Microsimulation study of the release of pneumonic plague and smallpox on a synthetic civilian population

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Abstract
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Keywords
smallpox, synthetic, civilian, population, release, microsimulation, pneumonic, study, plague

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Microsimulation Study of the Release of Pneumonic Plague and Smallpox on a Synthetic Civilian Population

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Abstract:
The confrontation in Syria is a cause for concern over the use of chemical and biological weapons. There have been reports of the use of chemical weapons including Sarin. While both sides accuse each other, there is very little ground evidence at this time (August 2013) to substantiate claims or to determine who is involved. Their use would demonstrate a total disregard for civilian casualties and UN conventions. Syria is thought to have stockpiles of a number of agents including anthrax, plague, tularaemia, botulinium, smallpox and cholera (Gordon, 2007). Some groups sympathetic to Al Qaeda might also have access to some of these through their terrorist networks. If chemical weapons have been used by either side, then the potential use of biological weapons cannot be disregarded.

Of concern is whether the response to an attack involving a single agent would be the same as when more than one agent is used. While there are a number of papers on the management of both smallpox and plague (Halloran, (2002), Rani et al, (2004)), there are few, if any, which discuss joint infection or the likely confounding factors that will affect outcomes in their post attack management. In this paper we explore the application of microsimulation modelling of a joint attack on a civilian population using plague and smallpox as an example. The literature suggests that plague affects the innate immune system by suppressing cytokine responses while smallpox activates the cytokine response. The possible interaction between the two diseases in people who are infected with both diseases is examined and its effect on the spread of disease and number of deaths.

The simulations involve a population of 1250 people based on NSW statistics for households and work. The structure of a community model of social mixing is briefly discussed, over which a multi-infection model is imposed that accounts for varying infectivity in different stages of each disease as well as confinement to home as each disease progresses. A number of simulations were run, assuming 10% immunity to both diseases, to establish a baseline for each disease in the community. Further simulations where both are released together with delay of the introduction of plague compared to smallpox of 0 and 35 days respectively. The strength of the interaction by smallpox on plague deaths was also investigated.

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Keywords: Bioterrorism, Microsimulation, Plague, Smallpox, Disease Management
1. INTRODUCTION

The current conflict in Syria has raised the serious issue of the use of chemical and biological weapons on civilian populations. Reports in the media have intimated that chemical weapons have been used in the conflict whilst urging caution in the interpretation of these reports. The more serious risk, because it has the potential to spread rapidly outside the conflict area, is the use of biological weapons. Syria is thought to have stockpiles of a number of agents including anthrax, plague, tularaemia, botulinium, smallpox and cholera (Gordon, 2007). These may also be available to other groups but a counterview suggests that biological weapons might not have been fully developed and non-state groups would not have the technology to home develop such weapons (Leitenberg, 2005). While the quality and viability of these stockpiles are unknown, and the difficulties in weaponising them documented, both state and non-state actors, through their state sponsors, might also have access to these weapons.

If their use is a credible possibility it raises the question of how release in a conflict zone can be countered effectively, particularly as refugee camps have extremely high population densities. Local and international response agencies will be stretched by a biological epidemic occurring in the context of other conflict-related issues. The principle impact will be on their ability to contact-trace cases to control the epidemic. Similarly, supplies of anti-bacterials and vaccines may not be readily available, necessitating their importation from international stockpiles and delaying their application. There have been several numerical studies of the spread and control of smallpox and plague, such as Halloran, (2002) and Rani et al, (2004), where the authors have used stochastic methods either to evaluate intervention strategies for control of outbreaks or to estimate the number of infecteds hidden from authorities in a community once the disease outbreak had occurred. Intervention strategies tended to be modelled on common procedures for tracing, vaccination and isolation of contacts. While many of these recommendations may work well in Western, non-conflict situations, conflict areas have problems that delay surveillance, delay access to medication and restrict the quantity and quality of trained staff. In addition the presentation of more than one disease may confound treatments.

In this paper we present development of our microsimulation framework, Simulacron, (Keep, 2012) to multi-infections with a preliminary investigation into the building of a model for studying the impact of multiple biological weapons releases on a population. In the work reported here we have used plague and smallpox as two indicative and plausible biological weapons.

