Will Type-CA MRSA become the Dominant Staph Bacteria in the Future? *

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1 Introduction

Methicillin-resistant Staphylococcus aureus(MRSA) is a grape-like cluster of bacteria that could infect humans and other animals. Based on WebMD, it is commonly more difficult to be treated than regular Staphylococcus aureus(MSSA) because it is resistant to most common antibiotics people are using today. There are two kinds of MRSA, one is Health-associated MRSA(HA-MRSA) and other is community-acquired MRSA(CA-MRSA). HA-MRSA usually infects people in illness while they are in the hospital or other healthcare organizations, while CA-MRSA is community-acquired MRSA that people are infected outside the hospital. From WebMD, the population of people who get CA-MRSA is on the rise while the population of people who get HA-MRSA is in decline. In this project, an SIS model, a similar model to SIR but the recovered will not have immunity instead, will be used to evaluate the growth rate of two different kinds of MRSA, a conclusion about whether CA-MRSA will take place to HA-MRSA in specific conditions will be drawn.

2 SIS Model

The SIS model has three systems, the population of patients who are infected by HA-MRSA, call it H(t), the population of patients who are infected by

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CA-MRSA(C(t)) and the susceptible group(S(t)). Suppose there is a hospital with patient N. Then the model will be set with the following parameters:

- e: entrance rate/day of the susceptible group
- l: death or discharge rate/day of the susceptible group
- lh: death or discharge rate/day of the HA-MRSA infected population
- lc: death or discharge rate/day of the CA-MRSA infected population
- rh: recovered rate/day of HA-MRSA infected population
- rc: recovered rate/day of CA-MRSA infected population
- ih: transmit rate/day of HA-MRSA between patients
- ic: transmit rate/day of CA-MRSA between patients

Thus the differential equation could be:

$$\frac{dS}{dt} = e - \frac{i_c * S * H}{N} - \frac{i_h * S * H}{N} + r_h * H + r_c * C - l * S$$

$$\frac{dH}{dt} = \frac{i_h * S * H}{N} - r_h * H - l_h * H$$

$$\frac{dC}{dt} = \frac{i_c * S * C}{N} - r_c * C - l_c * C$$

To simply the equation, suppose the hospital is always full, the entrance rate is equal to the sum of the exit hospital rate for CA-MRSA, HA-MRSA and Susceptible group due to discharge or death. In this case, total hospital population $N = S + C + H$. Since this paper concentrates on the dynamics of CA-MRSA group vs HA-MRSA group. The rate of susceptible group is not very important here. Thus, the model could be written as:

$$\frac{dH}{dt} = \frac{i_h * (N - C - H) * H}{N} - (r_h + l_h) * H$$

$$\frac{dC}{dt} = \frac{i_c * (N - C - H) * C}{N} - (r_c + l_c) * C$$

$$S = N - H - C$$

Suppose the hospital's population is 400, at the beginning, there is one patient infected by each type of MRSA bacteria, the dynamics of the infected group in one year (365 days) will be evaluated.

