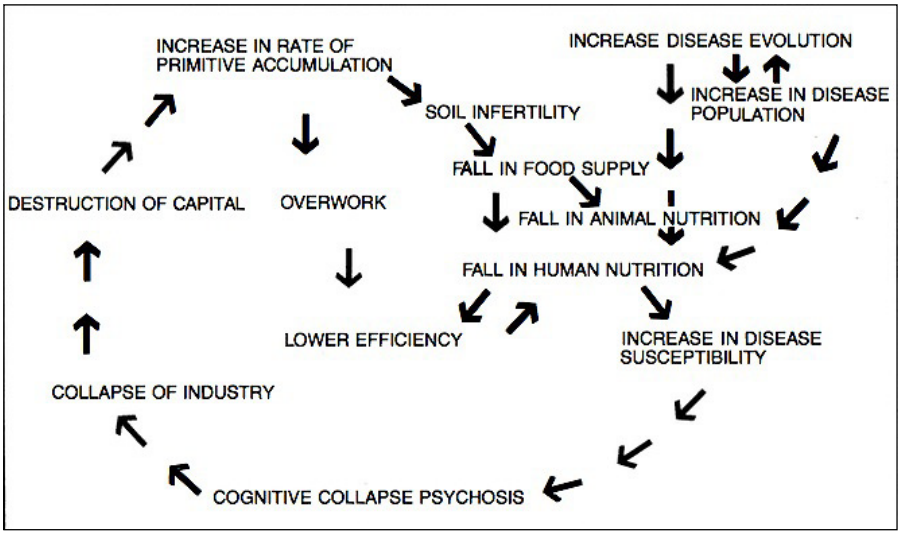
The Rapid Evolution of Dangerous New COVID-19 Variants Appears Related to Immune System Collapse

by Ned Rosinsky, MD

Jan. 17—The worldwide epidemic COVID-19 has so far killed more than 5.5 million people, including over 860,000 in the United States, and has sickened over 328 million people worldwide. This devastating epidemic was foreseen by Lyndon LaRouche 47 years ago, when he warned that the anti-industrial policy of Zero Growth would inevitably result in the development of new pandemic diseases.

In September of 1974, in support of his own policy, later expressed in his 1983 book, *There Are No Limits to Growth*, LaRouche formed an Ecological Holocaust Task Force to study and document the disastrous consequences of the policy of Zero Growth. The resulting study identified two interrelated causation loops. One loop started with Zero Growth, resulting in depletion of resources, fall in living standards, decreased human and animal nutrition, decreased immunity to disease, increased disease rates, collapse of the labor force, collapse of industrial production, and the circle closed with more extreme collapse of living standards. A second loop started with the increase in disease rates from the first loop, leading to an increase in the size of the diseased human and animal population, which would lead to an increase in the evolutionary potential for the creation of new diseases, and further increases in disease rates.

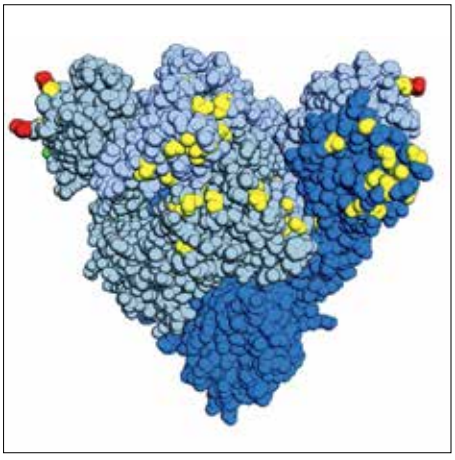


Source: *New Solidarity*, Jan. 16, 1975.

The main causal pathways of an "ecological holocaust." The driving factor is the increase in primitive accumulation (top)—using resources without maintaining them, such as materials, energy, or human labor. The result is the exhaustion of material resources and the exhaustion of the labor force, which result in decreased nutrition, weakened immune systems, increased disease, and further collapse of the labor force.

The first confirmation of this second loop after the formation of the Task Force was the development of the HIV/AIDS epidemic in the 1980s. This was a new disease originating in Africa—a prime example of an area of enforced Zero Growth—in which a monkey virus evolved to be able to infect humans. Further research by mapping gene evolution later showed that HIV/AIDS had started in Africa earlier, at the latest in the early 1930s at the time of the worldwide Great Depression. However, due to the slow progression of the disease, and the miserable health conditions, disease monitoring, and general medical care in Africa, it was not even recognized as a new disease until it invaded the advanced sector in the 1980s.

