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Reducing the impact of the next influenza pandemic using household-based public health interventions

Key Message

Household-based public health interventions can effectively mitigate the impact of influenza pandemic, and the resources and compliance requirement are realistic and feasible.

Introduction

Wherever a pandemic influenza strain evolves, there is a period of time during which the disease has not yet reached some populations. This allows these populations to implement interventions to reduce local transmissibility (measured by the basic reproductive number R_0) prior to the introduction of the strain. This may reduce the infection attack rate (IAR) once the pandemic arrives. We estimated the reduction in IAR after different household-based interventions using a mathematical model of influenza transmission within and between households. Household-based interventions, such as voluntary quarantine and antiviral prophylaxis, may reduce the IAR substantially, without consuming resources at the same rate as non-targeted population-level interventions. To estimate the impact of household-based interventions on IAR, we used an individual-based stochastic model of influenza transmission with explicit household, peer-group, and community settings.

Aims and objectives

To estimate the effectiveness of preventive measures that communities might implement to reduce the impact of pandemic influenza.

Methods

In this simulation, the distribution of household sizes and the average numbers of children in households of different sizes were made to be consistent with Hong Kong.[2] All interventions were active prior to the arrival of the infected individuals, and the population had a constant introduction of 1.5 infected individuals per day per 100 000 inhabitants for 365 days. Susceptible individuals reported with influenza-like-illness, caused by something other than the pandemic influenza strain, at a constant rate of 74 per day per 100 000 inhabitants (according to Hong Kong Centre for Health Protection, www.chp.gov.hk, Data and Statistics, Sentinel Surveillance).

Household-based interventions were simulated as an integrated process of voluntary household quarantine, voluntary individual isolation, and contact tracing. Quarantine referred to segregation of household contacts of a suspected patient from other members of the community within their own homes. Isolation referred to relocation of symptomatic individuals from their household to a separate facility. If an individual complied with household quarantine, his infectivity to other household members increased by a factor of ε_0 ($\varepsilon_0=2$ at baseline). Also, the level of transmission in isolation may be higher than elsewhere. The degree of transmission in isolation was assumed to be a factor of ε_1 greater ($\varepsilon_1=1$ at baseline). Individuals with symptoms severe enough to warrant hospitalisation were assumed to be isolated and to receive antiviral therapy. Compliance was modelled at the individual level (ie each member of the household made independent decision). We defined p_c to be the probability of compliance. These interventions were implemented using the following algorithm:

(1) An individual from households not in voluntary quarantine had the opportunity to enter the programme via one of the following three routes: developing symptoms, being contacted through contact tracing, being hospitalised.

We assumed that the subject actually reported with a probability p_c for symptoms and contact tracing, and with probability 1 for hospitalisation, and complied with the programme until released. After release, the subject was not bound by previous decisions to join or not join, ie being able to choose once again.

(2) Each of the other members of the household complied with intervention instructions with a probability p_c.

(3) After a delay of 1 day, all compliant non-symptomatic houshold members took one dose of prophylactic antivirals per day, when antiviral policies were in effect. Symptomatic household members took two doses of anitvirals per day.

(4) If contact tracing was in effect, each compliant adult member of the household would name, on average, five subjects (in their peer-group).

(5) If isolation was in effect, new symptomatic individuals who were compliant would enter voluntary isolation with a probability p_c after a delay of 1 day. If the isolated individuals no longer showed symptoms after 3 days, they would be released from isolation and rejoin their household, which might be quarantined. Otherwise, they would be isolated for a further 3 days. This cycle would be repeated until the subjects no longer showed symptoms or died.

(6) Isolated individuals were given two doses of antivirals per day, without a delay, in all simulations, regardless of the policy for the use of antivirals in households.

(7) If contact tracing was in effect, contacts (whether known or not already in the programme) of all new symptomatic or hospitalised household members would be traced with a mean delay of 1 day.

(8) In the absence of new symptoms in compliant or hospitalised household members for 7 days, the quarantined household would be released from the programme at that point. Otherwise, they would return to step 5.

