

Genetically distinct Middle East respiratory syndrome coronavirus variants from dromedary camels in Kenya

Brian M. Ogoti*¹, Victor Riitho*^{1,5}, Johanna Wildemann*², Nyamai Mutono^{1,6}, Julia Tesch², Jordi Rodon², Kaneemozhe Harichandran², Jackson Emanuel², Elisabeth Möncke-Buchner², Stella Kiambi⁷, Julius Oyugi¹, Marianne Mureithi¹, Victor M. Corman^{2,3,4}, Christian Drosten^{2,3}, Samuel M. Thumbi*^{1,6,8}, Marcel A. Müller*^{2,3} *contributed equally

¹University of Nairobi, Nairobi, Kenya; ²Charité – Universitätsmedizin Berlin, Berlin, Germany; ³German Center for Infection Research, Berlin, Germany; ⁴Labor Berlin–Charité Vivantes GmbH, Berlin, Germany; ⁵Queen Mary University of London, London, United Kingdom; ⁶Washington State University, Pullman, WA, United States; ⁷Food and Agriculture Organization (FAO), Dar es Salaam, Tanzania; ⁸University of Edinburgh, Edinburgh, United Kingdom

Background information

- Middle East respiratory syndrome coronavirus (MERS-CoV) is endemic in dromedary camels from the Arabian Peninsula and Africa with comparably high seroprevalence of >75%.
- Migration patterns, loss of maternal antibodies in calves, population density, seasonality might be linked to acute MERS-CoV outbreaks in camel populations.
- Field studies on nomadic camels are hampered by limited infrastructures in remote and resource-restricted regions of camel migration but nomadic camels are regularly transported to abattoir hubs enabling sustained regular testing.

Aim of the study

- Investigation of MERS-CoV incidence and genomic diversity in nomadic camels in Northern Kenya.

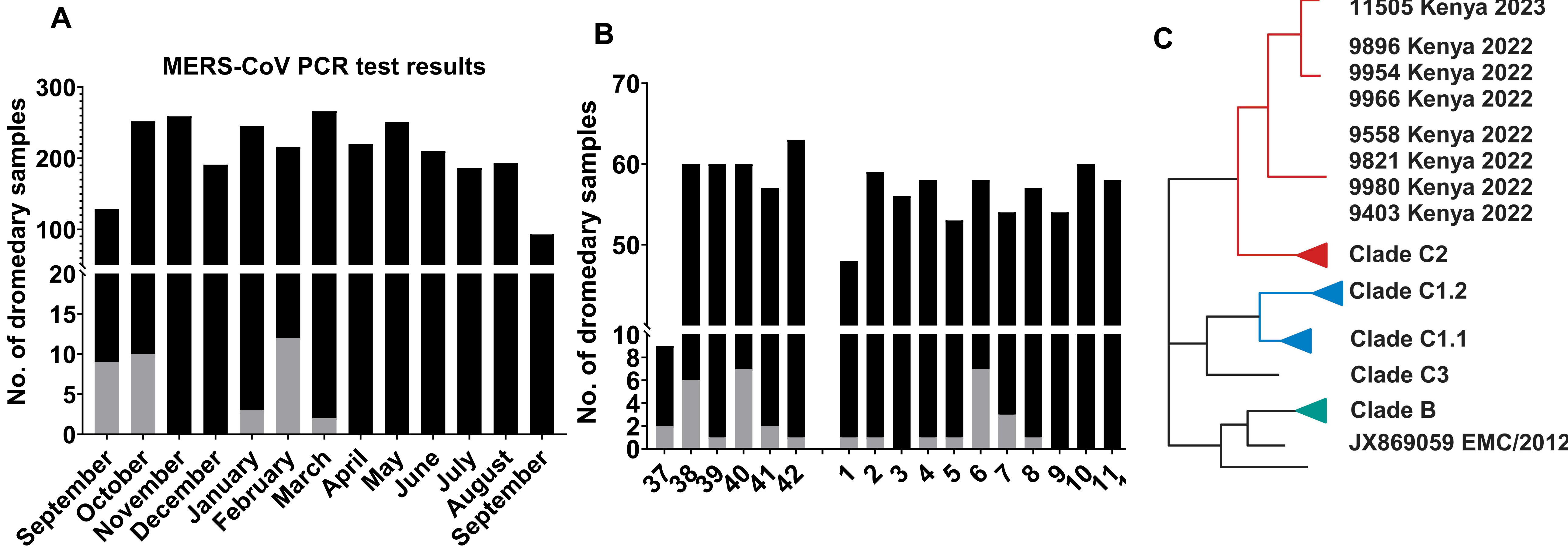
Methodology

- Sustained sampling of dromedary camels in an abattoir hub of Marsabit, Samburu, and Isiolo (Northern Kenya).
- Sampling of nasal swabs from 10-15 camels 3-4 days/week from Sept. 2022 – Sept. 2023 (total n=2,711).
- Sample testing for acute infections: UpE & ORF1a RT-qPCR.
- Generation of ORF1ab genomes from RNA samples with >1x10⁶ genome copies/mL using Illumina NGS
- MERS-CoV genome ORF1ab assembly and phylogenetic analysis.

Acknowledgement



Results (main findings)



A) MERS-CoV RNA detection rates in nasal swabs from dromedary camels were tested by the MERS-CoV upE RT-qPCR assay. **B)** Detailed weekly overview of months with MERS-CoV RNA detections. The cumulative MERS-CoV RNA positivity rate was higher in September–October 2022 with 19/381 (5.0%) compared to 17/727 (2.3%) in January–March 2023. **C)** Schematic phylogeny of MERS-CoV including newly identified MERS-CoV cladeC2.2 strains 2022–2023. The 9 ORF1ab sequences were highly similar (>99.93% nucleotide identity) and had 99.75–99.78% nucleotide identity with the closest MERS-CoV relative identified in Akaki, Ethiopia, in 2019

Conclusion

- Our sustained sampling of dromedary camels over 12 months showed a biphasic MERS-CoV incidence in an abattoir hub in Northern Kenya and MERS-CoV RNA was detected in 36 of 2711 (1.3%) nasal swabs.
- Phylogenetic analysis suggests at least 3 independent MERS-CoV clusters over 3 different weeks in dromedaries.

Recommendations

- Identification of defined factors driving MERS-CoV outbreaks in nomadic camels will assist in predictive epidemiology and genomic surveillance in African dromedaries will aid in understanding their diversity.