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Stealth Adapted Coronaviruses Resulting from the Use of Covid-19 Vaccines

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Abstract

The continuing emergence of variant forms of the SARS-CoV-2 virus is the probable consequence of using the current Covid-19 vaccines. These vaccines do not induce the same immunity as do naturally occurring infections. First, the vaccines are given by intramuscular injections. This is far less effective than natural infection in stimulating the development of virus specific immunoglobulin A (IgA) producing cells and cytotoxic T cells (CTL) within the respiratory mucosa. Virus exposure in a previously vaccinated individual with limited mucosal immunity increases the risk of a persistent, subclinical infection, which will initially be restricted to the superficial mucosa. NIH and CDC officials have alluded to this possibility in advising those who have been vaccinated to continue wearing masks lest they may infect others. The second major distinction between the Covid-19 vaccines and natural infection is the FDA allowance of using only one component as the antigen, namely the spike protein. Deletion or other modifications of a single targeted component can occur more readily as an immune evasion mechanism than concurrent genetic modifications of multiple antigenic components. Covid-19 vaccine evoked immunity will, therefore, exert a strong immunoselective pressure for major modifications or deletion of the spike protein. With successive additional changes in the few remaining viral components that are normally targeted by cellular immunity, as well as the incorporation of sufficient genetic sequences from cells and other microbes; non-immunogenic, pathogenic viruses will then emerge. These viruses will no longer be immunologically restricted to the respiratory mucosa and will become more widespread within the body. The immune evasion/escape mechanism utilized in this manner is termed stealth adaptation. It was initially identified in the cytomegaloviruses of monkeys used to produce polio vaccines. Not only were these viruses probably involved in causing AIDS, but they can account for the rise in many chronic illnesses, such as autism and the chronic fatigue syndrome (CFS). Until proven otherwise, the neuropsychiatric symptoms of the Long Covid syndrome in previously healthy individuals, are consistent with brain infection with stealth adapted coronaviruses. This illness is, therefore, likely to be infectious, including the possibility of transplacental transmission. Testing for stealth adapted viruses in these patients is best performed using virus cultures followed by genetic sequencing. Even though cellular immunity fails to effectively suppress stealth adapted viruses, these viruses as well as the conventional viruses from which they are derived, are still susceptible to a non-immunological anti-virus defense mechanism mediated by the alternative cellular energy (ACE) pathway. This pathway is reflected in an added kinetic activity of the body's fluids. The environmental life-force energy for the ACE pathway is called KELEA (Kinetic Energy Limiting Electrostatic Attraction). Water with high levels of KELEA is available for clinical studies.

Enhancing the ACE pathway in those who are susceptible to severe Covid-19 illness and in Long Covid syndrome patients is arguably preferable to risking the development of new forms of stealth adapted viruses by using the current Covid-19 vaccines.

Vaccine Induced Immunity is Not the Equivalent of Natural Infection

- Intramuscular route of vaccine administration achieves less mucosal immunity than does natural infection via the respiratory mucosa
- Lower secretory IgA and local cytotoxic T cells allows for persistent, asymptomatic infection in vaccine recipients
- Vaccine immunity is solely directed to the spike protein, whereas additional proteins are targeted in response to natural infection
- Immune selection against one protein occurs more readily, especially if the infection is persistent
- Vaccinated individuals will not be protected from infection with spike protein deficient viruses. Spike protein is not essential for infectivity.

Formation of Virus Variants

- Directly related to the number of infected individuals. Therefore, vaccinations will reduce the likelihood of more virulent variants by minimizing symptomatic infections.
- Vaccines can, however, specifically predispose to variants with deletions or major modifications of the spike protein coding gene. These viruses can subsequently lose the remaining viral components that are normally targeted by the cellular immune system.
- Thus, while vaccines may reduce the formation of more virulent viruses, they will likely facilitate the development of immune escape variants.

