Research Article

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Solar activity and COVID-19 pandemic

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Abstract: Solar activity (SA) dynamics increases mankind's evolutionary adaptability to pandemics. Flu pandemics from 1880 to 2020 took place during maximum or minimum of solar cycles. The article discusses several factors that modulated the development of the COVID-19 pandemic: SA dynamic, genetic population features, environment temperature, the effect of lockdowns, and vaccination in various countries. The population genetic composition turned out to be the most significant factor for coronavirus mortalities during a SA global minimum 2019-2020. COVID-19 pandemic is most severe in countries with a dominant haplogroup R1b (the relative number of deaths per million is more than 12-25). Local COVID-19 epidemics were more easily in countries with a dominant haplogroup N (relative number of deaths less than 3). The incidence per million people in haplogroups R1b: R1a: N has a ratio of about 7: 2: 1. This ratio does not depend on the pandemic waves and the population vaccinated rate. Vaccination effectiveness may depend on the population's genetic characteristics too.
It is expected to maintain extremely low solar activity during the 30 years. Under these conditions, a twofold increase in the number of pandemics (every 5-6 years instead of 10-11 years) can be expected with pronounced genogeographic differences.

Keywords: solar cycles, cosmic rays, influenza pandemics 1880-2021, haplogroups R1 and N

1 Introduction

Solar activity has a significant impact on the occurrence and development of pandemics. The contribution of solar activity to climate and biosphere differs at different time scales. It can range from 5% on a scale of 11-year cycles to 60-70% on cycles from 250 years or more. Modern ideas about a solar activity (SA), its cyclicity, and the SA future manifestations forecast are presented in (Obridko and Nagovitsyn 2017). Solar cyclicality is considered in a long-term perspective and on different time scales. Geomagnetic field, ultraviolet radiation variations, and solar cosmic rays (SCR) make a significant contribution to the evolutionary adaptation of living systems during solar activity maximum. Galactic cosmic rays actively modulate biosphere processes during the SA minimum (Belisheva *et al.* 2012; Obridko *et al.* 2020). A deep minimum of a quasi-secular and a minimum of an 11-year solar activity cycle were simultaneously observed in 2019-2020. Biosphere and epidemiological processes responded to low solar activity by increasing the difference in adaptive responses. A feature of the SARS-CoV-2 virus pandemic is the significant difference in the number of deaths per million of the population across regions of the world. The relative mortality in China, Australia, Turkey, Iran and Russia is 4-10 times less than in USA, Spain and Italy in the first wave coronavirus pandemic (Figure 1).

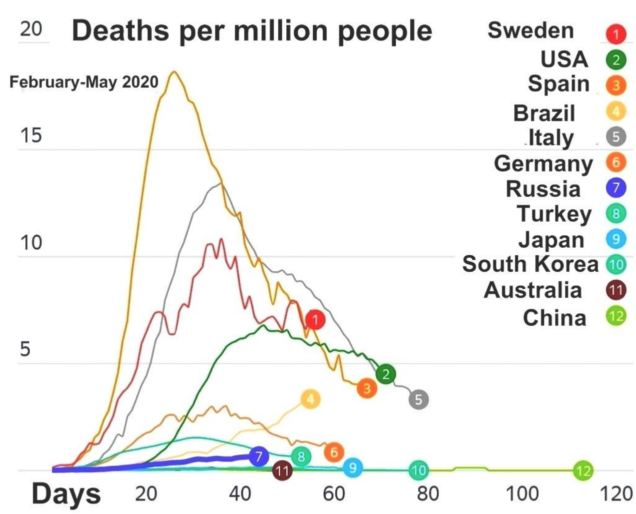

Figure 1. Deaths of coronavirus pandemic per 1 million people in February – May 2020; 12 countries from different continents represented

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This difference is paradoxical since, under conditions of common flu, the difference in mortality of different genetic groups is no more than 2 times. According to the CDC (USA) for seasonal influenza, the difference in the number of different ethnic hospitalizations is about 2 times (Figure 2).

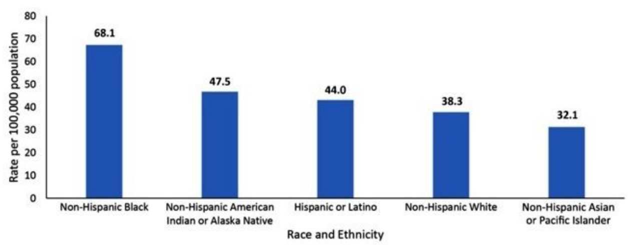

Figure 2. Age-adjusted Influenza-related Hospitalizations by Race/Ethnicity, 2009-2010 through 2018-2019 (Influenza Hospitalization Surveillance Network, FluSurv-NET)

Moreover, the maximum values of mortality are observed in fairly prosperous countries with a high level of medicine. This paradoxical variability of the deaths per 1 million people (more than 4-8 times in different countries) requires an explanation.

