THE CANADIAN SCIENCE FAIR JOURNAL

ARTICLE

Herd Immunity in Global Pandemics

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This project's goal is to determine the relationship between the basic reproduction number (R0) and vaccine effectiveness against transmission (E), and how they might affect the critical vaccination level (Vc) in different global pandemics. Furthermore, a central inquiry is "what are the common features that global pandemics have when it comes to vaccinations and how can one decline the infection rate?" Herd immunity first appeared as a threshold theory that allowed people to identify the minimum number of vaccines to fight against diseases effectively. Assuming that if only a certain group of people were vaccinated, this proportion of society that is immune would limit the spread of a contagious pandemic, as those that are immune are scattered everywhere in the society at random, preventing an infected individual from spreading the virus further to people around him or her. In consequence, this significant milestone of herd immunity promoted the vaccination program as a whole, especially in recent decades. Nowadays, the notion of herd immunity is more commonly used as a scientific method of mathematical models, together with some scientific terms.

HYPOTHESIS

This science fair project will explore the relationship between the critical vaccination level and basic reproduction number, whether they are proportional or inversely proportional. If the theory of herd immunity is applied to ancient diseases or previous global epidemics such as smallpox, yellow fever, Ebola, cholera, and influenza, their critical vaccination level will be proportional to their basic reproduction number, where the R0 is the amount of secondary infectious cases generated from the primary infectious case. The higher the value of R0, the larger the proportion of the immune population that is needed in order to reach the decline of the pandemic.

MATERIALS & PROCEDURE

Firstly, there must be research for reliable databases and to find the most recent scientific reports regarding the selected pandemics listed in the hypothesis. The second step is to gather information about the pandemics from multiple academic sites. They are NCBI, WHO, Science Direct and Oxford University Press. Third, one must calculate the value of the secondary infection cases, which equals the basic reproduction number, and the recommended vaccine coverage threshold of those pandemics. In the fourth step, one will calculate the vaccine coverage according to the formula (1-1/ R0)*100% (Becker & Dietz, 1996) and use the herd immunity simulator online (How Herd Immunity Works, n.d.) to test for accuracy. Finally, one will organize the data into a table and graph to prove or disprove the hypothesis. Last but not least, one must show how each factor found for herd immunity affects the final result, and one must reflect upon the result.

A herd immunity simulator was utilized as a tool to testify the accuracy of the project. The user could only control two variables, the basic reproduction number, from "low" to "high", and the critical vaccination level, from 0% to 100%. In the simulator, 300 people start in two states, most being susceptible and a few being infected. During the middle of the simulation, the population group could be in 4 different states: susceptible (shown as the unimmunized population), infected, recovered and vaccinated. When the vaccinated and the recovered make up the majority of the population, leaving a few people as susceptible, herd immunity is achieved, and the simulation would end.

Method	R_0 (95% CI for R_0)	Vaccination coverage (%)
Richard model	1.68 (1.45, 1.91)	40.47
AR	1.000388 (1.000383, 1.000392)[a]	0.04
	1.1164 (1.1163, 1.1165)[b]	10.43
EG	1.46 (1.41, 1.52)	31.51
ML	1.42 (1.27, 1.57)	29.58
TD	1.71 (1.12, 2.03)	41.52
Gamma-distributed generation time	1.49 (1.0, 1.97)	32.88
R_0 using the final size of the epidemic	1.0 (0.91, 1.09)	0

Figure 1. Influenza, the value of R0 and Vc according to different models. In this figure, the average value of R0 and Vc is calculated using different methods. The confidence interval for R0 is 95%. (Bahrampour et al., 2019)

OBSERVATIONS

Both the linear trend (from Graph #2) and bar length (from Graph #1) show that the difference between the critical vaccination levels reduces when comparing smallpox versus yellow fever (6.87 smallpox > 4.8 yellow fever | Graph #1) and cholera versus Ebola and influenza. (2.15 cholera > 1.88 Ebola >1.54 influenza | Graph #1)

The basic reproduction number of smallpox, yellow fever, cholera, Ebola, and influenza were ranked from the highest to lowest from left to right (Graph #2), their critical vaccination level was also ranked from highest to lowest, left to right.

Table 1. In this table, all the data required to complete the graph are assembled together to better show their original source, and the location and year of the pandemics.

	Basic Reproduction #	Critical Vaccination Level (%)	Location & Time	Source of Database
Smallpox	6.87	85	Abakaliki, 1967	Oxford Uni Press
Yellow Fever	4.8	79	Africa, Oct. 2016	Science Direct
Cholera	2.15	53	Haiti, Oct. 2010	Nature Science Report
Ebola	1.88	47	West Africa, 2014	NCBI & Science Direct
Influenza	1.54	35	Canada 2009	NCBI

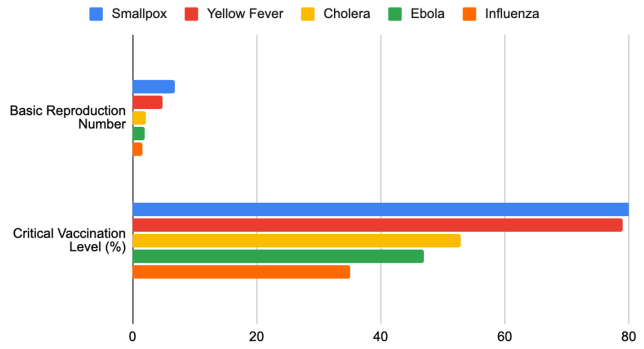

Figure 2. How critical vaccination level apply to different pandemics.

