

Solar Activity and Viral Pandemics



Maria Ragulskaya

Abstract The article discusses the influence of different-scale cycles of solar activity on the patterns of occurrence of viral pandemic. It is shown that in the twentieth century (during the maximum of the quasi-centennial cycle of solar activity), pandemics developed at the maxima of the 11-year SA cycle only. However, during the phase of growth, decline, and minimum of the quasi-centennial SA cycle, pandemics occurred both at the maximum of the 11-year SA cycle and at the minimum. The genetic composition of the population turned out to be the main factor in the difference in the dynamics of coronavirus local epidemics under the conditions of the global minimum of solar activity. Countries with haplogroup R1b show a synchronization of the dynamics of local epidemics and high values of relative coronavirus mortality in the first two waves of the pandemic (values from 15 to 30). It is discussed that for countries with haplogroup R1b, universal vaccination lowered the level of relative mortality by 5–8 times by mid-2021 (from 20 to 3). However, relative mortality increased by 2–4 times for countries with haplogroup N and R1a + N by mid-2022 compared to 2020 (from 2 to 8). It is possible that the fundamental change in the dynamics of local epidemics is partly due to solar and geophysical factors in connection with the growth phase of the 25th cycle of solar activity by end 2021.

Keywords SARS-Cov-2 pandemic · Solar activity cycles · Genetic composition of the population

1 Solar Activity and Viral Pandemics 1750–2020

Cycles of solar activity (SA) and space weather have a modulating effect on virus mutations and the dynamics of infectious diseases. Viruses react faster to changes in the external environment and space weather parameters due to the high rate of change.

M. Ragulskaya (✉)

Institute of Terrestrial Magnetism, Ionosphere and Radio Wave Propagation RAS,
Moscow 108840, Russia

e-mail: ra_mary@izmiran.ru

It is the mutations of viruses and bacteria under the influence of solar activity and space weather that have a significant impact on the dynamics of infectious diseases.

As a result, the number of infectious diseases doubles from the minimum to the maximum of the 11-year cycle of solar activity SA (while the incidence of general diseases changes by no more than 20%). A pronounced 11-year cycle is observed, coinciding in phase with the 11-year cycle of solar activity. For example, the dynamics of infectious diseases in Russia for 1998–2011 demonstrates a sinusoid with a maximum in 2001 (simultaneously with the maximum solar activity) and a minimum in 2005–2009 (an abnormally prolonged minimum of solar activity of 24 cycle SA) [1]. At the same time, the number of infectious diseases is 53 million cases at the maximum of solar activity and 27 million cases at the minimum of solar activity. This difference is more than 26 million cases per year in a country of 150 million people.

Figure 1 shows the onset dates of the 1889–2020 pandemics that occurred during the last quasi-centenary solar cycle. Figure 1 shows that in the twentieth century (during the maximum of the quasi-centennial cycle of solar activity), pandemics developed at the maxima of the 11-year SA cycle only. However, during the phase of growth, decline, and minimum of the quasi-centennial SA cycle, pandemics occurred both at the maximum of the 11-year SA cycle and at the minimum.

The general dynamics of solar activity in 1889–2020 is shown in Fig. 2. The discussed quasi-centenary SA cycle is highlighted with a vertical dashed line. It can be assumed, that during the minimum of solar activity, the main impact on the biosphere and virus mutations is exerted by galactic cosmic rays. During the maximum of solar activity, the bio-effect of solar cosmic rays and flare activity increases [2–7].

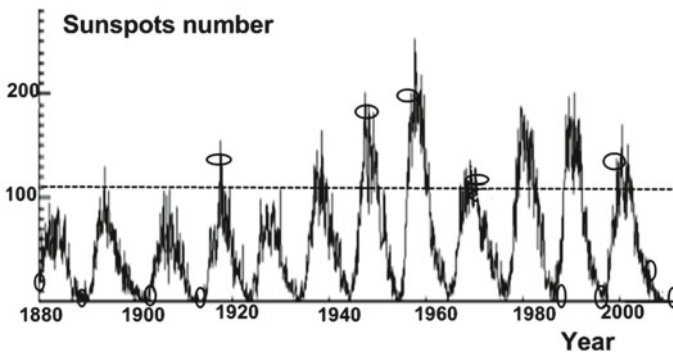


Fig. 1 The last quasi-centenary cycle of solar activity (1880–2020) and viral pandemics. Vertical ovals mark pandemics that developed during the minima of 11-year cycles of solar activity. The horizontal ovals mark the development of pandemics during the highs of the 11-year SA cycles. The broken horizontal line marks the estimated cycle height horizon during which pandemics can develop both at the maximum and at the minimum of 11-year cycles. Basically, this binary phenomenon is observed at the phase of growth and decline of the SA quasi-centenary cycle

