Solar activity global minimum and genogeographic features of the COVID-19 pandemic

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Abstract. The relationship between space weather and influenza pandemics of the 19th and 21st centuries and the COVID-19 pandemic is considered. All influenza epidemics of the 19-21 centuries developed only at the extremes of solar activity, and the difference in the number of infectious diseases in Russia in the minimum and maximum of 11-year SA cycles is more than 25 million people. The COVID-19 pandemic took start at the minimums of the 11-year and quasi-secular solar cycle. Weather factors and characteristics of the population genetic composition in each country can accelerate the development of a local epidemic, as well as increase its severity and mortality rate. Mortality by country during the COVID-19 pandemic varies by more than 5-8 times. This haplogroup is characterized by the rapid development of an epidemic with low mortality and a large number of asymptomatic patients. Genetic variations explain differences in the strength of leukocyte antigens immune responses. The article investigated the DNA oxidative damage degree as a molecular predictor of exogenous disorders to exposure to UV radiation and magnetic field different frequencies. The greatest number of DNA damage was observed in the age groups over 60 and under 20.

1. Introduction
The regulatory mechanisms of the biosphere respond to both high and low periods of solar activity (SA), but the contribution of the space weather factors is different [1]. At the SA maximum, the contribution of variations in the geomagnetic field, variations in the ultraviolet radiation of the Sun and solar cosmic rays (SCR) is significant. Galactic cosmic rays (GCR) claim the role of the main regulatory biotropic factor during solar cycle minimum [2-3]. A deep minimum of a quasi-secular and a minimum of an 11-year solar activity cycle were simultaneously observed in 2019-2020. This affected the epidemiological situation in the world. A feature of the SARS-CoV-2 virus pandemic is the significant variability in the number of deaths per million population in different countries (Figure 1 a).
The maximum values of mortality are observed in fairly prosperous countries with a high level of development and organization of medicine. At the same time, the most stringent quarantine measures are ineffective. So in the first wave, the relative mortality in Sweden without a lockdown was 4-5 times lower than in Spain and Italy with a hard lockdown. The relative mortality in Iran and Russia is 3-8 times less than in Great Britain, Switzerland, Belgium and the Czech Republic (in the first wave, the difference was more than an order). Figure 1a shows deaths per million people for Spain, France, the United States and Russia in 2020 (before the start of mass vaccination). The difference is 5-8 times. The number of infections with the SARS-CoV-2 virus in Belgium is 1600 people per million at the incidence peak, and in Russia 240 people per million. This difference is indeed unusual. According to the CDC (USA) for seasonal influenza, the difference in the number of different ethnic hospitalizations is about 2 times (Figure 1b).

The paradoxical difference in the number of cases and mortality in different countries (more than 4-10 times) requires a search for factors not related to the level of medical care and the severity of the lockdown in a particular country.

The article examines three factors that modulated the development of a pandemic: 1. Dynamics of solar activity and galactic cosmic rays; 2. Genogeographic distribution of the population; 3. Temperature regime of the environment and precipitation distribution. Genetic differences in the efficiency of leukocyte antigens in binding peptides of the SARS-CoV-2 virus are discussed. The effect of electromagnetic radiation (EMR) on human immunocompetent cells in vitro was carried out to confirm the hypothesis about the role of space weather and environmental factors in the
development of a pandemic. EMR is damaged to the primary structure of the DNA of lymphocytes, and as a consequence the accumulation of oxidized nitrogenous bases and the formation of single-strand breaks are observed. A nonlinear dependence of the degree of DNA damage on the frequency of the external magnetic field is observed [4, 5].