The article examines 5 factors that modulated the development of a pandemic: 1) Solar activity and cosmic rays; 2) Genetic population features; 3) Environment temperature; 4) Lockdown effects; 5) Vaccination process for different countries.

2 Materials and methods

Statistics data of coronavirus infections and deaths for countries were researched (based on the Johns Hopkins University database). 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 Solar activity and space weather factors during pandemics

Space weather and solar activity are insufficiently estimated in medical and biological approaches to the analysis of the dynamics of pandemics due to the nonlinearity of solar-terrestrial connections. The role of solar activity and cosmic rays in the development of the biosphere in general and pandemics, in particular, were considered by the author in articles (Ragulskaya 2020, 2021). However, we will allow repeating ourselves the main conclusions to preserve the presentation logic:

1. An 11-year SA cycle and a nearly 100-year SA cycle make a significant contribution to the emergence and development of epidemics. The number of infectious cases in the minimum of the solar activity is 2 time low than in the maximum. According to the Russian statistical agency, it is 53 million people a year are recorded in 2001 and 27-31 million people a year in 2007-2009.
2. Flu pandemics from 1880 to 2020 took place during maximum or minimum of solar cycle only. Those pandemics have occurred at the minimum of 11-year SA cycle at the beginning and end of the quasi-year solar cycle during the 19th and 21st centuries. Pandemics began at the peak of 11 years of solar activity during the high solar activity of the 20th century (Table 1).

Table 1. Flu pandemics and solar activity during 1880-2020. Legend: maximum of SA cycle number 23 – Maximum 23; minimum between 23 and 24 SA cycles – min 24 (Ragulskaya 2020)

Years	Disease	Phase Cycle SA
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
since 2004	Avian influenza, H5N1	Max23
2009–2010	Swine Flu, H1N1	min24
2019–2020	COVID19, SARS-CoV-2	min25

3. Viruses and human populations are involved in the emergence of pandemics as predator and prey, respectively. Virus mutations, the emergence of new species as competitors, or evolutionary-adaptive changes in the human body are significant factors in accelerating or slowing down the rate of development of a pandemic. Different factors of space weather have a predominant effect on the biosphere during solar activity cycles.
4. Sun ultraviolet (UV) radiation and cosmic rays are important factors for virus mutation (Güdel 2007; Gaucher *et al.* 2008). They dominate when solar activity increases and UV and X- ray intensities significantly enhance. X-Ray can change the atmosphere composition due to ionization of its various layers (Mironova 2016). Ultraviolet light passes through the

atmosphere and participates in the processes of evolutionary adaptation of living systems. During the years of maximum Solar activity UV variations near 200 nm are up to 7% and can be up to 50% for shorter wavelengths.

5. When solar activity decreases another factor such as Galactic processes (Atri and Melot 2014), ozone layer efficiency (McComas *et al.* 2013) become more important. The maximum of GCR intensity for the entire observation period was registered in 2008-2010 and in 2019-2020. The origin of new strains of influenza and coronavirus at the minimum of the 11-year CA cycle (swine flu 2009 and SARS-CoV-2 during 2019-2020), probably is associated with decreasing in the ozone layer. Increase of galactic cosmic rays intensity and significant change in the spectrum of UV radiation passing through the atmosphere is obtained in the period preceding the COVID-19 pandemic.
6. UV radiation can cause damage to the primary structure of DNA and the accumulation of oxidized nitrogenous bases, in particular 8-hydroxy-2-deoxyguanosine (8-OHdG). As a result, single-stranded DNA breaks can appear in immunocompetent cells. The main damaging effect is due to UV-A (320-400 nm) (95%) and UV-B-range (5%) radiation (Dizdaroglu 2012). The impact of electromagnetic radiation on T-lymphocytes of human peripheral blood leads to the formation of reactive oxygen species (ROS) (Manzella *et al.* 2015; Tekutskaya *et al.* 2020; Vanin *et al.* 2021). It is interesting to note that the adaptive response of the human body to UV and electromagnetic radiation is nonlinear both at the total and cellular levels. It depends on age, health status, and degree of fatigue, genetics and many more factors. The Gamalei Institute report says that the effectiveness of the Sputnik-Light vaccine also significantly depends on age. It ranges from 53% in the older age group to 85% in young people.

Thus, influenza virus mutations under the influence of solar ultraviolet radiation and general high solar activity could lead to the development of the 1918–2004 pandemics during the maxima of the 11-year solar activity cycle. The emergence of influenza pandemics in the 19th and 21st centuries at the minima of the SA cycle may be associated with a thinning of the ozone layer with a simultaneous increase in the intensity of galactic cosmic rays.