2. SIMULATION OF MULTI-INFECTION IN A COMMUNITY

Three essential components are required to simulate multi-infection spread within a community at the level of the individual.

First, a description of the community though which the infection will spread. This includes breaking down a population into age- and work-based compartments. The community model used in this study is based on the 2011 census data for NSW (ABS, 2012) and employment statistics for NSW (ABS, 2012a). Each member of the population is assigned to a household that matches NSW housing statistics and to a location, such as a school or place of work. These locations are associated with one of six compartments that are used to assign schedules for each individual: infants, primary school and secondary school children, full time employed, part time employed and unemployed including retirees. Workplace structures, like their household counterparts, conform to the overall industry sector statistics.

Second, a model of social mixing that emulates the complex patterns of locational behavior such as going to work, school or eating out at lunch or dinner. In the simulation this mixing occurs through a hierarchical structure of daily and weekly schedules. A daily schedule is chosen at random from a list of potential schedules that is dependent on the type of person and the day of the week and these are then combined into a weekly schedule. These selections for example take account of days off or sick days for full time employed or the sport activities of children on the weekend. Each daily schedule randomly selects the timing of events within time periods during the day, such as the start of work or lunch, and the place where this occurs. Individuals are moved by teleportation at each event time. Figure 1 is an example of a daily schedule for full time work over a day. At each event time, a person has a choice of alternative activities which are preselected

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1 An infectid is a person who has been infected with a disease.
2 A NSW community was chosen for convenience to progress understanding of the disease processes involved. Conflict areas, however, occur all over the world and are not confined to places like Syria; for example the Cronulla riots in NSW indicate that NSW is not immune.
3 A more detailed transport model involving path tracing, though available as a module within Simulacron, is not used in this study.
randomly for execution during the simulation. Complex mixing patterns occur from these very simple constructs and these patterns mimic typical social behaviours.

Third, a multi-infection module that allows spread of diseases through the community. Each infection is implemented as a chain model through six infection states (Green et al, 2011). As contact time is explicitly modeled through the social mixing process, a probability of infection (infection chance) is used to spread the disease and a probability of recovery allows progress to a state of either immunity or death. One innovation is the ability to specify the infection probability as a relative force of infection (infection strength) by infectids as shown by equation 1.

\[ A_{IC} = T_{IC} \frac{\Delta t}{t_I} \sum_{j=1}^{S_j} \delta_{ij} \]  

Where \( A_{IC} \) is the infection chance at a susceptible target with infection chance, \( T_{IC} \) is the tick time interval and \( t_I \) is average infectious time. \( S_j \) is the infection strength of an infectious peep, \( j \), with a compatible infection mask within the cell. The sum is over all such infectious peeps. Infection is determined by selecting a \([0, 1)\) uniform random variate, and comparing it to \( A_{IC} \). If the random number is less than \( A_{IC} \), infection spreads to the target peep.

The infection source is a biological weapon which can either be dropped randomly into an area or taken by a person to a specific area of release. In this study we have randomly selected locations from the workplace locations to emulate the former release mode rather than the latter which would tend to be targeted at specific high density locations for maximal effect. The weapon source has its infection strength increased compared to a natural outbreak of the disease in order to simulate an aerosolized weapon infecting individuals while subsequent spread between individuals will be similar to natural outbreaks.

\[ \sum \]  

\[ eq(1) \]  

The supression of immune response may increase virulence overall

\[ S1: No change to YP infection parameters \]

\[ S152: Change virulence up for VM by some parameter that is randomly selected \]

\[ S251: Change virulence down for VM by some parameter that is randomly selected \]

\[ S2: No change to VM infection parameters \]

\[ S15: No change to YP infection parameters \]

\[ S25: Change virulence up for VM by some parameter that is randomly selected \]

\[ S251: Change virulence down for VM by some parameter that is randomly selected \]

\[ S2: No change to VM infection parameters \]
As plague has evolved to suppress the production of cytokines by the innate immune response (Li et al, 2008) and smallpox promotes cytokine response (Fenner et al, 2013) there is the possibility that infection with both diseases may alter the recovery outcomes, as the innate immune system works in opposite directions for the two diseases. The use of additional states of infection extends the multi-infection module to allow interactions between the infections. Figure 2 shows the basic infection states and their function. The potential interaction is investigated in this paper. Triggers on change of infection state are used to place individuals into states where the infections can interact within a person either increasing or decreasing the recovery rate, depending on which infection occurred first. These triggers are also used to confine individuals to one of the bedrooms in their house. While other options such as hospitalisation are possible, they have not been modelled in this work. The actual model used is more complex than that shown in Figure 2: additional states are required to take account of varying infectivity over the course of infection as discussed below.