Results

With compliance rates of 50%, all intervention policies substantially reduced IAR. The baseline IAR of 74% was reduced to 49% when voluntary household quarantine was in effect. However, the peak proportion of households that were quarantined, even with compliance rates of only 50%, was 9.6%. The addition of voluntary individual isolation further reduced the IAR to 43% and the peak proportion of households that were quarantined decreased to 7.1%. Voluntary individual isolation provided an incentive for households to participate: presumed infectious individuals may have been prioritised for health care services and would have protected household members. However, this approach required isolation facilities for up to 0.9% of the population at the peak of the epidemic.

We also considered the use of antivirals with voluntary household quarantine. This policy had a similar efficacy to voluntary individual isolation (IAR, 44%) at a cost of 3.9

doses of antiviral per member but with a much smaller peak level of isolation of 0.5%. The use of antivirals in addition to quarantine and isolation further reduced the IAR to 40% and the peak proportion of households that were quarantined reduced to 6.2%. The addition of contact tracing reduced the IAR to 34% but increased the proportion of the population in quarantine considerably. The additional requirements of contact tracing are unlikely to be justified unless the reproductive number is reduced to near one by other interventions. The prevalence of quarantine and isolation specifies the resources required by these programmes over time, eg the total prevalence of quarantine and isolation on a given day indicates the number of antiviral doses that needs to be distributed, when the use of antivirals in addition to quarantine and isolation is in effect.

As the influenza strain that may cause the next pandemic has not yet been observed, it is not possible to estimate its level of transmissibility (other than by using historical data from other strains) or the balance of transmission in different settings.[1] We used extensive Latin hypercube sampling to conduct sensitivity analyses. This suggests that variations in the efficacy of policies in reducing the IAR is dominated by the basic reproductive number R_0.[3] All interventions are considerably more cost-effective for lower values of R_0.

The efficacy of quarantine plus antivirals was not substantially less than that of quarantine, isolation plus antivirals for most parameter combinations. The potential for increased transmission in isolation did not seem to substantially decrease the efficacy of the voluntary individual isolation. Even with isolation transmissibility levels 10 times greater than those outside isolation, the voluntary individual isolation was still effective (IAR, 45%), compared to voluntary household quarantine alone (IAR, 49%), because the overall proportion of susceptible individuals entering isolation was low. Although this proportion may have been high during the initial stages, it would likely be small when averaged over the entire course of the epidemic.

All estimated reductions in IAR were sensitive to the population compliance rate, p_c and to the proportion of transmission, θ, which was either asymptomatic or pre-symptomatic. Values of p_c=50% and θ=30% were assumed for baseline intervention scenarios. Our estimated changes in IAR were also sensitive to the average delay in the provision of antivirals and in voluntary isolation, although less so than to p_c and θ. In deciding whether to implement any or all of the policies described, local public health officials may wish to consider available epidemiological data (to assess R_0 and θ) and also estimate the levels of compliance that could be achieved for the different options in their populations. As compliance may be higher for policies that provide immediate benefits to the individual, compliance will be low for voluntary household quarantine alone, higher for voluntary individual isolation alone, and the use of antivirals with voluntary household quarantine, and highest

for the use of antivirals with voluntary household quarantine and individual isolation. It is likely that the provision of antiviral prophylaxis and treatment increases compliance substantially. Our baseline assumption of 50% is intended to be conservative. It seems that household-based interventions work when levels of compliance are high. Even moderate levels of compliance render household-based public health interventions effective. Also, the marginal benefits from the use of antivirals and isolation may not be justified if the average times for provision of these services exceed 3 to 4 days, given that the quarantine period is set at 7 days.

Levels of compliance with quarantine and isolation would likely improve in the early and late stages of the epidemic, when a viable diagnostic method is available. We considered the impact of virological testing as a diagnostic support for these policies. However, current low throughput (limited by both laboratory infrastructure and supplies of reagents) and low test sensitivity (due to difficulties in obtaining adequate specimens outside of specialised care settings) meant that it was not a worthwhile addition. If an inexpensive, easy-to-perform, rapid and accurate test was available, it would have a significant impact on transmission and on peak levels of quarantine, when used as part of a wider household-based programme.