4 Geographic factors and the COVID-19 pandemic

The genetic features of population have become one of the essential factors of the local coronavirus epidemic development to different countries. For the first time, this idea was expressed by the author in the spring of 2020 on the basis of studies on the ethnic characteristics of the functioning of the cardiovascular system and three-month European statistics of the incidence of coronavirus (Ragulskaya 2020). The introduction of this article shows the dynamics of relative mortality in different countries and continents in the first wave of the coronavirus pandemic. Further coronavirus epidemic dynamics also turned out to be strongly dependent on the genetic makeup of the population of different countries. The dynamics of morbidity and mortality for the second coronavirus wave (before the start of mass vaccination) was discussed in the author's article (Ragulskaya 2021). It was shown that the most vulnerable are countries with a dominant population of the haplogroup R1b. Morbidity and mortality are 4-6 times lower for a related haplogroup R1a.

The third coronavirus wave only confirmed the significant genogeographic differences in the course of local epidemics in during of the solar activity global minimum. Vaccination of more than half of the adult population of Europe did not lead to significant changes in the ratio of morbidity between haplogroups R1b and R1a. The largest number of victims per 1 million inhabitants is recorded in the territories of Italy, Spain, France, Belgium, Great Britain, and Portugal (12 – 30 death per million of the population).

Figure 3 shows a map of the distribution of haplogroups across Europe (genetic markers Y-DNA are passed on the Y-chromosome exclusively through the paternal line, from father to sons). The numbers indicate the values of the maximum mortality per million populations. Figure 5 implies that the rapid development of the COVID-19 epidemic is observed in European countries with Y-DNA haplogroup R1. The most severe course of COVID-19, high mortality, prolonged course of the disease and low lockdown efficiency are observed in countries with a dominant haplogroup R1b. The rapid of local epidemics development are observed in to the related haplogroup R1a too.

Haplogroup R1b is dominant in northern Italy, Portugal, France, Great Britain, Belgium, Armenia, the USA, and Spain. These countries have suffered the most severe losses due to the current pandemic. Most of the population has R1a haplogroup in India, eastern Germany, Russia, Ukraine, and Iran. The genogeographic features of local COVID-19 epidemics are clearly visible in the statistics of the relative

Figure 3. Haplogroups and distribution of deaths per million people into European territory

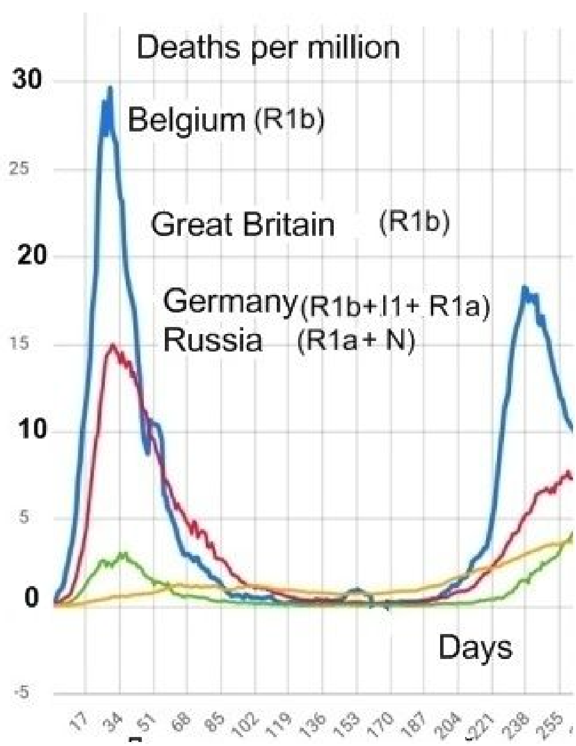

Figure 4. The development of the COVID-19 pandemic in various countries before the start of mass vaccination, per 1 million (based on the Johns Hopkins University data): the relative number of deaths in countries with haplogroups R1b and R1a. Blue line – Belgium, purple – UK, green – Germany, yellow – the European part of Russia (Ragulskaya 2021)

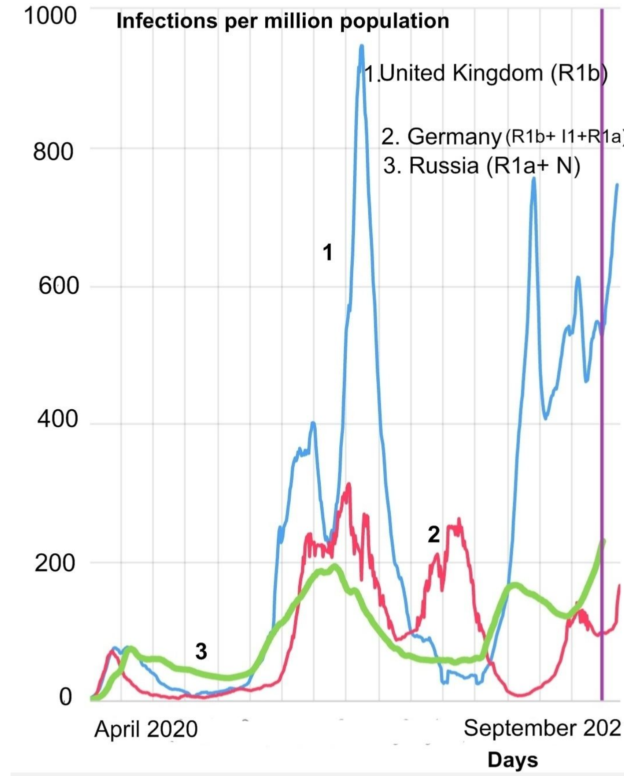

Figure 5. Infections per million following national vaccination programs. Blue line – Great Britain (74% of the vaccinated population, more that 700 infections per million population now); pink – Germany (69% of the vaccinated population, more that 200 infections per million population now); green – Russia (35% of the vaccinated population, more that 250 infections per million population now)