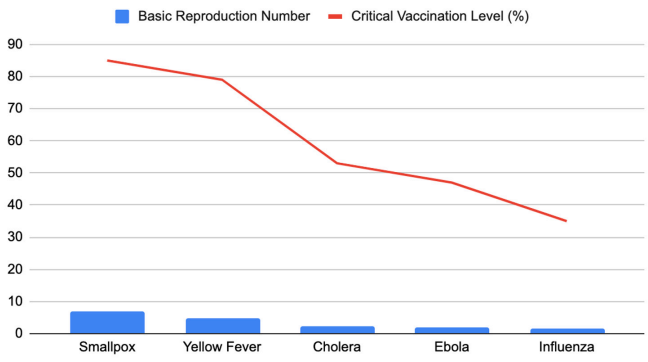

Figure 3. Basic reproduction number and critical vaccination level.

ANALYSIS

Two graphs are shown above. They consist of the exact same information and data, but they are plotted in different ways to better represent the result.

Graph #1 mainly emphasizes the relationship between the basic reproduction number and the critical vaccination level. In the Combo Chart, the two variables were compared under the specific contagious disease.

Graph #2 presented the two measured variables in decreasing order. One can see that the line descends as the bars range from highest to lowest.

The herd immunity simulator has verified the result in the calculation section. As illustrated in the simulator, the higher the basic reproduction number, the higher the critical vaccination level should be. Unfortunately, this simulator doesn't consist of an important factor called the "death rate", which indicates one death per thousand people. In real life, when this factor is applied, the low vaccine coverage would cause the basic reproduction numbers to stay at a relatively high level because there would not have not enough recovered and vaccinated populations to block the virus from the susceptible population. If the user slowly increases the vaccination rate, the vaccinated population will also contribute to the herd immunity, faster than the recovered population.

SOURCES OF ERROR

However, the project still encountered challenges throughout the research process; the refining of numerical information in a table full of other variables; finding the average value of the basic reproduction number, which varies according to the time period; the different threshold vaccine coverage is recommended by different websites; the critical vaccination level differs based on age and other factors.

All of the above challenges could cause inaccuracy in the final vaccine coverage. For example, the value of the basic reproduction number changes constantly according to the virus's living conditions, resulting in the limitations of this mathematical model, as follows: Mathematical models do calculate the value of a certain threshold efficiently and critically, but the dynamic of critical vaccination level does not fully depend on the R0. Furthermore, the population size (N), local human traditions (referring to the contact rate) and biological characteristics of the virus may also influence the final recommended vaccine coverage (referring to the infection duration). Certain deviations in the theorem of herd immunity are unavoidable, so when using it as a tool, constant updates regarding the virus are compulsory.

Speaking of the model's limitations, the value of the critical vaccination level is harder to handle in real life. Firstly, its value varies according to the efficacy of vaccines, and vaccine effectiveness against transmission wouldn't be 100% in real life. Especially as the immunizations provided by the vaccines always have a time limit, people will need to take a second or third shot after months. Generally speaking, the complexity of vaccine cov-

erage is a huge limitation when applying a mathematical model to the actual circumstances.

CONCLUSION

In conclusion, the hypothesis was proven correct. The graph overall shows the trend that the basic reproduction number is proportional to the critical vaccination level. According to observation (1), the higher the transmissibility of the disease (referring to R0), the higher the vaccination threshold. And according to observation (2), the larger the difference between the basic reproduction numbers, the smaller the difference there is between their vaccine coverages. When R0 took the role of the denominator in the formula: Vc = (1-1/R_0)*100% (Becker & Dietz, 1996), the bigger the denominator, the smaller the fraction, as the nominator stays the same. Subtracting this fraction (1/R_0) from one, one can see that the greater the value of 1/R_0 , the smaller the value 1-1/R_0 . After the calculations, the results show that the vaccine coverage will be proportional to the basic reproduction number.

The experiment originally planned to include the research of Spanish Flu (Influenza of 1918) and the Black Death Plague. Unfortunately, these diseases are fairly old and their value of R0 needs to be re-estimated, so it was impossible to get a recent, accurate database about these diseases. Moreover, neither WHO nor NCBI has ever provided their recommended vaccine coverage, so the backup plan was to change Black Death to Ebola and change Spanish Flu to Influenza. Another major issue was previously mentioned in the section called "Scientific Terms in the Model". When R0 equals or reaches a certain level, the value of E will be inversely proportional to the value of the critical vaccination level. Hence, a further optimization for this science fair project could include the factor effectiveness of vaccination against transmission to see the exact relationship E has with vaccine coverage.

The project "Herd Immunity in Global Pandemics" has successfully achieved its goal to figure out the relationship between R0, E and Vc. The greater the basic reproduction number, the greater the critical vaccination level.

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My name is Lang Zou (Amy), a fourteen-years old student who have studied in both Québec and Ontario, now attending Elmwood School in Ottawa. I have a great passion in science, mathematics and literature. During the pandemic of 2020-2021, I decided to further research about the spread of contagious diseases under the circumstance of COVID-19. The article "Herd Immunity In Global Pandemics" was written based on the science fair project that I had submitted to participate in the Canada Youth Science, Ottawa Regional Science Fair. From young age, I've always been fostering my curiosity in exploring the fantasy world of science. Moreover, I enjoyed sharing my insights and findings with the Canadian Science Fair Journal.