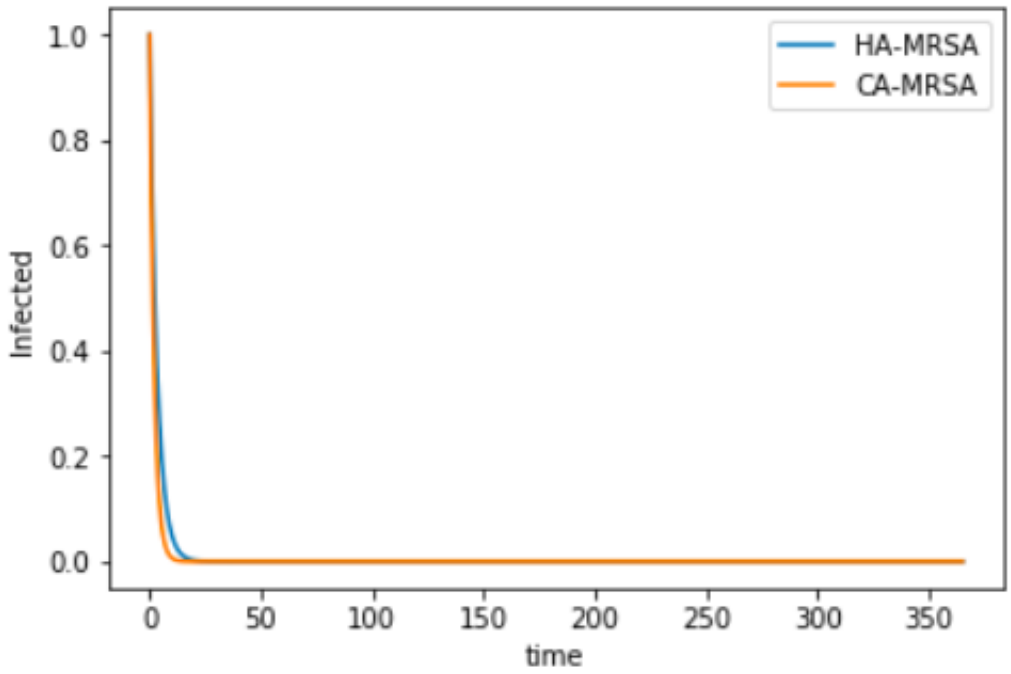

Figure 1: Situation when $r_c + l_c > i_c$, $r_h + l_h > i_h$

3 Analysis

By the model defined above, the equilibrium points could be found. There are three equilibrium points: $(0,0), (N*(1-\frac{r_h+l_h}{i_h}),0), (0, N*(1-\frac{r_c+l_c}{i_c}))$. Because the hypothesis is under positive condition, the nullclines should cross positive half part of both the X-axis and Y-axis. The equilibrium points should have values equal to or larger than zero. Thus, $\frac{r_c+l_c}{i_c} < 1$, $\frac{r_h+l_h}{i_h} < 1$. Figure 1 shows that the possible dynamics of infection, which will annihilate soon at the beginning if the equilibrium points have negative values. Furthermore, the stable property of two equilibrium points $(N*(1-\frac{r_h+l_h}{i_h}),0), (0, N*(1-\frac{r_c+l_c}{i_c}))$ are more important than $(0,0)$, because the paper concentrates on whether CA-MRSA or HA-MRSA will fade out.

Under this condition, the Nullclines' positions are strictly important to analyze the dynamic of the infective population. The model has three different situations:

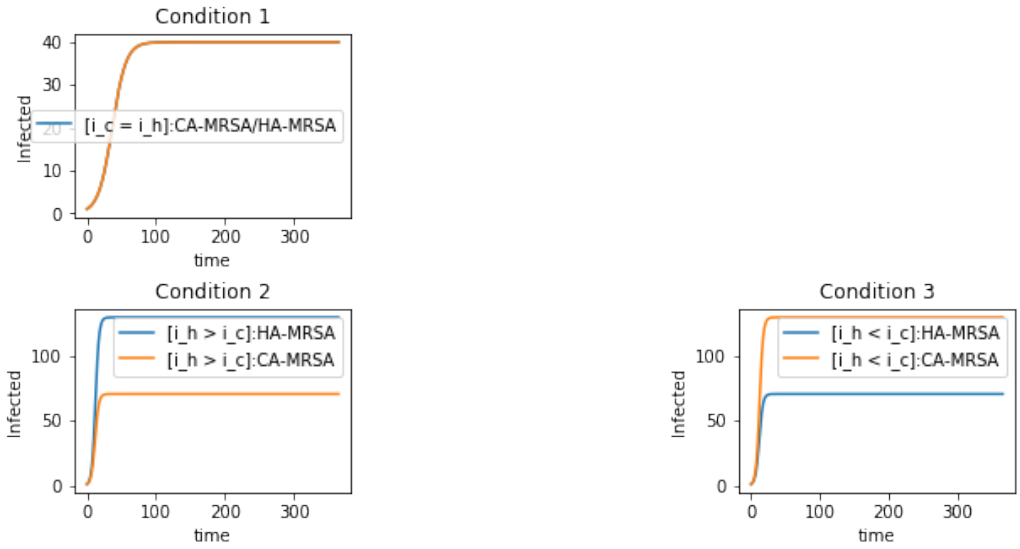

Figure 2: Infective population vs time in three conditions under $\frac{r_h+l_h}{i_h} = \frac{r_c+l_c}{i_c}$

• *Situation 1*: $\frac{r_h+l_h}{i_h} = \frac{r_c+l_c}{i_c}$

In this case, H-Nullclines and C-Nullclines overlaps. But the dynamic graphs would not be trivial. Figure 2 shows three different conditions when $\frac{r_h+l_h}{i_h} = \frac{r_c+l_c}{i_c}$. Whether the infective population of two types of MRSA will overlap or one is larger than the other depends on the illness rate. In condition 1, $i_c = i_h$, the dynamics of two types MRSA infective population are same. If $i_c > i_h$, the population of CA-MRSA will be **larger** than the population of HA-MRSA. What's more, $i_c < i_h$, the population of CA-MRSA will be **smaller** than the population of HA-MRSA.