incidence and deaths per 1 million people for various countries with dominant haplogroup R1b or haplogroup R1a. The article (Ragulskaya 2021) presented the dynamics of coronavirus infections in Belgium, Switzerland, Germany, and Russia until December 2020 (before the start of universal vaccination).

The incidence in Belgium with a dominant haplogroup R1b was at 1600 people per million populations; Great Britain (R1b) had more than 900 incidences. In Russia, with dominant haplogroups R1a + N, the incidence did not rise above 220 people per million. The difference is more than 4–7 times. The difference in mortality was also about 6 times. In Belgium, the maximum relative mortality was about 30 people per million, and in Russia about 5 (Figure 4).

Even after the start of vaccination, the difference in incidence in the UK is 3.5 times more than in Russia in September 2021 (Figure 5). At the same time, the number of vaccinated adults in the UK is 2 times more than in Russia. Vaccination significantly reduced the number of deaths but had little effect on the number of coronavirus incidence in these countries with different dominant haplogroups.

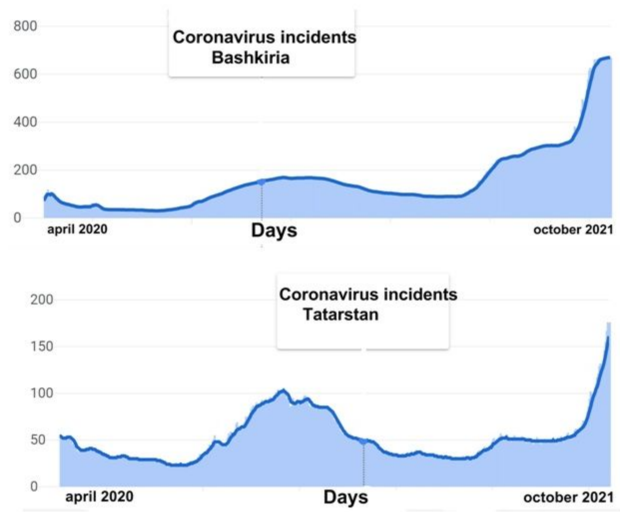

Figure 6. Dynamics of coronavirus incidents from April 2020 to October 2021. Above – Bashkiria, below - Tatarstan

Let's compare the current incidence in the republics of Bashkiria and Tatarstan. (Russia). Bashkiria has a dominant haplogroup R1b. The number of coronavirus cases is 4 times less in the neighboring republic of Tatarstan with other genetic characteristics of the population. The population of Tatarstan is a mixture of major European haplogroups with a slight predominance. Figure 6 shows the number of coronavirus incidents in Bashkiria and Tatarstan now (700 versus 150, respectively).

The haplogroup R1a is only 15% population in northern Russia versus 30% in southern Russian territories. At the same time, haplogroup R1a is replaced by haplogroup N in the northern regions of Europe (St. Petersburg, Karelia, Finland).

Haplogroup N is less susceptible to coronavirus according to statistical medical data. Finland with a dominant haplogroup N consistently shows the lowest relative mortality in Europe, regardless of the vaccination level (Figure 7).

Differences in the strength of immune responses can be explained by genetic variations in different haplogroups. This concept is confirmed in the article (Nguyen *et al.* 2020). Haplotype and the individual genetic variability can affect immune responses to the coronavirus. 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. Different genetic resistance of people to coronavirus can be explained by adaptation historical processes of the last 20-25 thousand years. Authors (Souilmi *et al.* 2021) apply evolutionary analyses to human genomic datasets to recover selection events involving tens of human genes that interact with coronaviruses, including SARS-CoV-2 that likely started more than 20,000 years ago. These adaptive

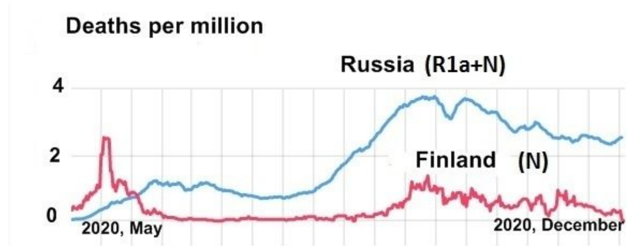

Figure 7. Dynamics of mortality in haplogroups R1a and N before the start of mass vaccination, per 1 million (based on the Johns Hopkins University data). Blue line – Russia (dominant haplogroup R1a+N); pink line – Finland (dominant haplogroup N)

events were limited to the population ancestral to East Asian populations. The lungs turned out to be the most severely mutated organ. The article shows that population selection was strong for the CoV-VIP coronavirus only over 500 generations (~14,000 years) ago. And it has been much weaker during the last 5000 years.

