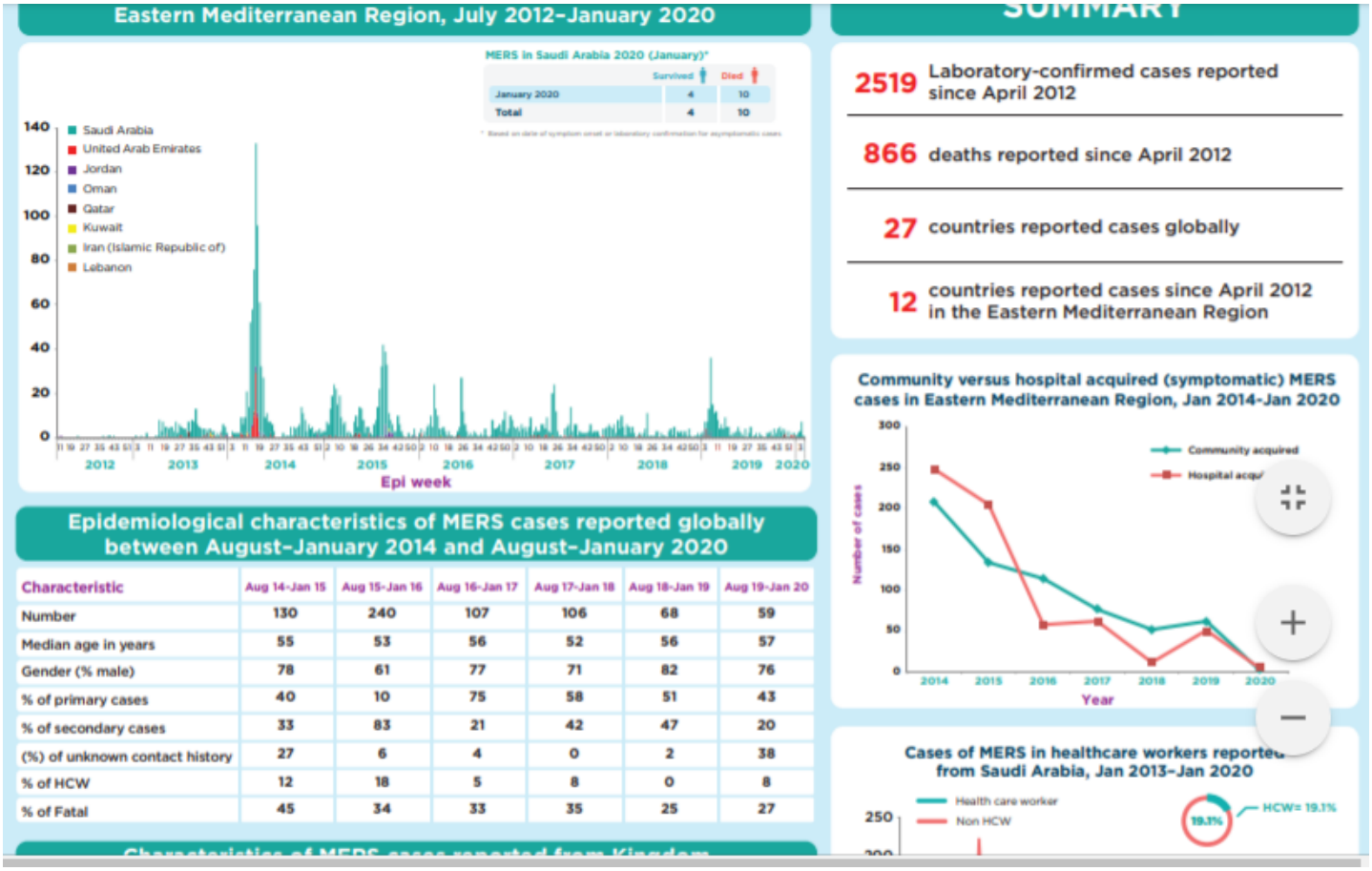
Twitter Thread by Billy Bostickson ■■&■ ■

Billy Bostickson ■■&■ ■
@BillyBostickson

@NCPV @Micro_MDPI Can you comment on Professor Gallaher's statement concerning the possibility of SARS-COV-2 recombining with

@Pirbright_Inst @NCPV @Micro_MDPI Gallaher's "Prophecy" Is it Likely?
MERS + SARS-COV-2 Combo Event
MERS Situation Update - January 2020
https://t.co/K2AB0fTpJT
SA Cases:
https://t.co/ix083ozN0v
UAE Cases:
https://t.co/eCBVg3oSPo



@Pirbright_Inst @NCPV @Micro_MDPI 1. "Specificity of S is largely responsible for widespread & rapid communicability of SARS-CoV-2, with relatively low virulence in most infected; in contrast, spread of MERS is more easily contained, but its virulence is much higher, at 35%."

@Pirbright_Inst @NCPV @Micro_MDPI 2. A virus with high communicability of SARS-CoV-2 & the virulence of MERS would be apocalyptic in its impact!
There is a breakpoint sequence in MERS S (25215CAGAT) that is similarly very close in relative position to 25047CAGAT in SARS-CoV-2.....

@Pirbright_Inst @NCPV @Micro_MDPI 3. There is a 4th breakpoint sequence, between the receptor binding domain of MERS & the S1/S2 junction, that is precisely conserved in sequence & position with the corresponding location of SARS-CoV-2:
23577CAGAC in MERS
23300CAGAC in SARS-CoV-2

@Pirbright_Inst @NCPV @Micro_MDPI 4. This breakpoint, is identical in both viruses at the same relative position in the S1 protein sequence, where it defines an identical dipeptide, QT
(see underlined section in the PDF)
https://t.co/Glh98zcbWP

@Pirbright_Inst @NCPV @Micro_MDPI 5. There is potential, based on closely apposed or identical breakpoint sequences, that the bulk of the S1A and S1B domains of the S1 attachemnt subunit could be exchanged between MERS and SARS-CoV-2 in any mixed infection.

@Pirbright_Inst @NCPV @Micro_MDPI 6. While there is no indication that this has occurred in the wild, during the SARS-CoV-2 pandemic we face the unique situation of SARS-CoV-2 being present simultaneously in a substantial number of human beings worldwide.

@Pirbright_Inst @NCPV @Micro_MDPI 7. Simultaneous outbreaks of MERS, within or without areas where it has been found prevalent, could produce mixed infections in humans that we know have resulted in frequent recombination among Covs in the wild or in captive populations of animals.

@Pirbright_Inst @NCPV @Micro_MDPI 8. To the viruses, there is no known theoretical difference!
"Public health authorities should especially guard against simultaneous spread of more than one coronavirus in the human population at the same time & location"
https://t.co/O2CHJQVCXP