Widespread outbreak of Middle East Respiratory Syndrome Coronavirus in a camel cohort and associated spillover to humans in Kenya

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Middle East Respiratory Syndrome Coronavirus (MERS-CoV) is known to be endemic in dromedary camels including Kenya's >3 million camels. We studied MERS-CoV infection in camels and people who work closely with camels and found widespread circulation of the virus which also affected the camel handlers. This study adds to our knowledge of MERS-CoV infection in camels and the public health threat it poses to humans who work closely with camels.

Abstract Reference

PP15

BACKGROUND

- Among the recently emergent coronaviruses of global public health concern that include severe acute respiratory syndrome coronavirus (SARS-CoV), Middle East Respiratory Syndrome Coronavirus (MERS-CoV), and SARS-CoV-2, only MERS-CoV has a domestic animal reservoir that serves as the primary source of human infections
- MERS-CoV is an emerging coronavirus that is endemic in dromedary camels, most of which reside in the Horn of Africa
- Kenya's >3 million camels have high seroprevalence of antibodies against MERS-CoV, with scant evidence of human infection, possibly due to a lower zoonotic potential of Clade C viruses, predominantly found in African camels.

METHODS

- Between April 2018- March 2020, we followed camels aged 0-24 months from 33 camel-keeping homesteads within 50Km of Marsabit town through collecting deep nasal swabs and documenting signs of illness in camels every two weeks (**Fig 1**)

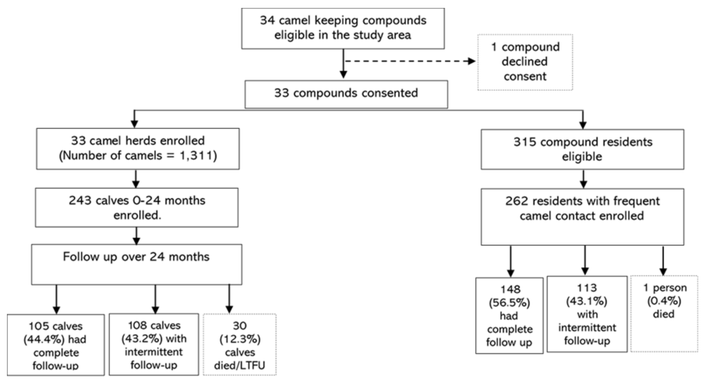

Figure 1: *Study flow chart showing screening, enrollment and follow-up of the linked camel-human cohort. LTFU- Loss to follow up. Intermittent follow-up was defined as calves/persons who missed intermediate study visits but were available for subsequent visits or final sample collection at the end of the study period*

- Swabs were screened for MERS-CoV by reverse transcriptase (RT)-polymerase chain reaction (PCR) testing and virus isolation performed on PCR positive samples with cycle threshold (CT) <20
- Both the isolates and swab samples (CT <30) were subjected to whole genome sequencing. Human camel handlers were also swabbed monthly and samples screened for MERS-CoV by RT-PCR.

RESULTS

- On average, the study achieved 9.1 follow up visits per calf with 105 calves (44.4%) reporting complete follow up, while 108 calves (43.2%) were available intermittently over the study period **(fig 1)**
- Among 243 calves, 68 illnesses were recorded in 58 camels (53.9%); 50/68 (73.5%) of illnesses were recorded in 2019, and 39 (57.3%) were respiratory symptoms (nasal discharge, hyperlacrimation and coughing)- **fig 2**

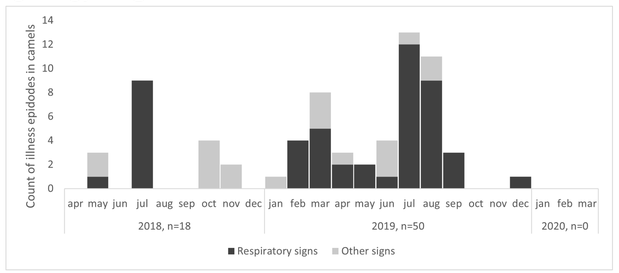

Figure 2*: Counts of clinical signs reported in camel calves during the 2 year-follow up period. The majority of clinical signs (50/68) were recorded in 2019 as shown with peaks in March and July and mainly comprised respiratory illness signs such as nasal discharge (28/50 or 56%), increased lacrimation (12/50 or 24%) and coughing/honking (7/50 or 14%)*