2. Materials and methods
The objects of research were data on statistics of infections and deaths of COVID-19 in various countries (based on the Johns Hopkins University database). We also examined samples of peripheral blood collected from healthy donors (20 people), men, nonsmokers, from 21 to 23 years. The degree of oxidative damage to DNA was assessed by the concentration levels of 8-OHdG in the blood serum. Determination was carried out by ELISA using monoclonal antibodies to 8-OHdG on a Thermo Fisher Scientific Multiskan microplate reader (Finland). The number of single-strand DNA breaks was estimated from the ratio of the fluorescence values of control and experimental samples [5]. Isolation of pure suspension of lymphocytes from donor blood was carried out in a density gradient of ficoll-urografin (density 1.077 g / ml). The laboratory diagnostic examination was carried out in accordance with the mandatory observance of the ethical standards set out in the 1975 Declaration of Helsinki, with the 1983 amendments. The results were processed statistically (StatPlus software). The significance of differences between the samples was assessed using the nonparametric Mann-Whitney U-test. Space weather and solar activity data are provided by the IZMIRAN Space Weather Forecast Center www.izmiran.ru and the website www.spaceweather.com.

3. Space weather factors and pandemics
The incidence waves of the COVID-19 pandemic (and any other epidemic) represent the implementation of the classic non-linear predator-prey equations. The SARS-CoV-2 virus acts as a predator, and the human population is realized as a prey. There is both competition between predators (the emergence of new strains of coronavirus) and adaptive and genetic competition of victims. The influence of space weather factors primarily affects the control factor of predators, and the success of medicine in combating the disease is manifested in the control factor of the prey number. Medical intervention artificially reduces natural competition among victims. The medical adjustment process leads to a strong “patchiness” of the intensity of the disease (the spread of the predator-virus), mainly due to the increasing role of fundamental genetic differences in the immune systems of victims. The introduction of national lockdowns and bans on the movement of victims also contributes to the emergence of unevenness in the dynamics of morbidity and mortality in different countries (see the solution of Voltaire’s equations with delay and dissipation, [6]). Space weather factors and local environmental factors also affect increases after artificial medical elimination of the main controlling factor of natural competition among victims.

Consider the possible influence of the dynamics of solar activity (SA) on the occurrence and development of pandemics. Solar activity has periods of varying duration. 11-year SA cycle and about a 100-year SA cycle are having the greatest epidemiological significance [1]. The statistics of infectious diseases within the 11-year cycle shows a twofold increase in the number of cases at the maximum solar activity [7]. So, in during maximum of 23 solar activity cycle (Max 23) in Russia the people number with infectious diseases was 53 million per annum (data from the Federal State Statistics Service of Russia). In the protracted SA minimum between 23 and 24 cycles (min 24) in 2006-2010, the number of cases was kept at the level of 27-30 million people per annum. Apparently, in Russia, as in a country with a bad climate, the constant dependence of the infectious diseases number on the phase of the solar activity cycle is especially pronounced.

There is a pronounced relationship between the dynamics of solar activity and the time of occurrence of pandemics. The last 140 years (coinciding with the rapid development of modern principles of organization of medicine and epidemiology), there has been a period of fairly high overall long-term solar activity (Figure 2). Therefore, both from a medical point of view and from the
point of view of solar-terrestrial physics, it will be correct to consider pandemics precisely for the period during 13 to 24 solar cycles.

Figure 2. Number of sunspots 1880-2018 (according to the Royal Observatory of Belgium).

Analysis of the SA dynamics and the dynamics of pandemics of this period shows:

1. Clear boundaries of the beginning and end of pandemics are present only in influenza pandemics and some typhoid epidemics. All influenza pandemics developed only at the extremes of the 11-year solar cycle.

2. All 20th century influenza pandemics occur at the highs of 11-year solar cycles. The typhus pandemics of 1847-1848, 1899, and the civil war of 1918-1919 also occurred at the maximum solar activity.

3. Pandemics also developed at the minima of 11-year solar activity at the beginning and end of the quasi-year cycle of solar activity in the 19th and 21st centuries (for example, the 1889-1990 flu pandemic, the 2009 swine flu pandemic, the 2019-2020 COVID-19 pandemic).

