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The Endgame

By  Geert Vanden Bossche

The Outcome of Vaccine-Associated Viral Phenotype Selection Will Overrule the Effect of Vaccine-Associated Human Genome Editing.

I regularly read the contributions of Julian Gillespie, who, along with his colleagues, tirelessly battles the Australian judicial system, regulatory authorities, and especially Moderna and Pfizer. They legitimately argue that these companies circumvented applicable laws by not seeking approval for their mRNA-based Covid-19 (C-19) vaccines under the GMO (Genetically Modified Organism) statutes. This particularly applies to the mRNA vaccines, as they are heavily contaminated with bacterial DNA from the manufacturing process (Australian DNA CONTAMINATION Confirmed .. in Australian vials of Pfizer and Moderna .. NOT safe for Humans (substack.com).

Those who make the effort to examine the remarkable evidence presented by Julian and his team regarding the safety concerns of the mRNA C-19 vaccines and the widespread fraud by the despicable lobby of governmental agencies and Big Pharma primarily ask one major question:

> To what extent could the integration of bacterial DNA, heavily contaminating Pfizer and Moderna vaccines, cause changes or damage to the genome of C-19 vaccinated individuals? Could such integration into germ cells potentially even lead to these changes being passed on to future generations?

There is growing evidence that this kind of insertional mutagenesis could, for example, lead to the activation of oncogenes or the inhibition of tumor suppressor genes, *effects that primarily manifest in the medium to long term*. How will highly C-19 vaccinated countries fare if it turns out that the mRNA-based C-19 vaccines have caused genetic impairments in millions? Will such societies remain viable and still be capable of producing healthy offspring?

The reckless and insane *genetic manipulation of large segments of the human*

yet targeted *genetic selection of Sars-CoV-2* (SC-2) *variants* by causing highly C-19 vaccinated populations to exert immune pressure on the virus without preventing its spread. This has led to significant *viral immune escape*. This means that among the many spontaneous viral mutants, phenotypes have been

selected that enjoy a competitive advantage in this hostile immune context, thereby dominating the original virus and less adapted variants.

It's important to note that depending on the strength of the collective immune pressure exerted by highly C-19 vaccinated populations, viral genotypes/variants with quite *remarkable* changes in their phenotypic characteristics may be selected (e.g., Omicron, BA.2.86/JN.1). As the replication cycle of SC-2 takes only about 10 hours, such new phenotypes can also increase their prevalence *very rapidly*. The combination of both factors therefore leads to *drastic and acute changes* in the viral population, contrasting with the mid to long-term changes in genetically manipulated (i.e., mRNA-vaccinated) individuals.

I believe it is evident that the global impact of the large-scale C-19 vaccination program on the virus's virulence *will manifest much sooner* than the detrimental impact of the DNA-contaminated mRNA vaccines on the population's health status (including reproductive health).

I've repeatedly emphasized that mRNA vaccines not only promote viral immune escape but also cause *immune refocusing* (https://tinyurl.com/vssiiep). This phenomenon involves the immune response increasingly targeting conserved spike-associated epitopes of the virus, often containing self-mimicking motifs.

Immune refocusing can slow the spread of the virus by delaying viral immune escape, benefiting the training of innate cell-mediated immunity in the unvaccinated. However, immune refocusing comes at the expense of the vaccinated population's health, leading to *autoimmune diseases, cancers*, and eventually more cases of long COVID. The combination of *long* COVID and the harmful genetic effects of the widespread, reckless use of mRNA-based C-19 vaccines that are heavily contaminated with bacterial DNA contributes to the *excess deaths and diminishes the productivity and survival chances of highly C-19 vaccinated populations.*

However, as the effects of immune derailment and genetic editing are likely to primarily result in premature death in the *medium to long term*, the current population-level immune pressure on viral transmissibility is currently only slightly reduced, allowing SC-2 to continue its catastrophic immune escape. This will eventually cause the virus to evolve into a form so adapted to the ongoing suboptimal immune pressure that it can spread unchecked within the host itself. Given the rapid selection of mutated viral genotypes/variants and the virus's quick replication, such evolution could happen overnight. For highly C-19 vaccinated populations, it has now merely become a matter of exerting sufficient collective immune pressure on viral *intra-host* transmissibility to enable the selection and dominant propagation of a new coronavirus that can spread unchecked within the fully vaccinated host (i.e., HI-VI-CRON[1]).