3. SIMULATIONS

The initial simulations involved a population of 1250 people in a small community. The two infections’ states and the recovery and infection probabilities are shown in Table 1 for individuals in the simulations. Smallpox was eradicated in 1972 and current populations under the age about 40 would have no immunity. Even those over that age are unlikely to have been vaccinated except when travelling to prone areas and, in a bioweapons attack, the strain might not match the vaccination strains. The immunity to smallpox was therefore assumed to be 10% for the population as a whole. While a more detailed model of immunity could be constructed, the approach taken was considered to be reasonable given the variation in other parameters. A similar value was used for immunity to pneumonic plague on the basis of sporadic natural outbreaks around the world leaving most of the world's population vulnerable. The infection strength was varied to account for changes in infectivity during the course of the diseases. It was reduced to 50% during hero time to take account of the increasing infectivity during the symptomatic phase of plague. With smallpox, the most infectious period is the prodromal period and the infection strength decreases once the rash appears.

The bioweapon infections were modelled as a static person in a cell who had a latency period that matched the time from the start of the simulation to the release of the weapon’s infection. This time was randomly selected from within a time window and the location was randomly selected from the workplaces in the simulation. The infectivity of the source was raised above 1.0, as shown in Table 1, to ensure a reasonable spread within the community in order that other effects of the two diseases could be studied. Other parameters came from analysis of outbreaks that had occurred for the two diseases.

An analysis of generational infection in an outbreak of plague in Mukden, Manchuria in 1946 (Tieh et al, 1946) is shown in Figure 3. In this outbreak 43 people were infected among 83 contacts. While the text did not explicitly state the contacts for the five that recovered, the text did allow identification of who was likely to have infected them. The infection chance for the present study is based on the average infection rate through the population in this case study.

Because the reproductive number (R0) in the literature for smallpox varied from 0 to 38 with a mean below 3 (Bhatnagaret al, 2006), an outbreak in Abakaliki, Nigeria, in 1967 was chosen to calibrate the infection rate in a naive population. In this outbreak, three population groups, a naive population belonging to a Faith group, a vaccinated group who lived in close proximity to the Faith group and a more general population who also had a high vaccination rate were used. There was sufficient detail in the published outbreak to be able to reconstruct the populations, their immunological status and their housing communities (Thompson et al, 1968, Ottenberg, 1960). The values for the infection in Table 1 were based upon this outbreak. Simulation of the outbreak calibrated the infection chance and the other infection parameters.

In the simulations, people who became infected with smallpox had a 50% chance of confinement to their home during the prodromal phase and 50% chance of confinement during the first observations of progression of the disease (Halloran, 2002). With plague there was no asymptomatic infectious stage and it was assumed that 50% of infectoids would be home confined during hero time and 100% thereafter. The variation in infection chance over the course of each disease increases the number of states required to 17 compared with Figure 2.

The initial simulations were undertaken to obtain a baseline for each infection separately. Figure 4 shows the results where infection was started in five locations over a two hour period, 12 hours into the simulation. Smallpox required lower infection strengths compared to plague to obtain infection of people in the locations.

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This study is not concerned with the efficiency of weapons. Consequently, an infection chance was chosen that consistently produced spread within the community for the two diseases.
Table 1  Infection Parameters

