MERS structure

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Abstract

Middle East Respiratory Syndrome coronavirus (MERS-CoV) is a zoonotic virus causing significant mortality and morbidity largely in the Arabian Peninsula. The epidemiology of the virus is relatively poorly understood with most MERS patients being older males with comorbidities, although large nosocomial have occurred, notably in Jeddah, Riyadh and South Korea. Our understanding of MERS-CoV epidemiology is further complicated by some patients not recalling contact with camels, the accepted reservoir for MERS-CoV, or any other livestock, suggesting significant cryptic MERS-CoV circulation in communities. Seroepidemiology has been employed extensively during the time since the discovery of MERS-CoV to understand the exposure and therefore risk among camels and humans alike, but various sequencing efforts have not been fully leveraged against this zoonotic virus. Here we use existing MERS-CoV sequencing data to estimate the number of times the virus has been introduced into humans and use the distribution of sequence clusters to estimate the reproductive number for the virus from sequence data alone. We confirm that MERS-CoV has relatively poor capacity to spread in humans and arrive at an estimate of at least 65 zoonotic introductions of the virus into humans.

Introduction

Middle East Respiratory Syndrome Coronavirus (MERS-CoV) is a zoonotic infection of humans in the Arabian Peninsula originating from camels. The virus, first discovered in 2012 **?**, has gone on to cause more than 1800 infections with at least 600 associated deaths. Its epidemiology remains obscure, largely because outbreaks are observed among the most severely affected patients, such as older males with comorbidities. Whilst contact with camels is often reported by patients, many do not recall contact with any livestock, suggesting a significant but unobserved community contribution to the outbreak. Studies into MERS-CoV epidemiology often rely on serology to identify factors associated with MERS CoV exposure in potential risk groups or hosts. The new era of genomic epidemiology, however, has repeatedly shown the utility of sequence data in outbreak scenarios. Often only sequence data can pinpoint sources of pathogens and discriminate between multiple and single source scenarios, which are a fundamental part of quantifying risk. Sequencing MERS-CoV has been performed as part of initial attempts to link human infections with the camel reservoir, nosocomial outbreak investigations and routine surveillance.

It is accepted that human MERS-CoV infections are a result of multiple introductions of the virus into humans, but no study has attempted to go beyond educated guesses about this number. Here we use existing MERS-CoV sequence data to investigate the population structure of the virus between two of its known hosts: humans and camels. By explicitly modelling the evolution of MERS-CoV between these two distinct host populations we show that human MERS infections are the result of frequent and unidirectional spillover events from camels into humans. Inter-outbreak evolution of the virus occurs exclusively in camels, highlighting the need for genomic surveillance of MERS-CoV in the reservoir as well. We also use the sequence clusters recovered from our population structure analyses to estimate the reproductive number for the virus (R_0), which is in agreement with previous findings that MERS-CoV is, on average, poor at spreading in human populations. Our analyses also capture seasonal variation in zoonotic transmission patterns, with indications that particularly large outbreaks are the result of zoonotic transmissions that take place at the beginning of each new year.

Results

Discussion

Methods

Data availability

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References