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Human MERS-CoV cases are falling but pose an ongoing pandemic threat

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Human cases of Middle East respiratory syndrome coronavirus (MERS-CoV) have declined in recent years, but continued surveillance and research is needed to understand this trend and mitigate future zoonotic threats.

Since its emergence in 2012, MERS-CoV has remained an endemic zoonotic pathogen in the Arabian Peninsula; most human cases come from the Kingdom of Saudi Arabia (KSA), where dromedary camels serve as the primary reservoir[1]. MERS-CoV can be classified by sequence analysis into three clades (clades A, B and C), each of which branches into more granular lineages that are continuing to evolve[2]. In addition to these lineages, circulating recombinant forms have emerged; there is limited knowledge on how the observed genomic diversity translates to specific viral traits[3]. To date, over 2,600 laboratory-confirmed human cases have been reported globally, with a crude case–fatality ratio of approximately 37%. MERS-CoV spreads in strikingly different ways across regions. In Africa, clade C dominates, but human Middle East respiratory syndrome (MERS) has so far not been officially reported – although there is increasing evidence that human infection is taking place[4]. In the Middle East, clade B drives frequent camel-to-human MERS-CoV infections, which intensify during calving season. Although laboratory evidence suggests clade differences in relation to virulence and infectivity, it remains unclear why these patterns diverge.

Recent years have seen a sharp decline in the number of human MERS-CoV cases reported from the Middle East, which raises questions about potential epidemiological shifts (Fig. 1).

Cross-protection from COVID-19 immunity

It has been hypothesized that widespread SARS-CoV-2 infection and vaccination may have indirectly contributed to reduced zoonotic MERS-CoV acquisition, or attenuation of symptoms. Studies suggest the presence of cross-reactive antibodies targeting the conserved S2 domain of the spike protein and robust T cell responses that could provide partial immunity[5,6]. Vaccination against COVID-19 has been shown to boost and reshape long-term humoral immune memory from previous MERS-CoV infection[6]. Broader evidence on SARS-CoV-2 and other seasonal coronaviruses also suggests the existence of some cross-protection[7]. The latter may help to mitigate the severity of infections or reduce susceptibility among individuals who are frequently exposed to camels.

Reduced zoonotic and human-to-human transmission via behavioural changes

Although no formal public health interventions targeted camel handlers specifically, several COVID-19-related factors – including increased mask use, heightened hygiene awareness and general infection-prevention behaviours – may have contributed to reduced MERS-CoV exposure in humans during the pandemic. In addition, travel restrictions and the cancellation of camel racing and related events, which are known to be a risk factor for MERS-CoV infection[8], probably limited camel movement and decreased opportunities for human–camel contact during this period.

These behaviours remain poorly documented and require further study. However, if behavioural changes were the primary driver, one would expect MERS-CoV cases to rebound following relaxation of COVID-19 public health measures. The majority of laboratory-confirmed MERS-CoV cases stem from nosocomial transmission in healthcare settings between 2013 and 2019, including large hospital outbreaks in the KSA, the United Arab Emirates (UAE) and South Korea[9,10]. Improved infection control guidelines with regards to aerosol-generating medical procedures may have resulted in substantially reduced nosocomial transmission potential (Fig. 1).

Attenuation of viral virulence and transmission potential

Current sequencing and virological data do not support the conclusion of reduced MERS-CoV virulence. Although full genome analyses are ongoing, preliminary in vitro studies show no evidence of attenuation[11]. However, there is a large variety in phenotypes of different MERS-CoV isolates observed in vitro and in vivo, with differential growth kinetics in human respiratory cells as well as distinct pathogenic phenotypes in a transgenic hDPP4 mouse model[12]. In contrast to SARS-CoV-2, limited information is available on the mechanistic drivers of transmission in animal models. Systematic mapping of functional traits such as replication efficiency, host range or immune antagonism across the

