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IMED abstracts

Oral Presentations: One Health – Emerging Threats Across Species Boundaries

03.002

A mathematical model of the transmission of middle East respiratory syndrome coronavirus in dromedary camels (*Camelus dromedarius*)



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Purpose: Middle East Respiratory Syndrome Coronavirus (MERS-CoV) remains an emerging disease threat, with regular reports of human cases on the Arabian Peninsula, driven by recurring camel-to-human transmission events. A prophylactic vaccine under development has been found to greatly reduce shedding in dromedaries, but there are major gaps in our quantitative understanding of the epidemiology of MERS-CoV in dromedary populations. The purpose of our work is to develop a mathematical model of MERS-CoV transmission in camels in order to address these gaps and to eventually inform the development of evidence-based animal vaccination strategies.

Methods & Materials: After reviewing publicly available data on camel demography and epidemiology of MERS-CoV in camels, we developed a stochastic, age-structured mathematical model of MERS-CoV transmission in single homogenous camel populations, and between coupled sub-populations.

Results: We show that if immunity is completely protective against future infection, a basic reproduction number (R_0) of 6 reproduces reported patterns of age-stratified seroprevalence observed in camel populations sampled in the Arabian Peninsula and North Africa. If immunity offers only partial protection, we estimate that R_0 is approximately 3. In large modelled populations where transmission persists long-term, epidemics are predicted to have an annual periodicity driven by seasonal births. Allowing reinfection (due to partial immunity) enhances persistence but disease extinction by chance is still expected in well-mixed populations of less than 1000 animals. Hence, we predict that single herds are unlikely to be able to sustain MERS-CoV transmission. Using a meta-population model of multiple coupled small populations, we show that transmission can persist in the population as a whole due to random reintroduction of virus into populations in which transmission has previously ceased via animal movements.

Conclusion: We conclude that the R_0 of MERS-CoV in camels is in the range 3–6, indicating moderate transmissibility. A meta-population model of MERS-CoV transmission reproduces the long-term persistence of MERS-CoV in camel populations in Africa and the Arabian Peninsula and may be useful for simulating camel vaccination strategies.

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03.003

Ebola in animals - our knowledge to date: assessing human exposure risks



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