

Introduction

Viruses like SARS COV-2 generally continue to evolve because of an alteration in the genetic sequences which occurred during replication of the genome. According to a lineage it is a genetically closely related group of virus variants which are derived from a common ancestor. Mutations are responsible for giving a virus certain variation among other viruses of SARS COV-2 viruses. There are several cases of SARS COV-2 that have been documented among different ethnic groups around the world including Africa and America. In order to inform local outbreak investigators and understand national trends, scientists compared the genetic differences between viruses in order to identify variants and how they are related to each other [1].

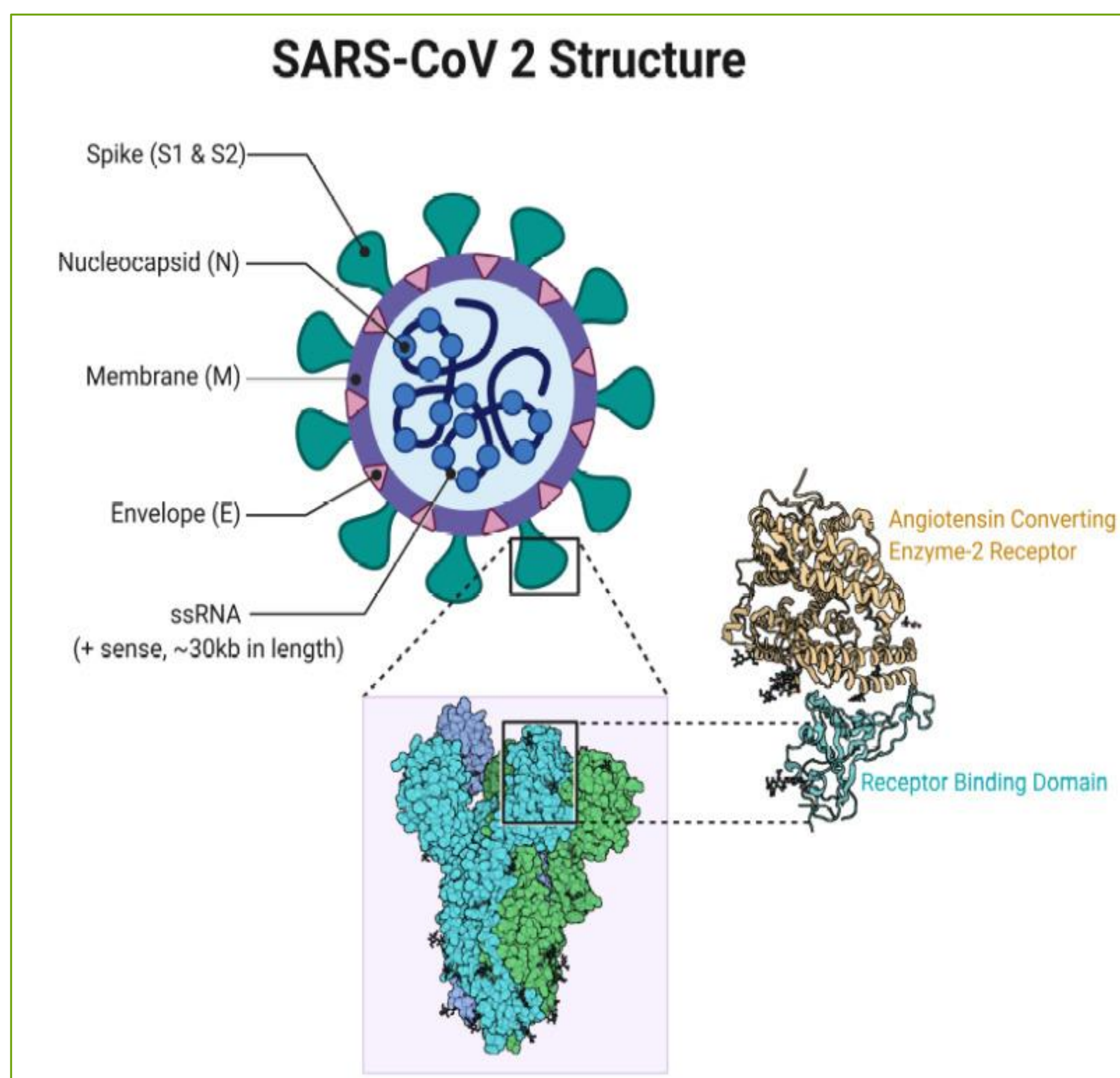


Figure 1. Structure of SARS COV-2.

How SARS COV-2 is different between ethnicities?

As known, the SARS COV-2 mediated COVID-19 pandemic has impacted mankind at an unprecedented scale. There has been many researches going around to understand the mechanism of viral infection and the development of vaccines or therapeutics to end this pandemic. The risk factors which increase the susceptibility to SARS COV-2 infection and manifestations of COVID-19 remain less explored. The HLA-systems play a major role in the virus. In order to understand this we used bioinformatics in many ethnic populations as it is responsible for effecting the recognition tools to probe all of the SARS COV-2 peptides which could elicit T-Cell response in humans. Scientists are trying to find out whether these potential epitopes were equally immunogenic across ethnicities. In order to find out, they must explore or study the distribution of the HLA alleles among different populations and their share of cognate epitopes [2].