Table 1 shows the years of pandemics and influenza strains and the corresponding extremes of solar activity. It can be assumed that the optimal adaptation of the human body occurs during the growth and decline phases of solar activity due to the constant activation of immunity by the gradient of environmental factors. The bioobjects exist in the over compensation phase at the SA maximum. The human body goes below the sensitivity threshold during SA minimum, and does not have time to respond in time and adequately to the virus introduction. At the same time, both very high, but constant solar activity at the maximum cycles, and the long-term constant absence of significant variations in the geomagnetic field and solar radiation at the minimum of SA activity contribute to the development of local epidemics into a pandemic.

Table 1. Pandemics of Influenza and solar activity cycles. Legend: maximum of cycle number 23 - Max 23; minimum between 23 and 24 CA cycles - min 24 [7].

| Years           | Disease              | Phase SA Cycle |
|-----------------|----------------------|----------------|
| 1889-1890       | Flu                  | min13          |
| 1918-1920       | Spanish Flu, H1N1    | Max15          |
| 1957-1958       | Asian Flu, H2N2      | Max19          |
| 1968-1970       | Hong Kong Flu        | Max20          |
| 1995-1996       | Influenza            | min23          |
| 2002-2003       | SARS, SARS-CoV       | Max23          |
| 2004-2005       | Flu                  | Max23          |
| 2004-2005       | Avian influenza, H5N1| Max23          |
| 2009-2010       | Swine Flu, H1N1      | min24          |
| 2019-2020       | COVID-19, SARS-CoV-2 | min25          |
The most active participant in the pandemic is the flu virus. The sharp deterioration of the epidemiological situation and the emergence of influenza pandemics in the 20th century at the highs of the solar activity cycle can be attributed to the increase in virus mutations under the influence of variations in ultraviolet radiation of the Sun. The intensity of ultraviolet (UV) and X-ray radiation from the Sun changes significantly depending on the phase of the solar activity cycle; maximum values are reached at the maximum of the SA cycle. Thus, changes in the X-ray range are more than 500%. X-ray radiation does not directly hit the Earth's surface, but it causes significant ionization of various layers of the atmosphere and changes in its composition. The passage of X-rays and short-wave UV through the atmosphere forms the Earth's ozone layer [8]. Also, X-rays can influence the formation of clouds. Soft ultraviolet light of the Sun passes through the atmosphere and participates in the processes of evolutionary adaptation of living organisms for all 4 billion years of the biosphere existence [2, 3, 9]. Variations in UV at a wavelength of 2000 Å are up to 7% during an 11-year cycle. Variations at shorter wavelengths can reach up to 50%. The total change in the intensity of solar radiation at all wavelengths is not large, and amounts to about 0.1%.

UV solar radiation and solar cosmic rays are the main mutagenic factor during the SA maximum years. Galactic processes become the dominant factor affecting the biosphere during the years of the minimum of the 11-year cycle of solar activity and at the minimum level of ultraviolet radiation [3]. Nearly a century of variations in galactic cosmic rays appear to be a significant biotrophic factor as well. GCR changes are in opposite phase with SA dynamics. Their intensity and mutagenic role are maximal at the minimum of any solar cycle [10]. The ozone layer of the Earth's atmosphere also significantly decreases with the prolonged absence of X-ray flares and a reduced intensity of UV radiation from the Sun during prolonged minima (for example, in 2008-2009) [11]. Thus, at the SA minimum in 2018, according to IZMIRAN data, the intensity of stratospheric radiation exceeded the level of 2014 (SA maximum) by 18%. The difference widened even more in 2019-20 during the onset of the COVID-19 pandemic.

Figure 3. GCR variations in solar activity cycles from 1964 to 2021 (www.spaceweather.com). The authors of the article have noted the maximum and minimum of the last two SA cycles. GCR changes are in opposite phase with SA dynamics.

The maximum GCR intensity for the entire observation period was recorded in 2008-2010 and in 2019-2020 (Figure 3). Apparently, the emergence of new strains of influenza and coronavirus viruses in the minimum of the 11-year SA cycle (swine flu 2009 and SARS-CoV-2 during 2019-2020) is associated precisely with a decrease in the ozone layer due to a decrease in the height of the last 23 and 24 cycles. A significant change in the spectrum of UV radiation passing through the atmosphere and an increase in the intensity of galactic cosmic rays appeared in the period preceding of the COVID-19 pandemic.