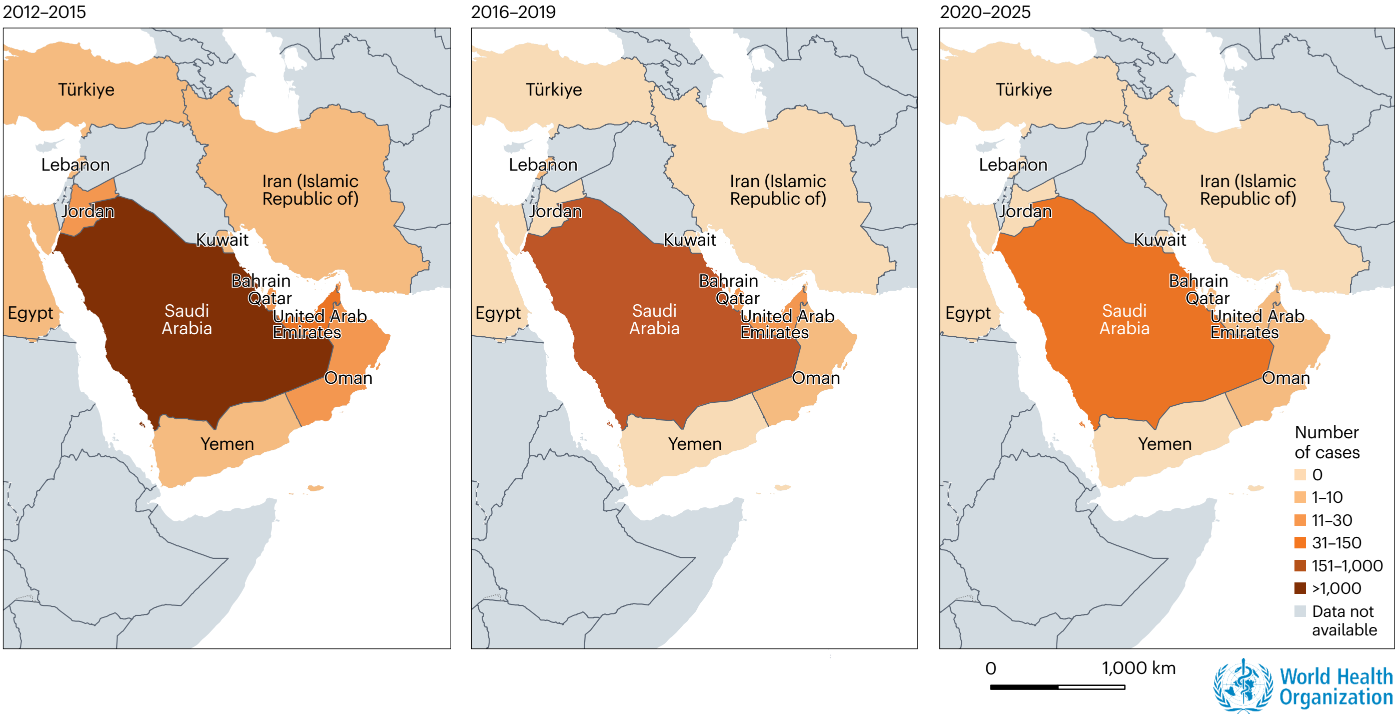

Fig. 1 | Trends in MERS-CoV cases over time in the Arabian Peninsula. The cumulative number of cases of MERS-CoV during three time periods (2012–2015, 2016–2019 and 2020–2025) are shown. The designations used and the presentation of the material in this publication do not imply the expression of any opinion whatsoever on the part of the WHO concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement. Source: WHO. Credit: WHO Health Emergencies Programme.

Merbecovirus genome is essential to identify mutations that could drive attenuation or altered zoonotic potential. Differences in replication dynamics have previously been invoked to explain the lower human transmissibility of clade C viruses compared with clade B, and even single amino acid changes can markedly alter replication efficiency in human cells[13]. Notably, clade B has recently been identified in African camel populations[14], which highlights the risk of introduction from the Arabian Peninsula and further spread within Africa in light of its potential growth advantage over clade C.

Assessing effect of genetic differences is further hampered by the lack of data on the effect of pre-existing comorbidities such as obesity or type 2 diabetes in the context of animal models. In nonhuman-primate models, MERS-CoV typically displays itself as a mild-to-moderate transient lower respiratory tract infection, which suggests that pre-existing comorbidities such as immunosuppression, obesity, diabetes or chronic lung disease may have a substantial effect on pathogenicity and the clinical outcome[15].

Reduced surveillance in humans

MERS continues to be a notifiable disease in the KSA and under the International Health Regulations, with established diagnostic infrastructure and mandatory reporting systems. There is no indication that decreased surveillance or underreporting is responsible for the decline in human cases. In 2023, the KSA added MERS-CoV testing to its integrated respiratory surveillance (which already included SARS-CoV-2, respiratory syncytial virus and influenza virus) and started to test all severe acute respiratory infections as well as over 80% of influenza-like illness cases. As many as 27,108 patients in 2024 and 16,744 patients in 2025 (as of May) were tested for MERS-CoV in the KSA, corresponding to 0.03% and 0.05% MERS-CoV detection rates for 2024 and 2025, respectively. Similarly, all severe acute respiratory infection samples have been tested for MERS-CoV since 2019 in the UAE, and strong contact-tracing systems are in place in both countries. The latest case in the UAE was reported in April 2023 and was an isolated case that did not cause secondary cases. There were five unrelated cases in 2023 and eight cases in 2024 (three of which were secondary cases) reported by the KSA. In 2025 and as of December, the KSA has reported 17 cases of MERS-CoV infection, including four deaths, and six of the cases (of which four were asymptomatic) were contacts of one of the cases.

