Added value of this study

We use a mathematical model to assess the feasibility of contact tracing and case isolation to control outbreaks of outbreaks in the model. Future research on the transmission characteristics could improve precision on control estimates.

virus disease,[8,9] Middle East respiratory syndrome (MERS),[10,11] and many other infections.[12,13]

The effectiveness of isolation and contact-tracing methods hinges on two key epidemiological parameters: the number of secondary infections generated by each new infection and the proportion of transmission that occurs before symptom onset.[5] In addition, successful contact tracing and reducing the delay between symptom onset and isolation are crucial, because, during this time, cases remain in the community where they can infect others until isolation.[6,14] Transmission before symptom onset could only be prevented by tracing contacts of confirmed cases and testing (and quarantining) those contacts. Cases that do not seek care, potentially because of subclinical infection, are a further challenge to control.

If COVID-19 can be controlled by isolation and contact tracing, then public health efforts should be focused on this strategy; however, if this is not enough to control outbreaks, then additional resources might be needed for additional interventions. Several key characteristics of the transmissibility and natural history of COVID-19 are currently unknown—eg, whether transmission can occur before symptom onset. Therefore, we explored a range of epidemiological scenarios that represent potential transmission properties based on current information about COVID-19 transmission. We assessed the ability of isolation and contact tracing to control disease outbreaks in areas without widespread transmission using a mathematical model.[6,15–17] By varying the efficacy of contact-tracing efforts, the size of the outbreak when detected, and the promptness of isolation after symptom onset, we show how viable it is for countries at risk of imported cases to use contact tracing and isolation as a containment strategy.

Methods

Model structure

We implemented a branching process model, in which the number of potential secondary cases produced by each individual is drawn from a negative binomial distribution with a mean equal to the reproduction number, and heterogeneity in the number of new infections produced by each individual.[6,15,17–19] Each potential new infection was assigned a time of infection drawn from the serial interval distribution. Secondary cases were only created if the person with the infection had not been isolated by the time of infection. As an example (figure 1), a person infected with the virus could potentially produce three secondary infections (because three is drawn from the negative binomial distribution), but only two transmissions might occur before the case is isolated. Thus, in the model, a reduced delay from onset to isolation would reduce the average number of secondary cases.

We initialised the branching process with five, 20, or 40 cases to represent a newly detected outbreak of varying size. Initial symptomatic cases were then isolated after symptom onset with a delay drawn from the onset-to-isolation distribution (table). Isolation was assumed to be 100% effective at preventing further transmission; therefore, in the model, failure to control the outbreak resulted from the incomplete contact tracing and the delays in isolating cases rather than the inability of isolation to prevent further transmission. Either 100% or 90% of cases became symptomatic, and all symptomatic cases were eventually reported.