The results have revealed that the immune recognition potential of SARS COV-2 epitopes tend to vary between different ethnic groups; while the south Asians are likely to recognize high numbers of CD8 specific epitopes. Europeans are likely to identify high numbers of CD4 specific epitopes. It has been theorized and provided clues that the latest mutations in SARS COV-2 are likely to alter the T-Cell mediated immunogenic responses among the studied ethnic populations [3].

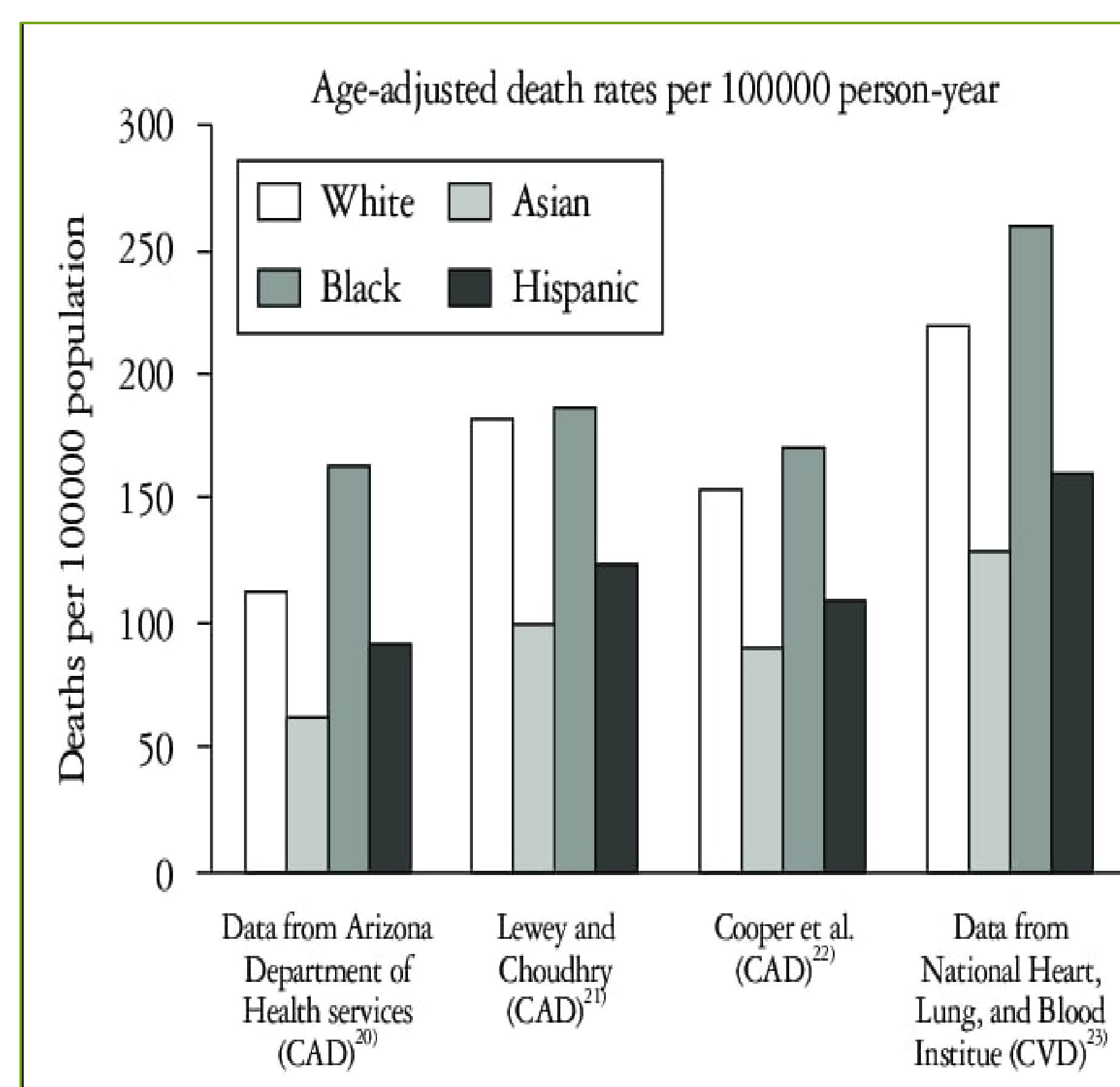


Figure 2. Mortality rates according to different datas.

