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Epidemiology and genomic features of MERS coronavirus in Africa: A systematic and meta-analysis review

Bibliography

Ogoti B, Riitho V, Wildemann J, Mutono N, Mureithi M, Oyugi J, Rodon J, Corman VM, Drosten C, Thumbi SM, Müller MA. Epidemiology and genomic features of MERS coronavirus in Africa: a systematic and meta-analysis review. *Int J Infect Dis.* 2026;165:108456.

Summary

This systematic review and meta-analysis examined why human MERS-CoV infection appears rare in Africa despite widespread infection in dromedary camels. Following PRISMA guidelines and a registered protocol, the authors searched major databases up to August 2025 for epidemiologic and virologic studies of MERS-CoV in African humans and camels. Fifty-three studies met inclusion criteria; 31 contributed to quantitative synthesis. Most were cross-sectional and concentrated in East Africa, particularly Kenya, Egypt, and Ethiopia. Using generalized linear mixed-effects models, the authors estimated pooled proportions for viral RNA positivity and seroprevalence, with stratified analyses by age group, region, and study characteristics, and assessed heterogeneity, publication bias, and robustness via sensitivity analyses. In parallel, they compiled all publicly available clade C MERS-CoV sequences from Africa and performed comparative polymorphism analyses of Spike and accessory proteins against the prototypic EMC/2012 strain and contemporary Arabian clade B5 viruses, focusing on high-frequency, regionally conserved amino acid substitutions.

In dromedaries, pooled MERS-CoV RNA positivity was 6.09%, with markedly higher detection in juveniles under two years (15.29%) than adults (4.51%), and higher RNA positivity in North than West or East Africa. Serologically, overall camel seroprevalence reached 73.67%, with adults showing about 81% and juveniles 36%, consistent with cumulative exposure and waning maternal antibodies. Camel age emerged as a significant predictor of seropositivity, whereas region and setting did not. Human data were far sparser: across 17 human-focused studies, only nine PCR-confirmed MERS cases were documented (six travel related, three autochthonous), yet pooled human seroprevalence based on ELISA screening was 2.4%, suggesting substantial under-recognized or subclinical infection among camel-exposed populations. The authors posit that surveillance limitations, differences in camel husbandry and slaughter practices, and health system constraints likely contribute to under ascertainment.

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Genomic analysis of African clade C viruses revealed a suite of characteristic polymorphisms in Spike and accessory proteins that may attenuate zoonotic potential. In Spike, conserved substitutions in the N-terminal domain (V26A, H194Y), receptor-binding domain (e.g., S390F, L450F, L495F/P), S1/S2 region (R626P), and S2 heptad repeat (A1163L/S) could modulate sialic acid or DPP4 binding, protease cleavage, and membrane fusion, possibly favoring camel-to-camel transmission over human infection. Accessory gene changes, including recurrent substitutions and deletions in ORF3, ORF4a, ORF4b, and ORF5, may alter interferon antagonism and innate immune evasion, consistent with previously observed reduced replicative fitness and pathogenicity of clade C strains in vitro and in animal models. The authors stress that these functional interpretations remain hypothesis-generating and require experimental validation. They conclude that Africa’s “apparent paradox” of high camel endemicity, but low recognized human disease likely reflects a combination of viral attenuation, ecological and husbandry differences, and major surveillance gaps. Ongoing evolution, recombination with clade B viruses in traded camels, and recent detection of a clade B lineage in Africa underscore the need for strengthened One Health-oriented genomic and seroepidemiologic surveillance to detect emergence of more human-adapted variants.

Comment

This review is methodologically robust and conceptually important, integrating epidemiology with genomics to explain regional differences in MERS risk. However, it remains constrained by substantial heterogeneity, heavy geographic concentration of data in a few countries, and reliance on cross-sectional and ELISA-based serosurveys that may over- or under-estimate true human exposure. The genomic inferences about attenuated zoonotic potential of clade C strains are plausible but still speculative without targeted phenotypic studies. Strengthening longitudinal human and camel surveillance, including standardized serologic cutoffs and functional characterization of key polymorphisms, will be essential to refine risk assessments as MERS-CoV continues to evolve at the human–animal interface.

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