Although the graphs are not trivial, the infection population of two kinds of MRSA all begin to increase at the beginning and stabilize to a certain number. In this case, the population of HA-MRSA infection and CA-MRSA infection will **co-exist**.

• *Situation 2*: $\frac{r_h+l_h}{i_h} > \frac{r_c+l_c}{i_c}$

In this case, C-Nullcline is one the right side of H-Nullcline. Assume $i_c = 0.5, i_h = 0.4, r_c = 0.1, r_h = 0.13, l_c = 0.2, l_h = 0.17$. According to Figure 3 Situation 2, HA-MRSA infective population will have a small outbreak at first, then the population will stable to zero, while CA-MRSA will take place of HA-MRSA. In this situation, $(0, N * (1 - \frac{r_c+l_c}{i_c}))$ is stable and $(N * (1 -$

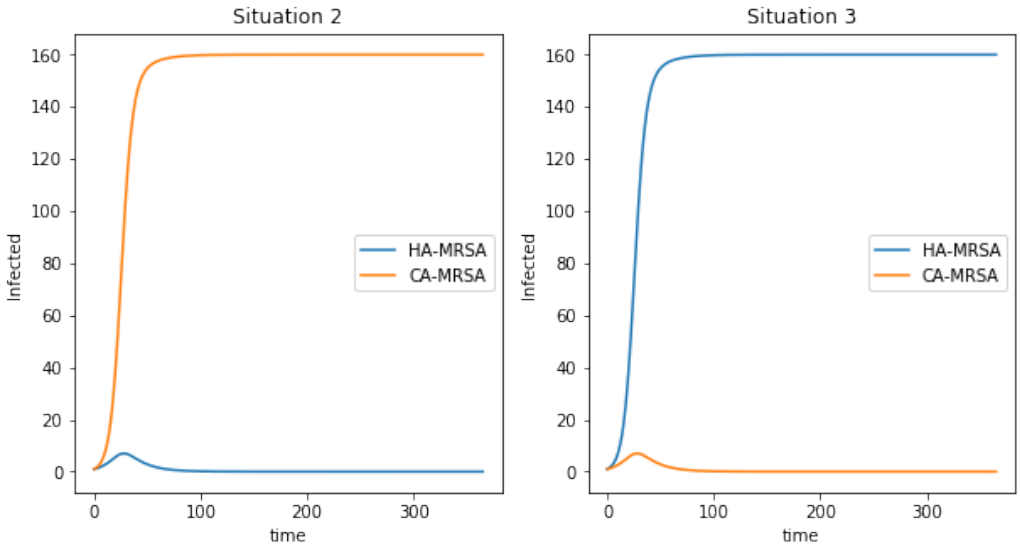

Figure 3: Infective population vs time under Situation 2 and 3

$\frac{r_h+l_h}{i_h}), 0)$ is unstable.

- Condition 3: $\frac{r_h+l_h}{i_h} < \frac{r_c+l_c}{i_c}$

In this case, H-Nullclines is on the right side of C-Nullclines. Under this condition, $(0, N * (1 - \frac{r_c+l_c}{i_c}))$ is unstable and $(N * (1 - \frac{r_h+l_h}{i_h}), 0)$ is stable. The plot proves the differential equation analysis. From Figure 3 Situation 3, the infective population of HA-MRSA will be stable. More specifically, CA-MRSA will face annihilation in the hospital.

Based on the analysis below, the role of the total population in the community is not important. It does not affect the dynamics. That is, if the population of the community is changed to 10000, the plot of infective population vs time will still be similar. (Shown in Figure 4)

4 Data Simulation in Real World

According to the data from Beth Israel Deaconess Medical Center which is obtained from Joanna Pressley,a Erika M. C. D'Agata,b and Glenn F. Webb's