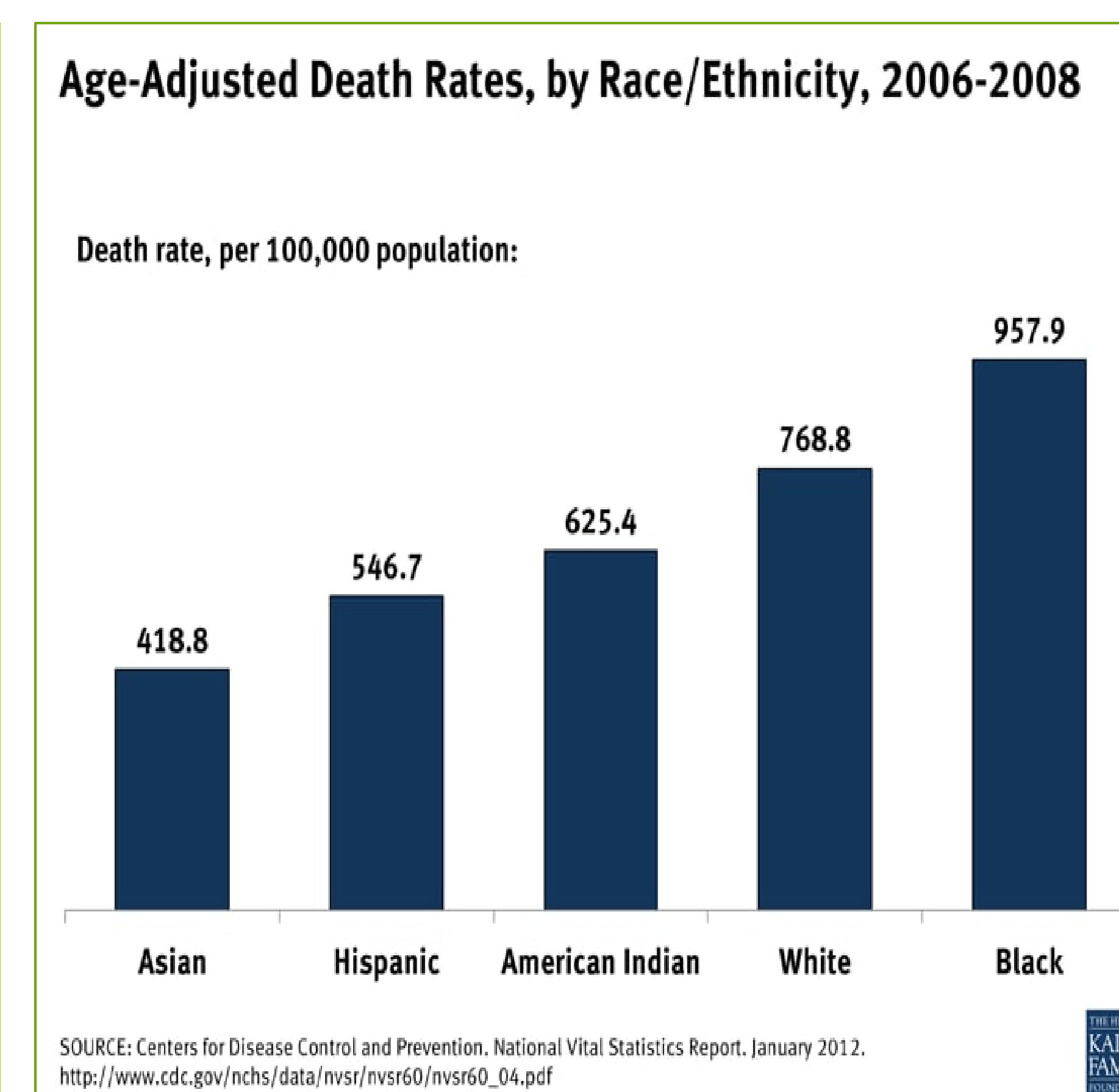


Figure 3. Mortality rates among different ethnicities.

Conclusion

Overall, the HLA-system plays a significant role in the variation of SARS COV-2 as it is expressed differently in different ethnicities. Epitopes were found out to be different among different groups of people around the globe, as there were variations in the number of CD8 and CD4 specific epitopes. It is believed that there are newer mutations of SARS COV-2 that could change the immune response of the T-Cell among different ethnicities. Treatment of the disease is still under studies as there are no current treatments available for the infected individuals.

Reference

1. CDC. Coronavirus Disease 2019 (COVID-19). Centers for Disease Control and Prevention. Published February 11, 2020. <https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-classifications.html>. [Accessed 3rd January 2022].
2. Gu T, Mack JA, Salvatore M, et al. Characteristics associated with racial/ethnic disparities in COVID-19 outcomes in an academic Health care system. JAMA Netw Open. 2020;3(10):e2025197. doi:10.1001/jamanetworkopen.2020.25197
3. Peng Y, Mentzer AJ, Liu G, et al. Broad and strong memory CD4+ and CD8+ T cells induced by SARS-CoV-2 in UK convalescent individuals following COVID-19. Nat Immunol. 2020;21(11):1336-1345. doi:10.1038/s41590-020-0782-6