The adaptive response of the human body to variations in electromagnetic and radiation turns out to be an equally important process of countering the disease. One of the exogenous factors causing DNA damage is UV radiation. The main damaging effect is exerted by UV-A-range (320–400 nm) (95%) and UV-B-range (5%) radiation [12]. Radiation in the UV-C range (<280 nm) and in the greater
part of the UV-B range (280–320 nm) is absorbed by the stratospheric ozone layer. Damage to pyrimidine bases is observed upon direct excitation of the DNA molecule by UV radiation. The generation of cyclobutane pyrimidine and thymine dimers, adducts and breaks occurs. This process can be a source of errors in DNA replication with subsequent development of cytotoxic and mutagenic effects.

The formation of reactive oxygen species (ROS) also occurs when T-lymphocytes of human peripheral blood are exposed to electromagnetic radiation (EMR). Exposure to EMR can damage the primary structure of DNA [5]. And also cause the accumulation of oxidized nitrogenous bases, in particular 8-hydroxy-2-deoxyguanosine (8-OHdG). The appearance of single-strand breaks of DNA is observed in immunocompetent cells. The amplitude-frequency variations of the geomagnetic field differ during the 11-year SA cycle. The authors irradiated blood lymphocytes with various magnetic frequencies to clarify the degree of DNA damage among different age groups. Enzyme immunoassay was used to determine the content of damage to nitrogenous bases 8-OHdG in the DNA of donor peripheral blood lymphocytes after exposure to EMR with a strength of 600 ± 30 A/m at frequencies of 3, 30 or 50 Hz in vitro (Figure 4). The increase in the level of oxidized modifications of nitrogenous bases 8-OHdG in the DNA of blood lymphocytes after EMR treatment is possibly associated with the generation of ROS.

![Figure 4](image_url)

*Figure 4.* Concentration of 8-OHdG in DNA of the whole blood lymphocytes of healthy donors after EMR treatment. Donor groups are formed by age (each group has 5 donors): 1 - over 60 years; 2 – 40 – 50 years; 3 – 30 -40 years; 4 – 20 – 30 years; 5 - less than 20 years.

As it can be seen from Figure 4, the greatest amount of oxidative damage to DNA is observed in the oldest and youngest age groups. This is consistent with the data of [13], which established a clear correlation between age and the accumulation of mutations in mtDNA, a drop in respiratory efficiency, and an increase in ROS production. The influence of ROS and reactive nitrogen species (RNS) increases under the influence of various exogenous factors on the cell. The authors of [14] propose to use this property of RNS metabolites as a probable drug for COVID-19.

In general, under the influence of external factors, the nature of the cellular response will depend on the duration and intensity of exposure. With moderate exposure, a nonspecific response is formed, which increases the body's adaptation to new conditions. The mechanism of the protective action is, apparently, in the redox modifications of sulfhydryl groups of sensory proteins, which leads to the activation of the tyrosine kinase pathway of the cellular response. When exposed to high intensity, for example, with deep hypoxia, including due to the direct damaging action of ROS, the adaptive capabilities of the organism are disrupted [5].

Thus, in the 20th century, influenza pandemics in the highs of the 11-year solar activity cycle against the background of the general high long-term activity of the Sun could arise due to successful mutations of viruses under the influence of ultraviolet radiation from the Sun. The emergence of
influenza pandemics in the 19th and 21st centuries at the minima of the SA cycle against the background of a low overall level of long-term solar activity may be associated with a thinning of the ozone layer in 2008-2009 and in 2019, with a simultaneous increase in the intensity of galactic cosmic rays as the main mutagenic factor.

Figure 5. Forecast of low solar activity. 25-28 SA cycles (V. Ishkov, [16]).