Another statement from a wonderful article (Souilmi *et al.* 2021) deserves a separate discussion. The genetic analysis carried out showed that about 5 thousand years ago, the coronavirus pandemics were replaced by influenza pandemics. The ancient strain of coronavirus has receded after 15 thousand years of domination. The authors do not discuss the possible reasons for the change of the viral predator. However, this fact is extremely interesting within the framework of our concept. We can assume 3 reasons for the change of coronavirus epidemics to influenza epidemics to East Asian populations 5000 years ago:

1. Adaptive genetic changes in the population of East Asia have become so significant that they have sharply reduced the food supply for the ancient coronavirus.
2. Influenza, as a more aggressive new predator, turned out to be more active and more successful than the ancient coronavirus.
3. It was about 5 thousand years ago that serious changes took place in the intensity of galactic cosmic rays and climate. The climate became more humid and colder. (Dergachev 2015). It might lead to successful mutations of the influenza virus and an increase in its aggressiveness and success.

Apparently, we are currently observing the opposite process. Significant warming of the climate, a high level of galactic cosmic rays, as well as mass vaccination against influenza have created optimal conditions for the active return of coronavirus pandemics. And perhaps those coronavirus pandemics will stay with humanity for the next 5-10 thousand years.

So, genetic population features have become one of the significant factors determining the development of local epidemics of the coronavirus during the period of low solar activity, not only in our time but also thousands of years before.

5 Lockdowns and the pandemic development

A social mechanism to reduce the number of coronavirus cases is the introduction of a lockdown. However, the effectiveness of this procedure and its long-term consequences differ significantly from country to country and even within different regions in one country.

The example of Germany and Sweden most clearly demonstrates the non-linearity of the long-term perspective from the introduction of lockdowns. The choice of these countries is not accidental: Germany is a country with low relative mortality among European countries, but at the same time, the country introduced a lockdown. Sweden did not introduce lockdown, but in Germany, it was observed quite strictly and for a long time. These countries are comparable in terms of life expectancy. In Sweden and Germany, it is 82 years and 81 years, respectively. Figure 8 shows the resulting dynamics of relative mortality per 1 million people in Germany and Sweden for 416 days of the pandemic.

It can be seen that the curves are almost identical. A slight excess in mortality was observed in Sweden during the first wave of the local epidemic. However, the herd immunity acquired by the country during this time allowed it to survive the second wave of coronavirus without the introduction of a lockdown. Thus, in the long term, the introduction of a second lockdown in Germany was not more effective than the acquisition of herd immunity by Sweden without a lockdown. It should be added that the genetic makeup of the population of Sweden and Germany overlaps with each other much more than Sweden and neighboring Scandinavian countries. However, the percentage of the population with a haplogroup R1b is higher in Germany than in Sweden (Germany – 46%; Sweden – 21%).

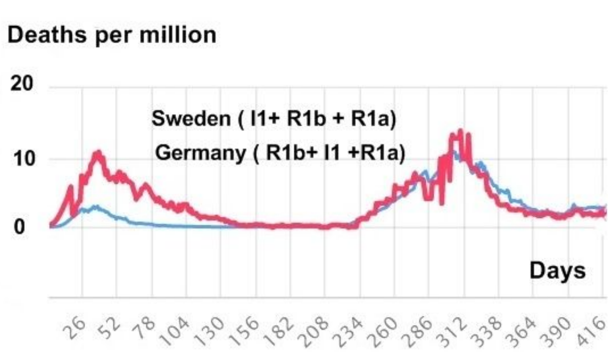

Figure 8. Dynamics of mortality per 1 million, February 2020 – October 2021: pink line – Sweden (haplogroups I1+R1b+R1a), blue line – Germany (haplogroups R1b+ I1+R1a)

The development rate of the first coronavirus wave in St. Petersburg was 10 times less than in Moscow (Figure 9). Population density, life expectancy and lockdown were almost the same in these cities. But the genetic makeup of the population differs in these cities. The number of the population with a haplogroup is 2 times higher in Moscow. In St. Petersburg, the haplogroup R1a is being replaced by the Finno-Ugric haplogroup N. Apparently, it was this factor that played a decisive role in the development of the first wave of local epidemics into Moscow and St. Petersburg.

