



Pharmacogenomics of Viruses

Kaitlyn Moore

College Park Scholars – Science & Global Change Program

Bioengineering

kamoore@umd.edu

College Park Scholars Academic Showcase, April 30, 2021



Introduction

Increased understanding of how to treat viruses and mitigate their spread has allowed the world to overcome many viruses and viral diseases that were once leading causes of death. Despite this progress, viruses such as influenza, Ebola, human immunodeficiency viruses, and coronaviruses remain a burden on human health. With the rise of human genome sequencing comes the opportunity to use such genetic information to determine drug interactions and patient responses in a field called pharmacogenomics. During the Spring 2021 semester, I was enrolled in CPSP359S: “Advanced Practicum: Research; Discovery Research”. Throughout the semester, I studied pharmacogenomics of viruses in order to determine if widespread preemptive pharmacogenomic testing could be used to reduce vaccine hesitancy in the event of a pandemic.

Methods

In CPSP359S, I learned about research processes and methods, then applied these discovery principles to articulate, investigate, and attempt to answer a research question in an area of interest. My research area was pharmacogenomics of viruses. The question I investigated throughout the semester was “How does drug individualization impact virus treatment efficacy and adverse effects?” My research method consisted of searching academic journals and publications on the use of pharmacogenomics and genetic testing in virus treatment. Many of the sources I used in my research were small-scale studies of the use of pharmacogenomics in treating viruses, such as hepatitis C virus (HCV) and human immunodeficiency virus (HIV), resulting in predications for future applications of pharmacogenomics in virus treatment. I also read current news articles regarding COVID-19 vaccine hesitancy to better understand the issue and its effect on efforts to achieve herd immunity.



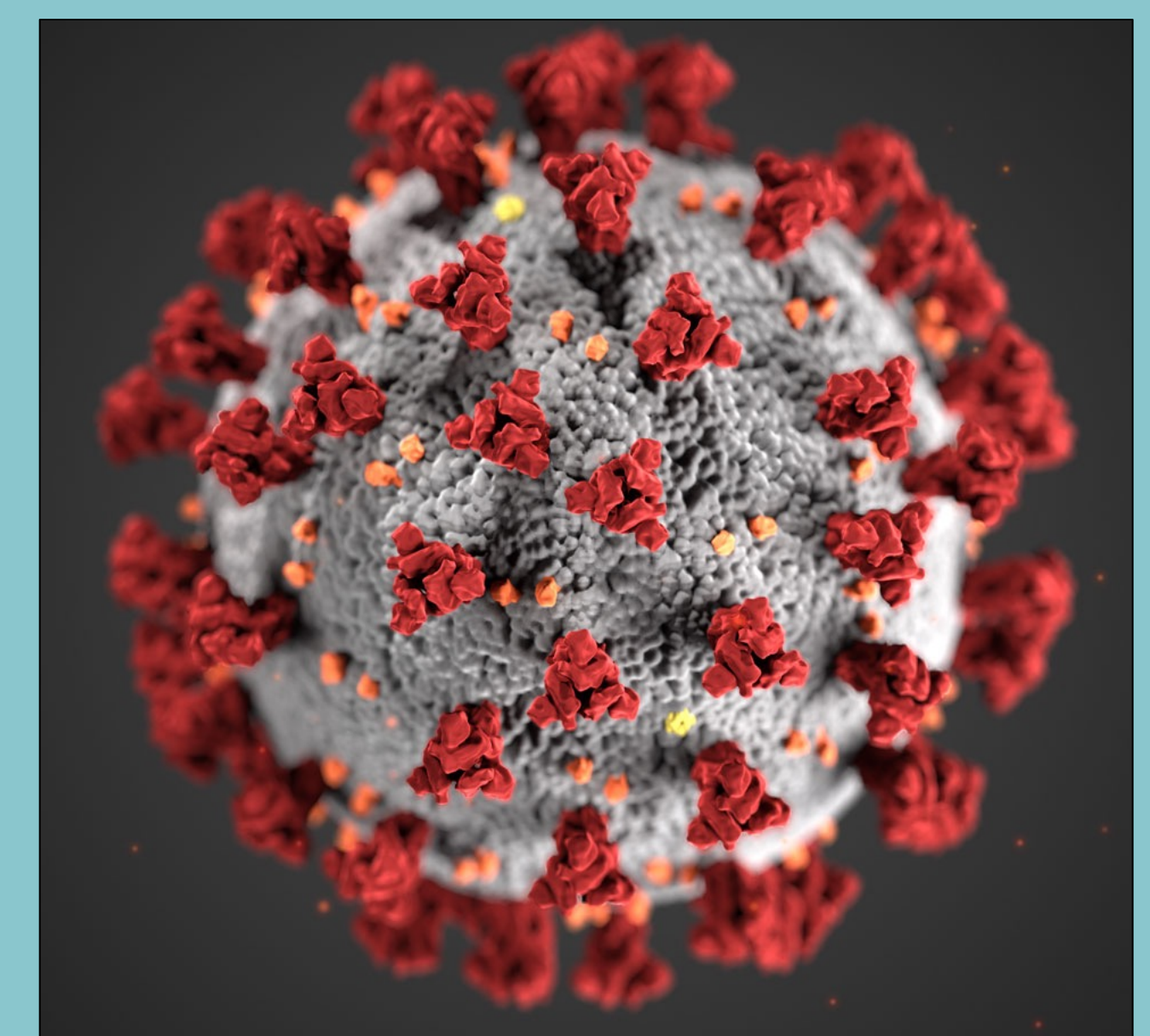
Graphic of pharmacogenomics. Genome sequence can determine a patient’s response to medicines. Image from <https://www.genome.gov/dna-day/15-ways/pharmacogenomics>