Solar physicists predict a low level of solar activity during the next three to four 11-year solar cycles [15]. Until 2070, it is assumed that the maximum number of sunspots will not exceed 100. Figure 5 shows the SA forecast from V.N. Ishkov (IZMIRAN) to 2070 [16]. With a low total activity of the Sun in the 21st century, the development of pandemics can be expected 2 times more often (both at the maxima and minima of the cycle). That is, in the 21st century, humanity will face the catastrophic consequences of pandemics not in 10-11 years as in the 20th century, but every 5-6 years.

4. Genographic factors and the COVID-19 pandemic
Genetic traits are a fundamental and irreducible difference between people. The role of other competitive processes between coronavirus victims has been significantly reduced in countries with a high level of medical development. Therefore, genogeographic factors begin to play a significant role in the dynamics of sick and dead people in each country. The rapid development of the COVID-19 epidemic is observed in European countries with Y-DNA haplogroup R1. At the same time, haplogroup R1b has the most severe course, high mortality, duration of the course of the disease, and low efficiency of quarantine measures. The rapid development of local epidemics and the lockdown ineffectiveness are also observed in the related haplogroup R1a (the division of the haplogroup R1 into R1a and R1b occurred about 22 thousand years ago). However, in R1a, few deaths and severe cases are recorded, and there is a fairly rapid recovery and a large number of asymptomatic patients. Haplogroup R1b is dominant in northern Italy, France, Great Britain, Belgium, Armenia, USA, and Spain. Haplogroup R1a is common in the European part of Russia, eastern Germany, Iran, and India.

Italy, Germany and Russia are a characteristic marker of the genogeographic features of the first wave of the COVID-19 pandemic. The most affected part of these countries turned out to be the northern regions (Italy) and the southwestern regions (Germany), where the number of the population with haplogroup R1b is significantly higher than the rest of the country. In Russia, a severe development of the pandemic was observed in Dagestan. The population of Dagestan also has a dominant haplogroup R1b. The percentage of the population with a dominant haplogroup R1a decreases by almost 2 times as we move to the north of the European part of Russia. Haplogroup R1a is being replaced by haplogroup N (St. Petersburg, Finland). Haplogroup N is less susceptible to coronavirus. The genogeographic features of the course of local COVID-19 epidemics are clearly visible in the statistics of the relative incidence and deaths per 1 million people in various countries with haplogroup R1b, haplogroup R1a and mixed population R1b + R1a (Figure 6).
Figure 6. Trends in relative incidence (left) and deaths (right) per million people in countries with dominant haplogroup R1, COVID-19 pandemic through December 2020 (before the start of universal vaccination). 1 - Belgium (haplogroup R1b), 2 - Switzerland and Great Britain (haplogroup R1b), 3 - Germany (haplogroup R1b + R1a), 4 - the European part of Russia (haplogroup R1a + N). The vertical line emphasizes the dis-synchronization of the highs of the second wave of the pandemic across countries.

Differences in the strength of immune responses can be explained by genetic variations in different haplogroups. This concept is confirmed in the article [17]. A. Nguyen et al. showed that haplotype and individual genetic variability affect immune responses and the ability of the population to respond to the SARS-CoV-2 virus. It was found out that the HLA-B * 46: 01 antigen (corresponding to one of the branches of haplogroup R1b) had the lowest peptide binding for both SARS-CoV in 2003 and SARS-CoV-2 in 2019-2020. Alleles of antigens HLA-B * 15: 03; HLA-A * 02: 02; HLA-C * 12: 03 (haplogroup R1a) showed the greatest ability to bind SARS-CoV-2 peptides, and hence greater resistance to the virus for their owners.

Apparently, it was the factor of replacing haplogroup R1a with N that slowed down the spread and rate of development of the first wave of the epidemic in St. Petersburg by almost 10 times compared to Moscow. The average age, population density and lockdown measures in these cities are almost the same.