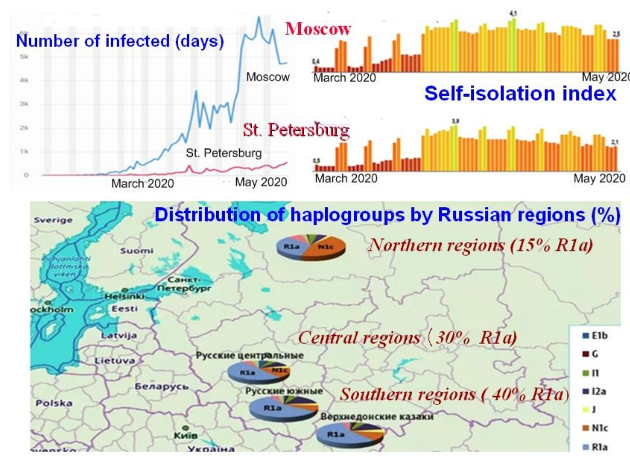

Figure 9. Local COVID-19 epidemics: Moscow and St. Petersburg (first wave)
Top right – the number of infections in Moscow (blue curve) and St. Petersburg (red curve) from March to June 2020. Top left – the lockdown compliance index in Moscow and St. Petersburg from March to June 2020. Below is a population genetic map of the European territory of Russia.

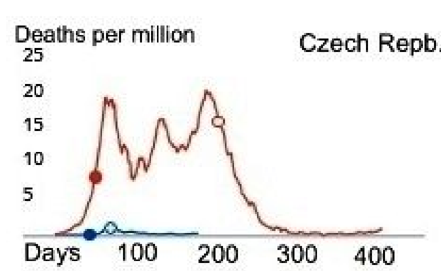

Figure 10. Czech Republic, deaths per million during 1 and 2 lockdowns. The blue line is the first lockdown; the red line is the second lockdown. The dots indicate the beginning and end of the lockdown

An unexpected non-linear lockdown effect was observed in the Czech Republic. This country introduced a very strict lockdown on its territory. In the first wave, this procedure helped to successfully prevent the spread of coronavirus infection. But later, persistent self-oscillating waves of coronavirus morbidity arose after the infection entered the country with a completely absent herd immunity (Figure 10).

As a result, the relative mortality rate from the new infection in the Czech Republic was one of the highest in Europe (about 20 people per 1 million).

A similar situation has developed in Georgia. And only total vaccination was able to reverse the dynamics of mortality.

6 Vaccination and COVID-19 local epidemic, the fourth wave

Total vaccination has helped to significantly reduce deaths from coronavirus in countries with a dominant haplogroup R1b. The number of deaths from coronavirus per million populations in the UK, Germany and Russia is shown in Figure 11. Vaccination rates are presented for the total population of each country. It should be recalled, however, that the age of vaccination initiation varies from country to country. It can be seen that in the 4th wave of the pandemic, the relative mortality rate fell 10 times in the UK and Germany (vaccination was more than 70%). The relative mortality in Russia, on the contrary, increased by 1.5 times (the number of fully vaccinated population was 35% at the beginning of November 2021). Apparently, the increase in mortality in Russia is associated with the entry into the pandemic of Siberian regions with other dominant haplogroups. The first wave of the pandemic bypassed these territories due to low ambient temperatures, and there was practically no coronavirus incidence in them (see paragraph 7).

However, the incidence of coronavirus demonstrates non-linear dynamics that is not directly related to the number of vaccinated in different countries. Apparently, depending on the dominant haplogroup, each country will have its own level of herd immunity formation. The Figure 5 shows the dynamics of infections in the UK, Germany, and Russia. In the UK, 74% of the all population was vaccinated, but the incidence rate in this country in August-September 2021 was almost 3 times higher than the incidence in Russia, with its vaccination rate of 35%. R1b is the dominant haplogroup in the UK (more than 67%). The European part of Russia has a population with dominant haplogroups R1a