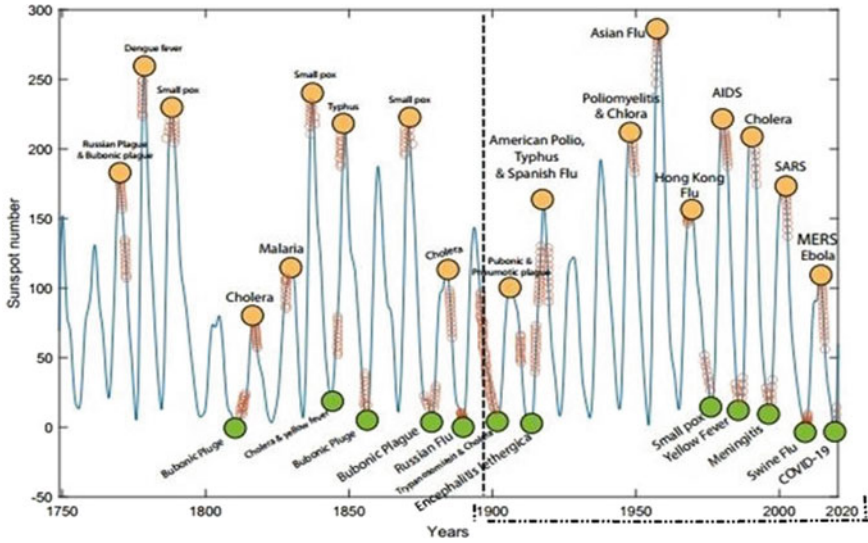


Fig. 2 World pandemics and sunspots number 1750–2020 (reconstruction from the article [8])

In [8], the joint dynamics of SA and pandemics 1750–2020 was reconstructed (Fig. 2). The development of pandemics in SA extrema was revealed. However, according to what regularity pandemics occur either at the maximum or at the minimum of SA are not considered in [8]. Meanwhile, an analysis of the dynamics of viral pandemics over the past 270 years shows that the development of pandemics, is typical at the maxima of the 11-year SA cycle in high SA cycles. During low cycles, pandemics occur at both the high and the low of the 11-year cycle. Moreover, the beginning of the development of a pandemic depends not only on the height of the 11-year cycle, but on its location in the SA quasi-centennial cycle. The pandemics of the mid-nineteenth century, occurring at the minimum of the 11-year SA cycle during the high of the quasi-centennial cycle, were bacterial (plague, cholera), but not viral.

Thus virus pandemics occur at extremes of solar activity, but depending on the ratio of the phases of the 11-year cycle and the hundred-year cycle. In further consideration of the problem of the relation of viral pandemics and solar activity, it is necessary to take into account the possibility that the conditions for the favorable development of local epidemics into a global pandemic could depend not only on the place of the 11-year cycle in the quasi-centenary cycle, but are also determined by the interaction of longer cycles (for example, 270-year and quasi-millennial solar activity cycles).

The SARS pandemics of 2002–2003 and the SARS-Cov-2 pandemic of 2019–2022 are prime examples of pandemics with low total solar activity during the quasi-centennial minimum (Fig. 2).

2 The SARS-Cov-2 Pandemic at the Global Solar Minimum. Genogeographic Features

The dynamics of morbidity and mortality strongly depends on the degree of variability of the victims, in particular on the genetic composition of the population. A significant genogeographic difference between local epidemics is characteristic of pandemics of the global minimum of solar activity. The difference in relative coronavirus mortality per 1 million people in the main European haplogroups R1b, R1a, I, N was more than 10 times in the first wave and up to 3–5 times during subsequent waves until about 50% of the population was vaccinated. Generally this difference in relative mortality is no more than 2 times for ordinary influenza. The question of the genogeographic features of the dynamics of the pandemic is considered in more detail in [9].

The largest number of victims per 1 million inhabitants is recorded in the territories of Northern Italy, Portugal, Spain, France, Belgium, Great Britain (Fig. 3a). All these countries have a high level of medical development. But the population of these countries has a genetic similarity and mainly belongs to the haplogroup R1b (Haplogroup is a group of similar haplotypes that have a common ancestor who has a mutation inherited by all descendants. R1b is a Y-chromosome haplogroup, the most common in Western Europe and the Southern Urals. It is also found in Central Asia, Eastern Europe, North Africa, Western Asia. It is transmitted through the male line. It is most common in Western Europe, and also in parts of Russia by several Bashkir clans and into Dagestan. In a lower content, the haplogroup is found in Eastern Europe, Western Asia. The R1b haplogroup arose from a mutation of the R1 haplogroup that occurred near 22 thousand years ago.) All countries with the highest relative mortality have a dominant population with haplogroup R1b. The relative coronavirus mortality per million people in the haplogroup R1b averaged 15–25, but in Portugal and Belgium it reached 30. This is one of the highest values of relative coronavirus mortality in the world.