5. Weather factors and the COVID-19 pandemic
The first maps of the distribution of COVID-19 across Europe in February - March 2020 coincided with the isoclines of the Earth's constant magnetic field. The transfer of wet ones turned out to be significant in the spread of local epidemics at the initial stage. The movement of rain clouds tends to be modulated by the isoclines of the geomagnetic field. However, this factor has ceased to play an important role in the further development of the pandemic.

Ambient temperature has shown itself to be a significant factor in the speed and geographical distribution of the first wave of local COVID-19 epidemics. Italian Bergamo was the most affected by the epidemic. The average temperature in February and March 2020 was about + 10 C in this city, and there was also fairly high air humidity. Weather conditions in northern Italy in February-March were close to optimal for the rapid spread of COVID-19. The temperature increased by more than 10 degrees during the second decade of April, humidity decreased, and after 10-14 days the increase in the number of infected people began to decrease. In April-May 2020, the optimal conditions for the
spread of coronavirus were registered in Moscow (Russia). The daytime temperature in the capital of Russia was close to +9 during the whole month of April and May. At the same time, in the main part of the territory of Russia, the air temperature was significantly less than zero. As a result, there was a rapid spread of the epidemic over a sharply limited European territory with temperatures above zero degrees, and at the same time, the spread of coronavirus was practically not observed over the Urals in Siberia until the beginning of May. Moreover, the presence of more than 4500 km of the Russian-Chinese border did not affect the geography and dynamics of the spread of the first wave of the COVID-19 pandemic in Russia. This fact once again emphasizes that the main “accelerators” of local epidemics were the genetic characteristics of the population and the temperature regime, and not the severity of the lockdown (note that the lockdown was very strictly observed in Moscow, and was practically not observed in the large cities of Siberia).

Countries with increased levels of ultraviolet radiation and high temperatures (Egypt, Thailand, and South Korea) showed a lower rate of coronavirus infection incidence spread and mortality. The exception was Iran with a genetic dominant of the population with the haplogroup R1a. As discussed above, haplogroup R1a is characterized by a large number of sick people with a fairly mild course of the disease. Thus, the weather regime of the area affects the localization of foci of coronavirus and the duration of the period of active infection of the population. However, ambient temperature is less significant than the genetic makeup of the population. It is the genogeographic features that determine the infection spread rate, the disease course severity and mortality in the local foci of the COVID-19 pandemic.

6. Conclusion
The number of pandemics could be double compared to the 20th century in the context of a long global minimum of solar activity until the 2060s (with a possible period of 5-6 years instead of 10-11 years). Understanding the genogeographic features of the COVID-19 pandemic contributes to optimize distribution of medical resources across regions, staff recruitment and makes it possible to quickly assess the possible severity of the disease in patients.

The COVID-19 pandemic occurs simultaneously during of 11-year SA cycle minimum and quasicentury SA cycle minimum. The genogeographic characteristics of the population became one of the essential factors determining the development of the first wave of local epidemics. Populations with a haplogroup R1b are dominant in the countries with the highest relative number of deaths and severe patients. One of the significant genetic differences between haplogroups from each other is the difference in the production of complexes of human leukocyte antibodies associating with the strength of the immune response of haplogroup representatives to the coronavirus. Haplogroup R1a is dominant haplogroup on the European territory of Russia. The R1a haplogroup is characterized by the rapid development of the COVID-19 pandemic with low mortality and a large number of asymptomatic patients. Studies of the degree of oxidative damage to DNA as a molecular predictor of exogenous disorders have shown that after treatment of blood serum and lymphocytes (isolated from the peripheral blood of healthy donors) with an alternating magnetic field and gamma radiation, a significant change in the level of 8-OHdG and single-strand DNA breaks is observed. The greatest amount of DNA damage was found in the age groups over 60 and less than 20 years old. The resulting effect can be associated with the generation of reactive oxygen species under the influence of radiation on the DNA repair process, and affect the adaptive capabilities of a particular organism. The space weather impact increases the variability of the adaptive capabilities of the human population as a whole. The dynamics of solar activity and geomagnetic field increases the evolutionary adaptability of mankind to the next pandemics.

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