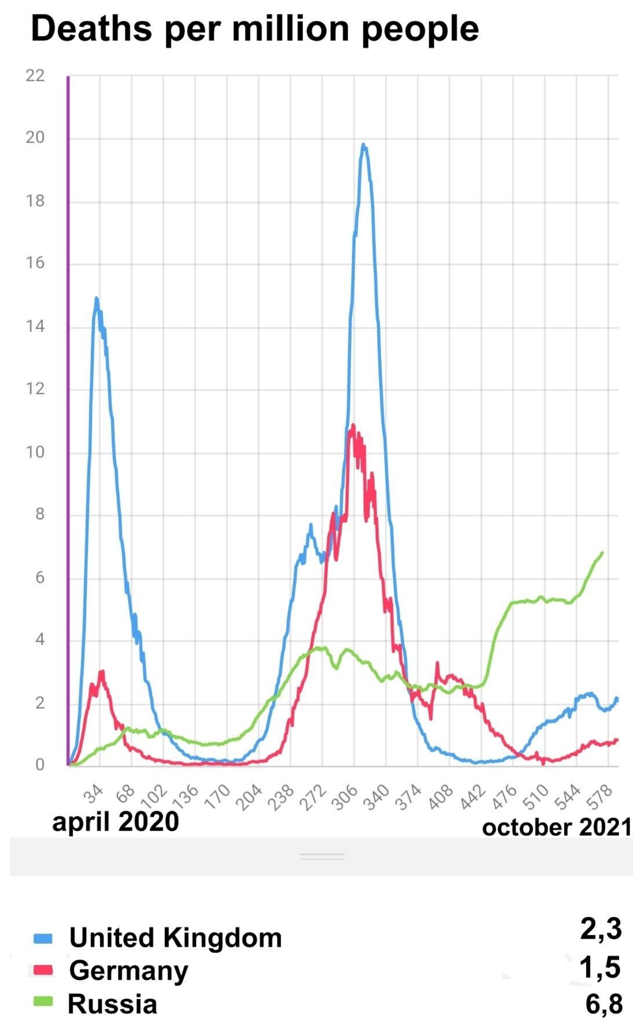

Figure 11. Deaths per million following national vaccination programs. Blue line - Great Britain (74% of the vaccinated population), pink – Germany (69% of the vaccinated population), green – Russia (35% of the vaccinated population). The relative mortality in each country is marked with numbers (at the beginning of November 2021)

and N (more than 75%, Figures 3 and 9, population genetic map of the European territory of Russia).

From the data in the Figure 5, it is possible to estimate its required level of vaccination of the population for the formation of herd immunity into the UK at least 80–90 %. This value may turn out to be at the level of 60–70% of the total population for Russia (recall that so far, only people over 18 are vaccinated in Russia).

The development of the fourth wave of the pandemic in some European countries with more than 68% vaccinated population is shown in Figure 12. The incidence did not decrease after total vaccination in countries with a dominant haplogroup R1b (compared to the first waves of coronavirus), but in some it even increased. Belgium, the Netherlands, and Austria have over 1000 coronavirus cases per million populations. At the same time, the relative incidence did not change significantly in countries with dominant haplogroups R1a and N (only 210 coronavirus cases per million populations are being registered now in Finland, and 350 in Russia).

A consistently low relative infections number (less than 230) and mortality from coronavirus (less than 3) are observed in Finland (haplogroup N). These numbers are regardless of population vaccinated rate. Recall that Figure 8 shows comparative dynamics of the relative coronavirus mortality in Russia and Finland before the start of mass vaccination. Apparently, the level of herd immunity required is even lower for Finland (about 50%). Currently, 75% of the population in Finland is vaccinated.

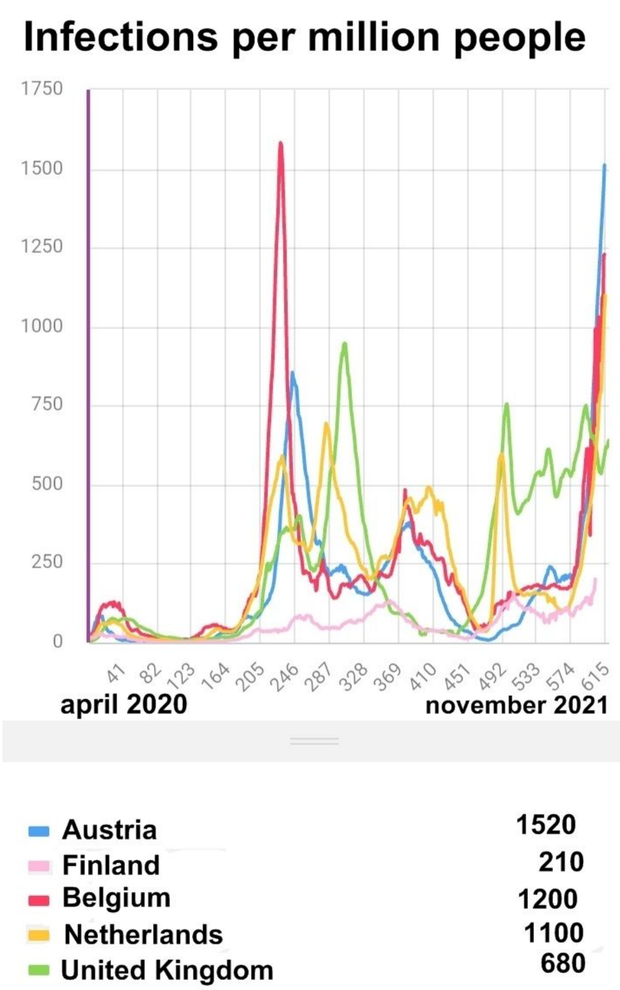

Figure 12. The fourth wave of the pandemic COVID -19 in Europe: infections per million following national vaccination programs. Blue line – Austria (68% of the vaccinated population); pink – Finland (75% of the vaccinated population); red line – Belgium (75% of the vaccinated population); yellow line – Netherlands (76% of the vaccinated population); green line – Great Britain (74% of the vaccinated population). The infections per million of population in each country are marked with numbers (at the beginning of November 2021)

Thus, the incidence per million people in haplogroups R1b: R1a: N has a ratio of about 7: 2: 1. This ratio no depends of the pandemic waves and the population vaccinated rate.