- A total of 124/4,702 camel swabs (2.6%) from 83 (34.2%) calves in 15 (45.5%) of enrolled compounds and 3/1,369 human swabs (1.1%) were positive for MERS-CoV RNA by RT-PCR
- Camel MERS-CoV cases were detected between May-September 2019 with three infection peaks, a similar period when three human PCR-positive asymptomatic cases were detected among camel handlers in these herds- **fig 3 and 4**

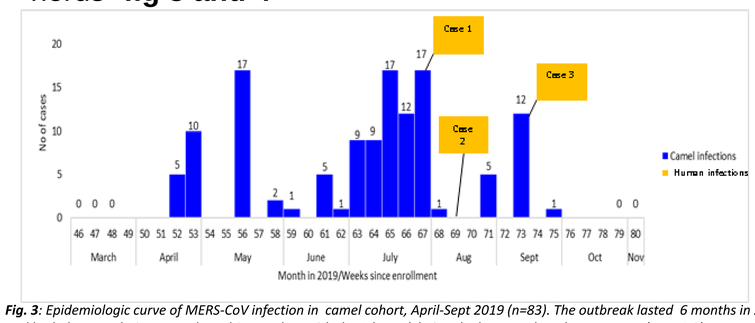

Fig. 3*: Epidemiologic curve of MERS-CoV infection in camel cohort, April-Sept 2019 (n=83). The outbreak lasted 6 months in 2019 and had three peaks in May, July and September, with the July peak being the largest. Three human cases (case 1-3) were detected in July, August and September*

- Sequencing of camel specimens revealed a Clade C2 virus with identical 12 nucleotide deletion at the 3' end of OFR3 region and one nucleotide insertion at the 5' region but lacked the signature ORF4b deletions of other Clade C viruses- **fig 5, 6 and 7**

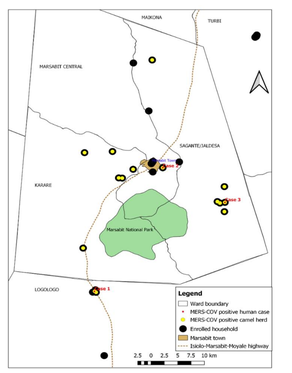

Figure. 4*: Spot-map of the study area showing location of enrolled camel herds (black spots), herds involved in the MERS-CoV outbreak (yellow spots) and human infections (red dots). The three human MERS-CoV infections clustered with camel infections*

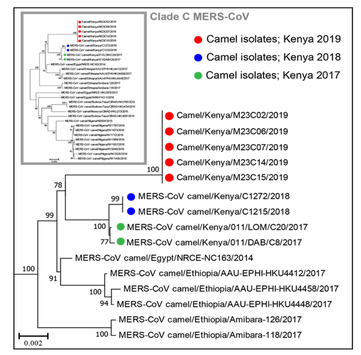

Figure 5. *Phylogenetic tree of camel-derived MERS-CoV sequences from Clade C. The sequences indicated by the green and blue colored dots were isolated from camels in Kenya in earlier studies. Sequences denoted by the red dots were isolated from our study*

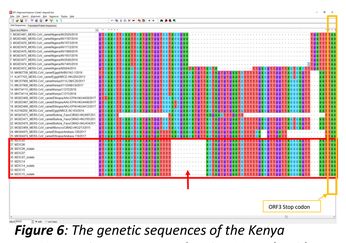

Figure 6*: The genetic sequences of the Kenya MERS-CoV virus sequences showing 12 nucleotide insertions at the 3' region of the ORF (arrow)*

figure 7: The genetic sequences of the Kenya MERS-CoV virus sequences showing 1 nucleotide insertion at the 5' uncoding region (arrow)

CONCLUSIONS

- We found high levels of transmission of distinct Clade C MERS-CoV among camels in Northern Kenya, with likely spillover infection to humans
- These findings update our understanding of MERS-CoV epidemiology in this region with possible implications for human morbidity and mortality.

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MORE INFORMATION / REFERENCES

1. Munyua PM, Ngere I, Hunsperger E, et al. Low-Level Middle East Respiratory Coronavirus Syndrome among Camel Handlers, Kenya, 2019 - Volume 27, Number 4—April 2021 - Emerging Infectious Diseases journal - CDC. DOI:10.3201/eid2704.204458
2. Ngere I, Munyua P, Harcourt J, et al. High MERS-CoV seropositivity associated with camel herd profile, husbandry practices and household socio-demographic characteristics in Northern Kenya. Epidemiol Infect undefined/ed; : 1–31

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