There is no doubt that SC-2's ability to spread from host to host is now close to reaching its maximum capacity in highly C-19 vaccinated populations. Consequently, it is clear that *Nature is highly unlikely to deal with countless long-term health damages caused by the C-19 mass vaccination program*, especially if conducted with mRNA-based vaccines. Nature will put a stop to this by intervening in a way to ensure that only the portion of the population whose health and immune protective capacity have not been compromised by the C-19 vaccines or severe C-19 disease following natural infection survives and reproduces. This implies that the part of the population that *exclusively* relies on obsolete antibodies from previous C-19 vaccination or SC-2 infection *cannot contribute to restoring a healthy human population*. This deficiency relates to a large group of C-19 vaccinated individuals and therefore also involves numerous individuals whose genomes may have been genetically modified due to mRNA vaccination.

Conclusion:

Because of all of the above, it must be stressed that the final outcome and health impact of this large-scale gain-of-function experiment on the very human species will be determined by the evolutionary dynamics of the virus, which is currently struggling to survive due to large-scale immune pressure on its transmissibility, rather than by vaccine-associated genetic or immune-mediated diseases.

[1] HI-VI-CRON refers to a new coronavirus that supplants the Omi**cron** family and is **hi**ghly **vi**rulent in C-19 vaccinees

Geert Vanden Bossche received his DVM from the University of Ghent, Belgium, and his PhD degree in Virology from the University of Hohenheim, Germany. He held adjunct faculty appointments at universities in Belgium and Germany. After his career in Academia, Geert joined several vaccine companies (GSK Biologicals, Novartis Vaccines, Solvay Biologicals) to serve various roles in vaccine R&D as well as in late vaccine development.

Geert then moved on to join the Bill & Melinda Gates Foundation's Global Health Discovery team in Seattle (USA) as Senior Program

Officer; he then worked with the Global Alliance for Vaccines and Immunization (GAVI) in Geneva as Senior Ebola Program Manager. At GAVI he tracked efforts to develop an Ebola vaccine. He also represented GAVI in fora with other partners, including WHO, to review progress on the fight against Ebola and to build plans for global pandemic preparedness.

Back in 2015, Geert scrutinized and questioned the safety of the Ebola vaccine that was used in ring vaccination trials conducted by WHO in Guinea. His critical scientific analysis and report on the data published by WHO in the Lancet in 2015 was sent to all international health and regulatory authorities involved in the Ebola vaccination program. After working for GAVI, Geert joined the German Center for Infection Research in Cologne as Head of the Vaccine Development Office. He is at present primarily serving as a Biotech / Vaccine consultant while also conducting his own research on Natural Killer cell-based vaccines.

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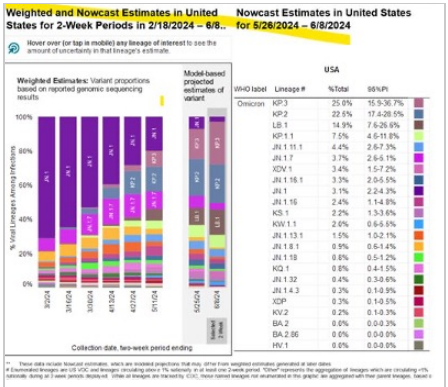

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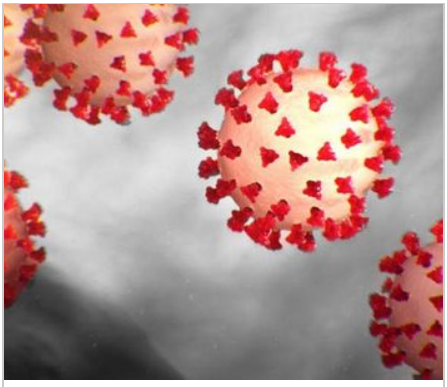

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