At the time of the formation of the Task Force, the second loop describing the evolution of new disease seemed evident, but the detailed explanation in biological terms was not available, due to the state of the science. With the recent explosion of research potential—including the development of rapid gene sequencing in the 1990s, the full sequencing of the human genome in



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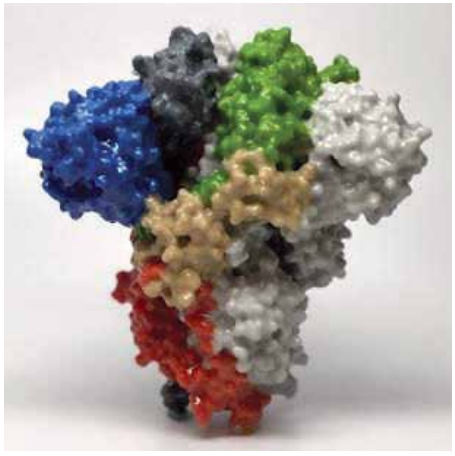

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The Omicron spike protein (left) attaches to a protein on the surface of cells of the respiratory tract, the ACE enzyme. Successful attachment requires a specific fit between the two proteins. The attachment site is a target for protection by the immune system. Compared to the Delta spike (right), the Omicron spike has large top bulges surrounding the attachment site, making it hard for the immune system protein (antibody) to intervene. Thus Omicron can partially evade the immunity provided by vaccination for the original COVID-19.

the early 2000s, and the more recent development of the ability to produce the genetic material RNA in the lab—we are beginning to fill in the gaps in understanding how low living standards facilitate the evolution of new contagious and deadly diseases. To explain how these advancements have improved our understanding of disease evolution, I will first discuss some basic aspects of genetics and evolution.

Gene Expression

Living organisms' genetic material takes the form of DNA in bacteria, plants and animals. DNA is a very large molecule, consisting of a string of molecular subunits called bases (actually, there are two intertwined strings, forming a double helix). There are four possible bases, so the string reads like a series of "words" made from four possible molecular "letters." The "words" are three "letters" or subunits long. The total possible number of letter arrangements in each of these words is 4x4x4, or 64 possible combinations of the letters.

The gene expresses itself in the organism by coding for the formation of proteins. The proteins are themselves large molecules composed of subunits called amino acids, and also arranged as strings of the subunits. There are 20 different possible protein amino acids. The genetic code identifies each of the "words" in the gene, with the choice of a specific amino acid in the protein, and there is a molecular apparatus in the cell that links up specific choices of amino acids according to the series of words in the gene. (Since there are 64 distinct "words," and only 20 amino acids, there is a redundancy in the code in which more than one DNA "word" is identified with some of the amino acids.)

Each of the 20 amino acids has a molecular side chain with specific chemical or structural properties, such as positive or negative charge. These side chains contribute to the structure and function of the completed protein. The protein activities in the cell include forming supporting structures—contracting in muscle movement, acting as antibodies if fighting infections, and facilitating the many chemical reactions in metabolism when acting as enzymes.

Proteins guide the functioning of the living state, and the code for producing the proteins lies in the genes.

Gene Mutations

When living organisms grow and produce more cells, the genes of the organisms are copied into new DNA, and copies of all the genes are present in each new cell. Most of the time, only a small proportion of the genes in any particular cell are active, just the genes needed for the functioning of that cell type. The switching on and off of the activity of the genes is determined by an elaborate molecular control mechanism that is only partially understood. When organisms reproduce, copies of the genes are passed on to the offspring. Most of the time the new copies of genes are identical to the original genes. However, occasionally a mistake is made in the copying process, the new DNA is not identical to the original DNA, and one or more of the base unit letters has been changed. This change is called a mutation. The molecular word formed by the three-subunit group that includes the mutation change becomes another word. This word change then may code for a different amino acid when the DNA gives instructions to build a protein, and the different amino acid may have important effects on the functioning of the protein.

In addition to single base copying errors, mutations can occur due to entire segments of multiple bases

being inserted into genes, or multiple base segments being deleted from genes.