On the contrary, for European countries the mortality rate drops significantly (up to 10 times) with a vaccination rate of more than 70%. It is logical to assume that the level of herd immunity achieved by vaccination also can be depends on the genetic makeup of the population too. Its value is highest for countries with a dominant haplogroup R1b. These differences may be less noticeable if the pandemic occurs during maximum solar activity. However, the COVID-19 pandemic began during the global minimum of solar activity, and the genogeographic factor plays an important role in the dynamics of morbidity and the formation of herd immunity.

7 Weather factors and forecast

Temperature and weather conditions proved to be important factors in the speed and geographical distribution of the first wave of local COVID-19 epidemics. The highest morbidity and mortality were observed for countries, regions, and cities with an average temperature of about +9°C (for example, Bergamo in February 2020 and Moscow in April 2020).

However, the part of Russia with temperatures below zero was not affected by the first wave of the coronavirus pandemic. Figure 13 demonstrated the coronavirus incidence distribution into Russia for 20 April 2020. It can be seen that there are no local foci of the epidemic in the territory with negative temperatures.

So, the weather regime of the area affects the localization of foci of coronavirus and the infection velocity of

Figure 13. Distribution of coronavirus infection into Russia in April 2020

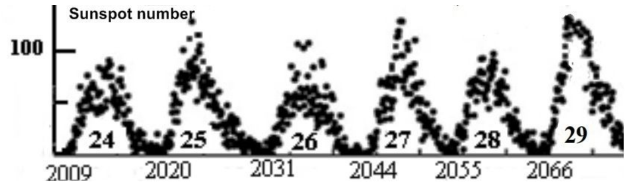

Figure 14. Forecast of low solar activity. 25-28 SA cycles (Ishkov 2017)

the population. However, ambient temperature is less significant than the genetic makeup of the population. Thus, solar activity and the gene-geographical distribution of the population have a great influence on pandemic development. Solar dynamics and galactic cosmic rays modulate the activity and mutations of viruses and also affect the adaptive resistance of a human. Solar activity forecasts are highly likely to suggest that the next 3-4 cycles will be low (for example, Ishkov 2017).

Figure 14 shows the SA forecast for 2070 from V.N. Ishkov. The emergence of viral pandemics can occur 2 times more often during the solar activity global minimum due to the mutagenic properties of cosmic rays. Humanity will face the catastrophic consequences of pandemics every 5-6 years during the 21st century.

8 Conclusion

Solar activity and space weather factors primarily affect mutations and variability of the virus and also increase the adaptive resistance of the human population. The article examines 5 environmental factors and social measures that could explain the large difference in coronavirus mortality in different countries (4–8 times versus 2 times during common influenza epidemics). These are factors such as: 1. Space weather factors; 2. Genetic population features; 3. Temperature; 4. Lockdown effects; 5. Vaccination process for different countries.

Solar activity dynamics and the genetic variability of humanity increase the chances of human survival as a biology species during pandemics. Influenza pandemics 1880–2019 were registered only at a maximum or minimum of the 11-year solar activity cycle. COVID-19 pandemic took the start at the minima of the 11-year and quasi-century solar cycle too. Genetic population features played a decisive role in the development of local epidemics in these conditions. This effect can be explained by genetic differences in leukocyte antigens, adaptive changes in the generation of nitric oxide and oxygen in the human body under the influence of space weather factors. It is also necessary to take into account the difference in the historical processes of adaptation to influenza viruses and coronaviruses for different haplogroups in the last 20,000 years. The most severe course of COVID-19 and the highest mortality rate are characteristic of countries with the dominant haplogroup R1b. The related haplogroup R1a is characterized by the rapid spread of coronavirus with a large number of asymptomatic patients. The easiest development of local epidemics was observed in European countries with a predominance of haplogroup N.

The incidence per million people in haplogroups R1b: R1a: N has a ratio of about 7: 2: 1. This ratio depends on little of the pandemic waves and the population vaccinated rate. The level of herd immunity achieved through vaccination also may depend on the genetic makeup of the population. Its value is highest for countries with a dominant haplogroup R1b. In conditions of a global minimum of solar activity, a twofold increase in the number of pandemics is expected in the next 30 years (every 5–6 years instead of 10–11 years) with pronounced genogeographic differences. The results obtained can interest a wide audience and draw the attention of specialists in solar physics to this actual topic for its further development.

Understanding the role of genetic variation in different haplogroups in the course of COVID-19 will help identify individuals at higher risk of the disease. Combining HLA typing with COVID-19 testing will improve estimates of viral severity in a population and adapt future vaccination strategies to genotypically vulnerable populations. Genetic diagnostics of medical personnel helps to identify hospital and ambulance workers who are more resistant to SARS-CoV-2 while optimizing the provision of medical care to the population and the protection of the doctors themselves. Also, an understanding of the genogeographic features of the spread and severity of the course of a pandemic, taking into account the dynamics of solar activity, can help in planning epidemiological and organizational-quarantine measures in the advance distribution of funds and medical resources.

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