Reduction of circulation in camels

The notion that reduced MERS-CoV incidence is due to reduction of virus circulation in camels is not supported by recent evidence. Surveillance conducted in the KSA from late 2023 through early 2024 revealed that 39% of over 550 camel nasal swabs collected from camel local farms tested positive for MERS-CoV RNA[11]. These findings confirm that the MERS-CoV remains enzootic and capable of zoonotic spillover. It should be noted, however, that surveillance among camels remains limited and the epidemiology of MERS-CoV in this reservoir population is still poorly characterized, which constrains the ability to fully assess the implications for camel-to-human transmission.

Recommendations

The recent decline in human MERS-CoV cases may be attributed to a combination of modest cross-protection from SARS-CoV-2 immunity, changes in behaviour among camel-exposed populations that have not been fully assessed, and reduced interactions between camels, at least for the first few years of the COVID-19 pandemic. Reduced virulence of circulating strains remains under investigation, but current sequencing and virological data do not support attenuation as an explanation. Importantly, the proposed hypotheses to explain decline in human MERS-CoV cases are not mutually exclusive.

To address these uncertainties, the following actions are needed:

- Expand sero-epidemiological studies to better characterize cross-reactive T cell and antibody responses following SARS-CoV-2 exposure (while acknowledging that in vitro data alone are not sufficient to establish meaningful cross-protection and that conceptual support from in vivo validation studies would strengthen the evidence base);
- Conduct behavioural research and strengthen awareness programmes to assess shifts in exposure risk among camel handlers, discourage close contact and reinforce good hygiene practices;
- Investigate patterns of animal handling and movement in relation to virus circulation;
- Maintain genomic surveillance and integrate it with systematic phenotypic assessment of selected camel and human viruses to map viral determinants and identify genomic regions that may influence attenuation or zoonotic potential; and
- Continue supporting MERS-CoV vaccine research, including platforms with potential cross-protective benefits across coronaviruses.

Although it is critical to understand the drivers of apparent epidemiological shifts, MERS-CoV remains a priority pathogen with pandemic potential and the current reduction in reported cases should not lead to complacency. The recent detection of two MERS cases in France, exposed in the Arabian Peninsula, serves as a reminder for any country to be prepared and have appropriate surveillance, diagnostics and infection prevention and control measures in place. Given that MERS-CoV is a zoonotic virus that typically causes only mild disease in camels (animals that are economically and culturally important in affected regions), it is essential to maintain strong collaboration between animal and human health stakeholders. Such sustained, cross-sector engagement helps to ensure that the full picture of MERS-CoV ecology is kept in view and supports a more complete understanding of the disease and any evolving epidemiology in humans.

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References

1. Reusken, C. B. et al. *Lancet Infect. Dis.* **13**, 859–866 (2013).
2. Chu, D. K. W. et al. *Proc. Natl Acad. Sci. USA* **115**, 3144–3149 (2018).
3. Rebendenne, A. et al. *Nat. Genet.* **54**, 1090–1102 (2022).
4. Munyua, P. M. et al. *Emerg. Infect. Dis.* **27**, 1201–1205 (2021).
5. Grifoni, A. et al. *Cell* **181**, 1489–1501 (2020).

6. Kim, S.-H. et al. *Sci. Adv.* **10**, eadk6425 (2024).
7. Murray, S. M. et al. *Nat. Rev. Immunol.* **23**, 304–316 (2023).
8. Holloway, P. M. et al. *Lancet Microbe* **5**, 100866 (2024).
9. Chowell, G. et al. *BMC Med.* **13**, 210 (2015).
10. Hunter, J. C. et al. *Emerg. Infect. Dis.* **22**, 647–656 (2016).
11. Hassan, A. M. et al. *Emerg. Infect. Dis.* **31**, 57–65 (2025).
12. van Doremalen, N. et al. *Emerg. Infect. Dis.* **27**, 3052–3062 (2021).
13. So, R. T. Y. et al. *J. Virol.* **97**, e0136923 (2023).
14. Gomaa, M. et al. *J. Virol.* **99**, e0064125 (2025).
15. de Wit, E. et al. *Proc. Natl Acad. Sci. USA* **110**, 16598–16603 (2013).

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Competing interests

The authors declare no competing interests