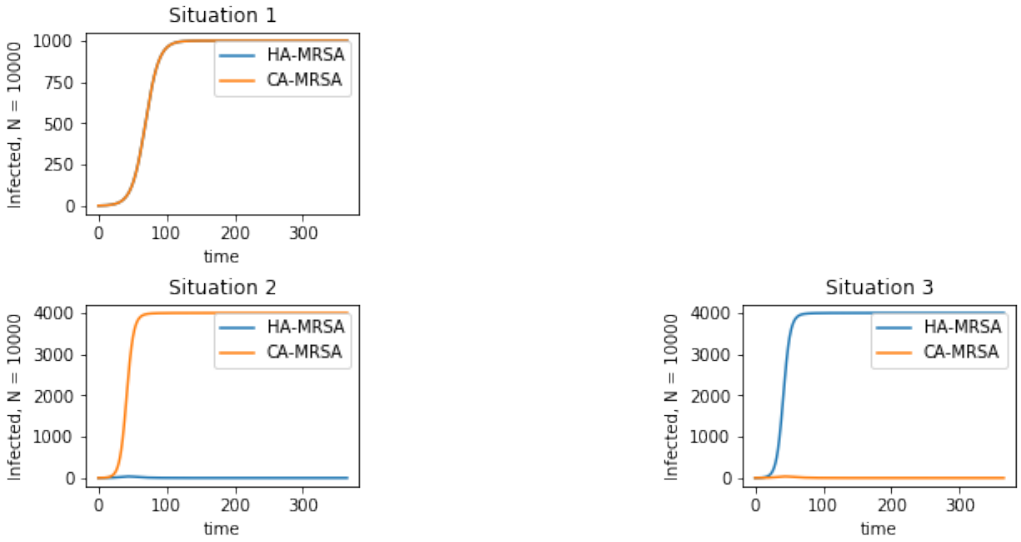

Figure 4: Infective population vs time (N = 10000)

Parameter	Symbol	Value
Total population in the hospital	N	400
Length of Stay		
Susceptible	$1/l_s$	5 days
Colonized CA-MRSA	$1/l_c$	7 days
Colonized HA-MRSA	$1/l_h$	5 days
Transmission rate per susceptible patient to Colonized CA-MRSA per colonized CA-MRSA	i_c	0.45 per day
Colonized HA-MRSA per colonized HA-MRSA	i_h	0.4 per day
Decolonization rate per colonized patient per day per length of stay		
CA-MRSA	r_c	0.1 per day
HA-MRSA	r_h	0.1 per day

Table 1: Parameter values for the infection dynamics of CA-MRSA and HA-MRSA colonization

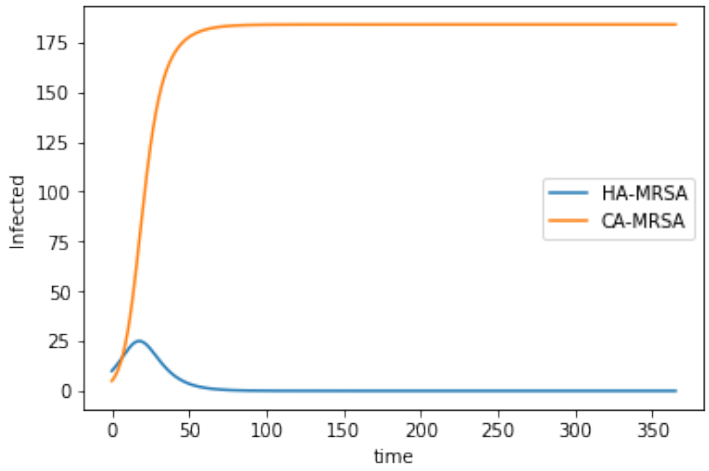

Figure 5: Infective population prediction overtime Based on Data Provided by Beth Israel Deaconess Medical Center

article *The effect of co-colonization with community-acquired and hospital-acquired methicillin-resistant Staphylococcus aureus strains on competitive exclusion*, the parameter values could be known. Plugged into the model, it is cleared that under this condition, the community is facing condition 2, that is, CA-MRSA will be dominant in this case. The plot of the dynamics is shown in Figure 5.

5 Conclusion

In conclusion, the total population does not influence the dynamics of infection. To prevent Community-Acquired MRSA, the rate β of CA-MRSA should be larger than the rate β of HA-MRSA, where β = (recovered rate per day + death or discharge rate per day)/transmit rate per day between patients. Because CA-MRSA can transmit to healthy people while HA-MRSA cannot, it is important to prevent CA-MRSA be the dominant Staph bacteria in any community. Therefore, the disease control department could consider the following suggestions.

First, the parameter β of CA-MRSA could be increased by increasing the discharge rate of patients who colonized by CA-MRSA. The infective population should be strictly controlled in any community. Furthermore,

decreasing the transmit rate i_c by isolating the CA-MRSA infective group with the Susceptible group could also increase β. Another suggestion is that boost research fundings to new potential antibiotics that MRSA is not resistant to could also prevent CA-MRSA to be the dominant Staph Bacteria in the future.

Apart from that, the analysis result may be infected by missing parameters. For instance, the mutation rate of MSSA to MRSA, and the competition may exist between two types of MRSAs. Thus, further analysis may need to consider other parameters.

Reference

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