Stealth Adaptation

- Stealth adaptation is an immune evasion mechanism in which there is deletion or mutation of the genes coding for the relatively few virus components that are normally targeted by the cellular immune system

Long Covid Syndrome

- Combination of symptoms resulting from residual damage from the initial infection, plus a new symptoms consistent with brain damage.
- Fatigue, cognitive impairments, mood disorders, and autonomic nervous system dysregulation are in common with CFS
- More likely to occur in patients with multiple early symptoms of Covid-19 infection. (Possibly related to activation of a preexisting stealth adapted virus infection)
- Conventional culturing may be inadequate to detect the presence of stealth adapted corona and other viruses
- Potentially infectious illness with long-term consequences

- Incorporation of additional genetic sequences from cellular genome and from other microbes to restore infectivity and transmissibility
- Genetic instability of the remaining genes of the originating virus and of the incorporated "renegade" cellular and microbial genes
- Generic process potentially applicable to all viruses, including SARS-CoV-2

Initial Indications of Stealth Adapted Viruses

- ✓ Positive PCR assays using low stringency conditions in the testing of blood and cerebrospinal fluids (CSF) of patients with various neurological diseases, including the chronic fatigue syndrome (CFS).
- ✓ Positive PCR in brain biopsy from a woman with periventricular opacities on MRI and a severe cognitive disorder. The biopsy showed neuronal and glial cell damage, yet there was no inflammation.
- ✓ Positive virus cultures on the blood of a PCR positive CFS patient and on the CSF of a comatose patient with a history of bipolar psychosis.
- ✓ Foamy vacuolated cells with syncytia seen in the two cultures.

Molecular Characterization of the Initially Cultured Stealth Adapted Virus

- One of three PCR amplified sequences showed partial homology to human cytomegalovirus. *Am J Path* 145: 440-451, 1994.
- Subsequently this and some other cloned sequences were shown to be nearly identical with regions of African green monkey simian cytomegalovirus (SCMV). *Clin Diag Virol* 4: 93-103, 1995
- Implied origin from monkeys used to produce polio vaccines
- Potential relevance to origin of HIV
- Imposed restriction on further clinical testing at University

Updated Molecular Characterization of Stealth Virus-1 (Sequence Data on GenBank)

- ✓ Most of the DNA migrates in agarose gel electrophoresis at a band size of approximately 20 kb. EcoR1 and Sac1 derived clones
- ✓ 200 clones match to approximately half of the SCMV genome. Uneven distribution of the matching clones with several parts of SCMV genome being repeatedly represented and no matching to other regions of SCMV
- ✓ 14 clones match to non-coding regions of the human genome. Some of these cellular sequences have presumably replaced previously present African green monkey cellular sequences by homologous recombination
- ✓ 18 clones match to Ochrobactrum; 10 to mycoplasma, 6 to undefined bacteria
- ✓ Closely related SCMV sequences in viruses from several other patients e.g., stealth virus-2 from a comatose patient with history of a bipolar psychosis

Heterogeneity of Cultured Viruses

- Only some cultures yield similar PCR products as do cultures of stealth virus 1 and stealth virus-2, using the same set of PCR primers.
- Partial sequencing of PCR products generated using this set of primers in cultures from three other CFS patients have identified cellular sequences derived from the rhesus monkey genome.
- Positive PCR in another culture only after reverse transcription of RNA to DNA using the same set of primers
- Evidence of genetic instability of similar cellular-derived sequences in viruses cultured from different patients

Stealth Adapted Virus Infections

- Brain is particularly susceptible to symptomatic illness resulting from the limited localized cellular damage caused by the virus.
- Illness may also occur from specific cellular genes present in virus
- Illness can be misidentified as a bacterial infection due to the presence of bacteria-derived sequences, e.g., chronic Lyme, PANDAS
- Potential of person-to-person transmission, as well as transplacental transmission to offspring. (Autism, ADHD, etc.)
- Molecular & serological markers are unreliable indicators of infection
- Cultures are required, possibly followed by genetic sequencing