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Why Indiscriminate Mass Vaccination Has Worsened the Pandemic

SARS-CoV-2 Readily Mutates and Thrives in the Vaccinated

By Dr. Peter McCullough
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Courageous Discourse

Theme: Science and Medicine

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A principle of infectious diseases is "antimicrobial stewardship" which involves choosing the right antibiotic for the right patient and never over-prescribing or blanket covering patients who don't need treatment.

Another principle is "narrowing the spectrum" of a drug once the organism is identified by culture or other methods. These fundamental approaches to the use of antibiotics work to limit the problem of bacterial resistance and the development of "superbugs." Every year hospitals each produce their antibiogram or report of their common infections encountered and what antibiotics either are effective (organism is sensitive) or ineffective (organism is resistant). In the SARS-CoV-2 pandemic these principles have been applied to the use of monoclonal antibodies and the process explains why various EUA products (e.g., bamlanivimab) were pulled from the market when they were understood to be no longer effective at neutralizing SARS-CoV-2. This entire thought process has been thrown out the window for COVID-19 vaccines. For 18 months the ancestral strain Wuhan Institute of Virology Spike protein was the featured antigen for Pfizer, Moderna, Janssen, AstraZeneca, and Novavax vaccines. Within a few months, there was mounting evidence that SARS-CoV-2 easily mutated to escape the reach of antibodies generated by the vaccines which would apply to serious invasive illness (IgG and IgM). Because the COVID-19 vaccines have never been demonstrated to neutralize SARS-CoV-2 in the nasopharynx, the only theoretical benefit would be for systemic disease. It has now become apparent that nature has the upper hand over the vaccine manufacturers as SARS-CoV-2 has far greater alacrity. Because replication can allow changes in genetic code that rapidly allow continued survival, SARS-CoV-2 enjoys a library of ~28k mutations of which ~4.5K are in the receptor binding domain of the Spike protein or the tip of the spear.

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Article

Emerging Vaccine-Breakthrough SARS-CoV-2 Variants

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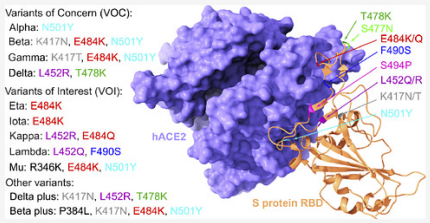
ABSTRACT: The surge of COVID-19 infections has been fueled by new SARS-CoV-2 variants, namely Alpha, Beta, Gamma, Delta, and so forth. The molecular mechanism underlying such surge is elusive due to the existence of 28 554 unique mutations, including 4 653 non-degenerate mutations on the spike protein. Understanding the molecular mechanism of SARS-CoV-2 transmission and evolution is a prerequisite to foresee the trend of emerging vaccine-breakthrough variants and the design of mutation-proof vaccines and monoclonal antibodies. We integrate the genotyping of 1 489 884 SARS-CoV-2 genomes, a library of 130 human antibodies, tens of thousands of mutational data, topological data analysis, and deep learning to reveal SARS-CoV-2 evolution mechanism and forecast emerging vaccine-breakthrough variants. We show that prevailing variants can be quantitatively explained by infectivity-strengthening and vaccine-escape (co-)mutations on the spike protein RBD due to natural selection and/or vaccination-induced evolutionary pressure. We illustrate that infectivity strengthening mutations were the main mechanism for viral evolution, while vaccine-escape mutations become a dominating viral evolutionary mechanism among highly vaccinated populations. We demonstrate that Lambda is as infectious as Delta but is more vaccine-resistant. We analyze emerging vaccine-breakthrough comutations in highly vaccinated countries, including the United Kingdom, the United States, Denmark, and so forth. Finally, we identify sets of comutations that have a high likelihood of massive growth: [A411S, L452R, T478K], [L452R, T478K, N501Y], [V401L, L452R, T478K], [K417N, L452R, T478K], [L452R, T478K, E484K, N501Y], and [P384L, K417N, E484K, N501Y]. We predict they can escape existing vaccines. We foresee an urgent need to develop new virus combating strategies.



KEYWORDS: *COVID-19, SARS-CoV-2, comutations, vaccine-breakthrough, vaccine-resistant, infectivity*

Wang R, Chen J, Hozumi Y, Yin C, Wei GW. Emerging Vaccine-Breakthrough SARS-CoV-2 Variants. ACS Infect Dis. 2022 Mar 11;8(3):546-556. doi: 10.1021/acsinfecdis.1c00557. Epub 2022 Feb 8. PMID: 35133792; PMCID: PMC8848511.

Wang and colleagues using detailed modeling techniques of the mutations prevalent in the more intensely vaccinated countries has shown indeed mass vaccination is backfiring and fueling more viral resistance to the limited antibody library that could be generated by the vaccines.[i] Wang's analysis suggests that future vaccine development against SARS-CoV-2 is hopeless. The virus is simply too nimble and can manipulate the "binding free energy" between the RBD and its human target the ACE2 receptor. This means the more vaccinations are delivered the greater the number of mutant stains and the longer the virus will propagate and extend the pandemic. Thus, a key step in ending the pandemic will be termination of mass vaccination. The virus doesn't stop until mankind stops.

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Note

[i] Wang R, Chen J, Hozumi Y, Yin C, Wei GW. Emerging Vaccine-Breakthrough SARS-CoV-2 Variants. ACS Infect Dis. 2022 Mar 11;8(3):546-556. doi: 10.1021/acsinfecdis.1c00557. Epub 2022 Feb 8. PMID: 35133792; PMCID: PMC8848511.

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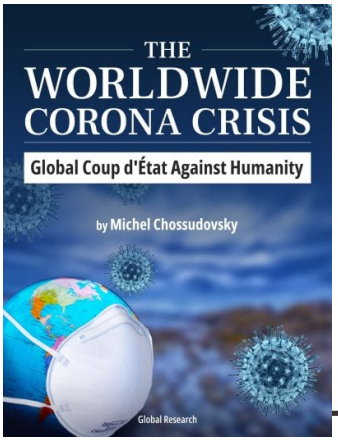

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