Viral Genes, Viral Mutations, COVID Variants

Viruses have genes. The viral gene material may be DNA, or the closely related RNA. The genetic material RNA, like DNA, consists of strings of four possible base subunits, and with each three bases forming a genetic "word." RNA can mutate when it is miscopied during the reproduction of the virus. Viruses are small, and the number of genes is likewise small. Viruses typically reproduce by gaining entry into the cells of higher organisms, such as plants or animals, and using their cells to reproduce the virus genes and virus proteins. These virus components are then assembled into complete viruses, which then leave the host cell. COVID-19 has 29 genes, and the total number of subunit bases composing these genes is approximately 30,000. In comparison, humans have approximately 20-25,000 genes, and the human DNA is composed of three billion base pairs.

A key step in viral reproduction is gaining entrance into the host cell. In the case of COVID-19, this step is facilitated by the spike protein, a protein on the surface of the virus. It attaches to a specific site on the host cell termed angiotensin-converting enzyme (ACE). ACE is a protein that functions as an enzyme on the surface of some normal cells, particularly in the lungs, and its activity is involved in the maintenance of normal blood pressure. The COVID-19 virus makes use of this ACE protein by attaching to the protein in a molecular lock-and-key fashion, ultimately bringing the entire virus into the cell. The transmissibility of COVID-19 is related to the efficiency of this spike-ACE interaction. Like other proteins used by COVID-19, the spike protein is produced in the host cell by a specific viral gene, the spike gene. Mutations in the spike gene produce changes in the spike protein, which is a major source of variants seen in the epidemic.

Most of the mutations that occur have either no effect or a negative effect on the ability of the spike protein to facilitate cell entrance, but occasionally a mutation helps this process. The Delta variant has a significant increase in transmissibility, due to changes in the spike gene. Likewise, Omicron has a further increase in transmissibility for a similar reason. However, the occurrence of new variants, such as Delta or Omicron, usually involve more than one mutation to produce the final active variant.

Since most COVID-19 mutations affect the virus' activity negatively, there is selection pressure against them, and they die off. This is termed purifying selection, since it tends to maintain the current gene structure in the viral population. Occasional mutations that have a positive effect on viral activity, such as increased transmissibility, or resistance to a current vaccine, have selection in their favor.

COVID-19 has a molecular "proofreading" mechanism involved in its gene reproduction, which can check the accuracy of the copying as it is done, and repair mutations as they occur. For an actively transmitting single line of individual virus particles, the rate of failure of this process allows approximately one mutation per month.

COVID-19 Compared to HIV

HIV, human immunodeficiency virus, is also an RNA virus. HIV is transmitted sexually and through body fluids, unlike COVID-19, which is easily transmitted through respiratory means, such as air droplets from sneezing or coughing. Both of these viruses were originally active in other species, and then jumped to humans. HIV came from monkeys, and COVID-19 most likely came from bats, with possible involvement of passage through another species, such as pangolins.

HIV has infected approximately 100 million people and killed approximately 25-40 million people since the first major outbreak in the advanced sector in the 1980s. COVID-19 has infected over 328 million people and killed approximately 5.5 million people in the two-plus years since its arrival in late 2019.

COVID-19 genes are made of RNA, which can be used to code for production of viral proteins in the host cell, or to produce copies of itself. COVID-19 has a rapid onset of action, within days of infection, and usually is cleared by the host within approximately a week. HIV requires more genetic steps to function. After gaining entrance into the cell, it makes a DNA copy of itself which is incorporated into the DNA of the host. This DNA copy then produces RNA copies, which are used to make viral protein and more viral RNA.

HIV typically takes at least several years to affect the health of the person infected. HIV can also enter certain white blood cells and remain dormant for prolonged periods of time, during which it may not be accessible to the medications used in treatment. HIV does

not have a proofreading ability, so mutations are approximately four times as likely as in COVID-19 over similar time periods. Mutations are so likely in HIV infections over the long course of illness, that each infected person has a large number of mutations active simultaneously on a continuous basis, and the HIV infection in each patient has a mutation profile that is genetically unique to that patient. This is one of the reasons that it has been so difficult to create a vaccine for HIV, whereas a vaccine for COVID-19 was developed in 12 months.

NASA

This gene-sequencing machine, used by an astronaut, reflects advances allowing smaller, lighter machines suitable for space flight. Gene-sequencing machines perform multiple chemical reactions that originally required significant human labor in labs and large amounts of time. The technology was first developed in 1974, became completely automated by 1986, and became very rapid and largely free of errors over the past 10 years.