From Fig. 3a, it follows that countries with haplogroup R1b show an amazing synchronization of the dynamics of local epidemics in different countries and high values of relative coronavirus mortality in the first two waves of the pandemic (values from 15 to 30). For comparison, Fig. 3b shows relative coronavirus mortality for countries with a dominant haplogroup R1a (values from 4 to 8). Fundamentally different dynamics of the development of local epidemics is observed for these countries, and the values of relative mortality are 4–8 times lower (notwithstanding a lower availability of medical care and a lower level of healthcare).

Figure 3c shows a map of the distribution of haplogroup R1b across Europe. The figures indicate the values of the relative coronavirus mortality by country in the first 2 waves of the pandemic (before the start of mass vaccination). Figure 3c shows that relative mortality increases as the proportion of the population with haplogroup R1b carrier's increases from values of the relative coronavirus mortality 10–12 to 30.

Eastern Europe and the European part of Russia have a predominant population with the haplogroup R1a. Iran, India, Germany and Sweden also have a part of the

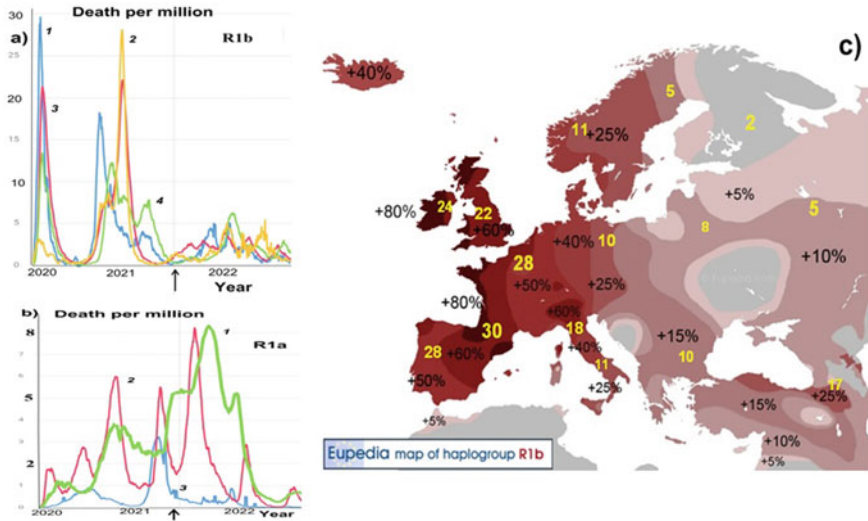


Fig. 3 Relative coronavirus mortality in different countries: **a** Relative mortality for European countries with dominant haplogroup R1b, 1—Belgium, 2—Portugal, 3— Great Britain, 4—Italy (the maximum value is 30); **b** Relative mortality for countries with dominant haplogroup R1a; 1—Russia, 2—Iran, 3—India Italy (the maximum value is 8); **c** Map of haplogroup R1b

population with haplogroup R1a. In these countries, there were a large number of cases without death, as well as asymptomatic patients. The average relative mortality rate for countries with R1a was about 5, and the maximum values did not exceed 8 (Fig. 3b). At the same time, it must be emphasized once again that the level of medicine and the availability of medical care in Western European countries are much higher than in Iran or India, but the mortality rate from Covid-19 in non-European countries was up to 5 times lower. In the North-West of Russia, the population with the haplogroup R1a is half replaced by the population with the haplogroup.

N. Finland also has a dominant population with the haplogroup N. The lowest relative mortality among European countries was observed in the haplogroup N. Its values did not exceed 4 prior to mass vaccination moment [9].

It was shown in [10] that leukocyte antigens of R1a haplogroup carriers are more effective in preventing coronavirus replication than R1b haplogroup antigens. This may be due to the fact that the R1b haplogroup was the first to leave the Asian region more than 20 thousand years ago, and did not have time to acquire the evolutionary mutations found in [11]. These facts confirm the conclusion about the significant role of the genetic diversity of coronavirus victims in the dynamics of the pandemic occurring at the global minimum of solar activity.