<table>
<thead>
<tr>
<th>Variable</th>
<th>Plague</th>
<th>Smallpox</th>
</tr>
</thead>
<tbody>
<tr>
<td>Latent time</td>
<td>100 ± 40 hours</td>
<td>330 ± 48 hours</td>
</tr>
<tr>
<td>Asymptomatic or prodromal time</td>
<td>0 hours</td>
<td>50 ± 20 hours</td>
</tr>
<tr>
<td>Hero time</td>
<td>&lt;24 hours</td>
<td>48 ± 13 hours</td>
</tr>
<tr>
<td>Infectious time</td>
<td>62 ± 30 hours</td>
<td>420 ± 60 hours</td>
</tr>
<tr>
<td>Immune time (assumed)</td>
<td>100000 hours</td>
<td>100000 hours</td>
</tr>
<tr>
<td>Infection chance</td>
<td>0.0022 ± 0.0003</td>
<td>0.01 ± 0.002</td>
</tr>
<tr>
<td>Recovery chance</td>
<td>0 - 0.1</td>
<td>0.6 - 0.7</td>
</tr>
<tr>
<td>Infection strength of infected people</td>
<td>1 (0.5 during hero time)</td>
<td>1 (0.2 during infectious time)</td>
</tr>
<tr>
<td>Infection strength of the initial infecting source</td>
<td>1000</td>
<td>10</td>
</tr>
</tbody>
</table>

While smallpox tended to spread throughout the population, plague did not spread as much and exhibited bimodal behavior. The frequency between the two modes is shown in Figure 4: about 2/3 of simulations showed low propagation. This behavior seems to be relative to the number of people going through the release locations over the 2hr period the release was active. A larger population density might change this finding.

Figure 5 shows the plague and smallpox outbreaks when there were five release points for each infection over the same time period and the interaction was not considered. The high plague propagation has about 30 less infections on average than when it is the only disease and occurs for about 10 days longer. The smallpox numbers are very similar to the single infection numbers but the main rise in the curve occurs a few days later. Both infections are affected by home confinement reducing the susceptible population available for further infection by a second infection as there is no interaction between the infections in this simulation. Note that the plague still has bimodal behavior similar to the single outbreak in Figure 4, left.

A second series of simulations involved adding interaction parameters between plague and smallpox. This was achieved by having two parameters controlling the change in recovery compared to no interaction for each of the two diseases. Figure 6 shows the results for adjusting the strength of the interaction when smallpox is caught first, leading to a reduction in the chance of death from plague. The simulations show that while there is a reduction in plague deaths due to the delay in the release of plague, it is not clear how the strength of the interaction between smallpox and plague is affecting the number of deaths.

Since any interaction in a double infection simulated here has to occur within a certain time period from infection with smallpox, the number of smallpox cases that would influence the outcome of plague was extracted from the simulations. In Figure 7 two sets of data are plotted against the number of plague deaths for the release of plague on the 1st and 36th days of simulation: firstly the number of smallpox cases that result in an interaction together with a regression estimate of the trend and secondly the effect of the reduction in the chance of death. The simulations show that the number of plague deaths depends on the delay in release of plague compared to smallpox as well as the strength of the interaction between the two diseases provided that there are enough smallpox cases where the interaction can make a difference. Increasing the number of available interactions does tend to decrease the number of deaths.

4. DISCUSSION

These preliminary simulations have shown that it is possible to construct a community based infection model based on individual spread of multiple diseases. In this case the two diseases, smallpox and plague, are assumed to interact through different channels in the innate immune system. Quite complex outcomes can be expected when more than one biological weapon is released into a conflict zone.
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Figure 4 Individual simulation of plague (left) and smallpox (right)

Figure 5 simultaneous releases of plague and smallpox

Figure 6 Deaths from Plague release 0 and 35 days after start of simulation.

This has potential ramifications on emergency preparedness and practical steps that can be taken to reduce mortality and morbidity.

Current WHO guidelines are based on accessible health professionals and the progress of individual diseases. They also assume point entry between countries rather than regional phased movement across porous borders. It also ignores two affects: the possibility of interaction between diseases (in this case through the innate immune system) and the human behavior constraints in delivery of health care. The latter affects the timing of the discovery of both diseases, the supply of drugs to the area, the presentation of patients at doctors’ clinics or hospitals and the reluctance of health workers to volunteer to go to conflict zones; particularly where approved preventative prophylaxis is not available, such as with plague.
The use of microsimulation has a benefit in that many of the human factors can be easily incorporated into the simulation without affecting the other components of the simulation. For example, vaccine and drug supply can be added as additional peeps that move to hospitals or doctors' surgeries and then interact with the human population through creation of additional states based on these locations.

Further work is planned to assess the impact of these human factors on preventing epidemic spread within and outside of conflict areas.

5. REFERENCES


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