COVID-19 in Patients with Impaired Immune Systems

People with weakened immune systems due to cancer may have prolonged COVID-19 infections, with the production of a wide variety of mutations. This has been reported repeatedly in individual case reviews. For example, a peer-reviewed report published in the *International Journal of Infectious Diseases* in October 2021 describes a 21-year-old woman with B-cell acute lymphocytic leukemia, a form of blood cancer, who contracted COVID-19. She had tests showing the virus for 78 days, and continued to have positive PCR tests for 97 days. During this time multiple sequencing tests showed that she developed 12 mutations. The last sample, at 97 days, contained seven mutations, indicating that the virus had evolved and eliminated five variations. Another case was reported Dec. 23, 2020, in the journal *Cell* by lead author V.A. Avanzato, involving a woman with chronic lymphocytic leukemia, who continued to shed COVID-19 virus for 70 days after the infection was diagnosed, and showed viral RNA on tests up to 105 days. The study stated, "We observed marked within-host genomic evolution of SARS-CoV-2 [the COVID-19 virus —ed.] with continuous turnover of dominant viral variants."A case report of a patient with HIV in South Africa showed that the COVID-19 virus was carried for seven months, with the patient producing 32 mutations. While not yet peer reviewed, this case is consistent with the numerous reports of proliferation of mutations in patients with cancer and immune system weakness.

A research group at Stanford University is working on a model of a possible link between HIV/AIDS, when it is not treated, and the development of the Omicron variant. Omicron has numerous mutations that make it unique. The Stanford group reported that a patient with untreated HIV/AIDS who was infected with COVID-19 was producing a large number of COVID-19 variants over several weeks. After starting an AIDS medication, her immune system improved, and she quickly fought off the COVID-19 infection and stopped producing COVID-19 mutations. The scientists reasoned that untreated HIV infections result in an impairment of the immune system. Thus, HIV/AIDS can cause prolonged infections with other diseases such as COVID-19, and increased mutations. It is noted that half of the approximately 23.8 million people on the African continent with HIV infections are currently untreated with medication, principally due to lack of availability of medical care. This population may be a huge reservoir for COVID-19 mutation.

The Stanford scientists are working on a computer model of the generation of multiple simultaneous mutations which appear to be responsible for the Omicron variant and other past variants. They reason that untreated HIV/AIDS, weakening the immune system, reduces the purifying selection that normally occurs with healthy immune systems, and which decreases mutations and even more powerfully suppresses multiple mutations. This decrease in purifying selection, allowing mutations to persist which may have negative ef-

fects on the virus, gives the virus the opportunity to develop further mutations which ultimately combine to create a strong advantage for positive selection. That is, this may be how a multiple mutation situation advantageous for the virus could arise, even if each of the individual mutations conveys no significant advantage or even a disadvantage.

Think of remodeling a house: there may be several steps, such as removing a wall in one step, and then building an addition in the second step. Removing the wall does not convey an immediate advantage; it actually conveys a disadvantage, a hole in the house. The overall advantage is not conveyed until the final step, when the addition is completed. Mutations likewise may cause changes in the shape or geometry of the spike protein, and an advantage in transmissibility of the virus may require several parts of the spike to be changed to become advantageous overall. This kind of jump using several mutations is characteristic of many of the examples of COVID-19 evolution.

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A bank of gene sequencing machines, showing how the technology can be scaled up as needed.

In the alternative evolutionary path, each mutation would convey some degree of advantage, and the final result of numerous such mutations would be a significant evolutionary advantage to the virus. It is likely that both types of pathways exist in a person with a weakened immune system.

The public health implication of these studies is that all HIV/AIDS patients should be treated with HIV medications as a measure against other pandemics. This means raising the standard of medical treatment in impoverished regions such as Africa. Also, a major study of 103,099 patients admitted for COVID-19 disease at 56 U.S. hospitals showed that malnutrition was correlated with a more severe course of illness. Anything that weakens the immune system, such as malnutrition, may be associated with more severe and longer COVID-19 infection. A Chinese study of hospital stays for COVID-19 patients documented longer hospitalizations for patients with malnutrition.

Having multiple infections at the same time, also can lead to immune system weakening. Tuberculosis, which is widespread in Africa, worsens the course of COVID-19. Since much of the disease transmission in Africa is water-borne, clean water is required. Refrigerators are required to keep food safe and edible, and to preserve vaccines. Electricity is required to run refrigerators. More hospitals and medical clinics are required. Transportation to and from hospitals and clinics is needed. The public health measures required to address the issue of disease evolution require raising overall living standards worldwide.