Results

- Challenges exist in optimizing the treatment of viruses
 - Low efficacy and adverse effects of antiviral therapeutics
- Vaccine hesitancy worldwide – millions delay or refuse vaccination
 - Vaccine hesitancy reduces efforts to achieve herd immunity
- Personalized medicine may be used to improve the treatment of viruses
 - Use of drug-gene associations and genetic markers in clinical medicine to select the optimal treatment for each patient
- Not enough data currently for widespread use of pharmacogenomics in the treatment of viruses, including COVID-19

Discussion

Knowledge of drug-gene associations and discovery of genetic markers has proven helpful in studies of HCV and HIV treatments, and recently in studies of COVID-19. A literature review suggests pharmacogenetic data may improve virus therapies; however, the potential impact of pharmacogenomic testing on virus treatment efficacy is unclear without additional data. Access to large quantities of genetic data becomes increasingly vital during a pandemic, when treatment outcomes are uncertain and treatment efficacy is of the utmost importance. Unfortunately, there is not enough data available for the widespread use of pharmacogenomics in treating the current COVID-19 pandemic. In the future, as multigene pharmacogenomic testing is made more accessible, genome screening will likely be able to identify profiles linked to viral disease and predict drug response, which may prove useful in the event of a future pandemic. If individuals learn about their own risks for getting vaccinated through genetic screening and pharmacogenomic testing, they may be less likely to develop negative attitudes about virus treatments solely based on stories of patients experiencing adverse effects that spread quickly through news headlines and social media. In the future, if pharmacogenomic testing is made more widespread and concrete evidence is obtained indicating pharmacogenomics improves virus treatment efficacy, predicting the optimal virus treatment for individual patients based on their own genetic data may be an approach to reduce vaccine hesitancy and help optimize treatment during a pandemic.



COVID-19. Image from <https://www.fda.gov/food/food-safety-during-emergencies/food-safety-and-coronavirus-disease-2019-covid-19>

Acknowledgments

I’d like to thank Dr. Lindemann for teaching me how to conduct research and enjoy the research process, as well as for her constant support and encouragement throughout the completion of my project. I would also like to thank Dr. Holtz and Dr. Merck for their amazing instruction and guidance over the last two years, and for making SGC an enjoyable and memorable experience. Lastly, thank you College Park Scholars for providing me this opportunity to learn and grow.