Discussion

For lower transmissibility strains of pandemic influenza, the combination of voluntary household quarantine, individual isolation, and the prophylactic use of antivirals was highly effective and feasible across a range of transmission scenarios, even with only moderate levels of compliance. We have quantified the resources consumed by this and similar policies in terms of numbers of people quarantined, numbers of people isolated, and doses of antivirals required.

We assume that the natural history of the next pandemic strain will be similar to that of the 1918 strain, a reduction in IAR from 74% to 40% would avert 16 000 deaths during the period of the initial pandemic wave in a city about the size of Hong Kong (6.8 million people). Our results suggest that such a reduction can be achieved using the combination of voluntary quarantine, individual isolation, and antiviral therapy. Isolation on such a large scale may be somewhat controversial, given the infrastructure requirements of such a policy. Therefore, when large stockpiles of antivirals are available, the marginal benefit of the additional use of isolation may not be justified. However, when stockpiling of antivirals is not feasible, individual isolation is the best possible addition to household quarantine.

Our results build on previous modelling studies of pandemic influenza which focus on the possibility of containment using geographically targeted antiviral therapy.[1,4] Effective strategies have been identified for mitigation rather than containment.[5,6] The key outcome of mitigation is the reduction in IAR, rather than the likelihood of complete control. Given that many epidemiological parameters associated with the next influenza pandemic are unknown, comparison of results from different modelling studies is not straightforward. Our results are consistent with the reduction in IAR from 34% to 20%.[5] However, they are not consistent with other studies, in which a 10 fold reduction in the numbers of ill people is reported for the use of targeted anti-viral prophylaxis.[6] This large discrepancy is likely due to the optimistic nature of their policy: they assume that households, household clusters, schools and workplaces can be targeted very efficiently for prophylactic antiviral therapy. We suggest that a highly efficient contact tracing process be required to achieve high levels of coverage between socially connected households, which is particularly true in modern urban populations. Such a process requires large numbers of households to be recruited during short periods of time, which is not feasible.

Reducing the first-wave IAR should be the primary goal of influenza preparedness planning. When complete transmission control is not achieved, this necessarily implies a longer epidemic. If the mortality rate of the pandemic strain is considered to be low, it is likely that some governments will place priority on reducing the duration of the outbreak than on reducing the number of infections. For a longer period of societal disruption, policy should be designed to reduce mortality and peak stresses on the society as a whole. For example, for the baseline case, a combination of voluntary household quarantine, individual isolation, and use of antivirals could reduce the peak incidence of infection from 3.7 to 0.8%. Although such analyses are beyond the scope of this work, the likelihood of maintaining uninterrupted key societal services (such as law enforcement, food distribution and utility provision) may improve substantially across this range. Therefore, the potential massive adverse economic implications of a temporary breakdown may justify extending the expected period of disruption.

Conclusions

Household quarantine was not successfully implemented on any significant scale during the 1918 city-level epidemics upon which estimates of transmissibility are based.[1,7] Therefore, the likely impact of the interventions we described is real and not already incorporated into estimates of transmissibility. Modern transport and communication infrastructures are much more advanced than those available in 1918, so it is reasonable to expect that such interventions can now succeed. Many countries have put in place formal pandemic preparedness plans following a World Health Organization framework. These national plans mention the interventions included here, but they do not specify the implementation of intervention processes in even the broadest terms, nor do they attempt to predict the levels of resources required. Our findings and future studies, which match detailed descriptions of

interventions with realistic transmission models, can help to inform pandemic preparedness plans by quantifying both the benefits of, and resources required by, household-based interventions against pandemic influenza.

Our measures to increase social distance consume substantial resources and therefore detailed planning is required. To allow quarantined individuals to remain at home, provision of food, water and medicines must be made for. This may be achieved through a central system or a neighbourhood assistance scheme. For isolation, careful planning and investment is required so that large facilities can be made operational in time to reduce transmission in the early stages of the epidemic. For antivirals to be provided efficiently, a dedicated distribution system is required.

Acknowledgements

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Wu JT, Riley S, Fraser C, Leung GM. Reducing the impact of the next influenza pandemic using household-based public health interventions. PLoS Med 2006;3:e361.

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