The Biological Science Driver

The astonishingly rapid development of the COVID-19 vaccine in 2020 was a spinoff from the biological science driver which had been accelerating for the past 100 years, and particularly since the 1990s. The development of biological techniques such as gene sequencing, gene fabrication in the laboratory, and use of RNA, such as by injection, to produce virtually any missing or defective protein, means hope for people who have any of the 50,000 currently known abnormal protein diseases. Already we have such treatments of this kind for muscular dystrophy, some forms of macular degeneration of the eyes, and many other genetic diseases. This state of the science represents a Riemannian singularity, so named after the great mathematician Bernhard Riemann, who developed a mathematics for describing how an entire fluid flow pattern within a given boundary could be changed in a coordinated way by introducing a flow singularity, a new fluid source or drain. In economics, an invention can likewise change the flow of production and consumption in an entire segment of the economy in a coordinated fashion.

The biological science driver goes further, in that the entire state of science has moved to a higher level, a game-changing qualitative advance with enormous numbers of possible uses for improving the human condition. The use of this science in the investigation of COVID-19 evolution in patients with weak immune systems has required the gene sequencing of hundreds of thousands of samples from many thousands of patients, and likewise required the interpretation of these sequences as affecting the functioning of proteins in the living state. This is yet another example of the power of this singularity in scientific advancement.

LaRouche's Testimony in Congress

LaRouche provided his analysis of the relation of living standards to new pandemics in Congressional testimony on November 26, 1974, during hearings before the House Judiciary Committee. In his testimony, LaRouche stated that the economics of Zero Growth, a policy promoted by financial elite families, including the Rockefellers, would result in "A massive collapse of the world's cooperative labor process … The concomitant neglect of those portions of the Earth's biosphere that depend on the intervention of human labor for their maintenance [such as farmland requiring fertilizer to remain productive —ed.], the accompanying deterioration of public health on a large scale, and the general deterioration of life processes will inevitably result in the outbreak of pestilence in unpredictable varieties and numbers."

LaRouche further concluded that the areas of most extreme poverty and economic breakdown would be the first to spawn new diseases, which would then be able to spread to the areas with higher standards of living. The continued division of the world into "have" nations and "have not" nations would end with worldwide epidemics that would invade and destroy the "haves" and well as the "have nots."

LaRouche had come to his conclusion regarding the destructive effect of a Zero Growth policy from his basic notion of what is required for an economy to survive. Every economic system is based on a certain level of technology, and every level of technology requires specific resources to function. Beginning with energy as a basic need for any technology, LaRouche traced the evolution of energy sources in the history of human society, beginning with human physical energy used in hunting and gathering, to wood for making fire, proceeding to coal as a more concentrated energy source, then oil, and then nuclear fission. Each of these technologies uses specific finite resources, and after a certain period of time the resource becomes increasingly depleted. As the human population grows and develops, new sources of energy are discovered and utilized. Thus, technological progress is required to sustain the growth of human society. If a society adopts a policy of Zero Growth, whatever technological status it has achieved will, after some time, deplete the energy source it depends on. The energy source will become increasingly scarce, and the society will collapse. LaRouche concluded that human economies are either growing or collapsing, and so it is not surprising that the advocates of Zero Growth urge population reduction and living-standard reduction as required features of their program.

Backing up yet another step to get a broader overview, LaRouche understood that human technological progress requires scientific development, and more generally cultural development, which are both dependent on the creativity of individual human beings. He identified human creativity as the ultimate source of value in an economy, and concluded that an economic system, combined with the accompanying political system, must foster individual human creativity to survive.

LaRouche's entire economic model of human advancement is based on the central importance of singular states of major scientific advancement. His model of a productive economy requires science drivers, to produce the knowledge we need, to inspire our youth to participate in the creation of progress, and to raise the level of culture to engage our citizens in this grand enterprise.

But an economy requires adequate infrastructure development, long-term investment that plans for the future 20- to 40-year time span, which includes a Hamiltonian-type national bank to lead in this investment. And for any major investment program to succeed, the parasitical derivatives market must be driven out of business by reinstating Glass-Steagall banking regulation. These four areas together—science driver, infrastructure development, Hamiltonian national bank, and Glass-Steagall banking regulation—comprise a comprehensive program that will bring the economy up to the level needed for healthy growth on an ongoing basis. This is the plan that will defeat pandemics like COVID-19.