3 Effects of Vaccination: Genetics and Solar Activity

The relative mortality for European countries with haplogroups R1b, R1a and N from the beginning of the pandemic to the present Fig. 4a shows. Relative mortality in countries with the haplogroup R1b was many times higher than in countries with R1a and N before the start of universal vaccination. The incidence ratio in the R1b: R1a: N haplogroups in the first and second waves of coronavirus (before the start of universal vaccination in December 2020) was approximately 7:2:1 during 2020–2021 (Fig. 3a and b). However, the situation has changed dramatically since mid-2021. Figure 4a shows the relative coronavirus mortality into countries with haplogroups R1b, R1a, N and R1a + N during 2020–2022. By mid-2021, mortality began to decline due to mass vaccination (this period is marked with an arrow from below in Fig. 4a), especially in countries with haplogroup R1b. However, by the end of 2021, relative mortality increased again, its fluctuations became chaotic, and the values became comparable in all countries.

In Fig. 4 on the right, the vertical bar highlights the mortality rate in the UK, Belgium, Finland and Russia in mid-2022. It can be seen that vaccination significantly affected the dynamics of relative mortality in most European countries, significantly reducing it in the third and subsequent waves for territories with a dominant haplogroup R1b (up to 5–8 times). However, relative mortality for regions with a predominance of the population of the haplogroup N (Finland, northern regions of Russia) increased by 2–4 times (Fig. 4a, right). Vaccination rate for

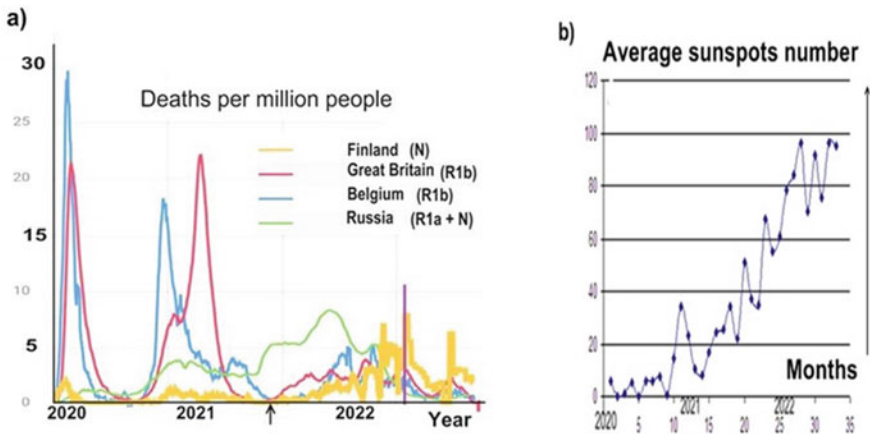


Fig. 4 **a** Relative coronavirus mortality into countries with haplogroups R1b, R1a, N and R1a+N during 2020–2022. The value “30” determines the maximum level of relative mortality during the coronavirus pandemic. The value “15” is a conditional limit of relative mortality values between countries with a dominant haplogroup R1b (above “15”) and countries with populations of other haplogroups (below “15”). The value “5” is the average level of relative mortality fluctuations after mid-2021; **b** Monthly number of sunspots at the beginning of 25 solar activity cycle

different countries: Portugal-91%, Belgium, UK, France, Germany, Finland-about 80%, Russia-52.5%.

It should be noted that Finland and Russia carried out mass vaccination with various vaccines, have different density and age composition of the population, but both of these countries have haplogroup N in the population. This fact once again confirms the conclusion that the genetic composition of the population plays a significant role in achieving collective immunity and consequences mass vaccination. Vaccination also shifted the disease population from the actively vaccinated older population to the unvaccinated younger population and children.

Another factor in the possible equalization of relative mortality across countries can be the sharply increased solar activity by the end of 2021. The dynamics of relative coronavirus mortality changed dramatically in mid-2021 in all countries (marked with arrows in Figs. 3a, b and 4a. After a significant decrease, mortality began to raise sharply, the sinusoidal dependence approached chaotic, and the values of relative mortality approached each other in almost all countries with a difference of no more than 2 times. Simultaneously with this process, active growth of the 25th cycle of solar activity began (Fig. 4b). It is possible that the fundamental change in the dynamics of local epidemics is partly due to solar and geophysical factors and not only to a sharp decrease in the effectiveness of all vaccines simultaneously.

Regardless of the main operating factor, these processes have led to the alignment of the ratio of relative mortality in various haplogroups to the standard coefficient of about 2 by 2022.

4 Conclusions

Thus, the dynamics of solar activity and galactic cosmic rays, as well as the geo-geographic distribution of the population, make a significant contribution to the development of the coronavirus pandemic under the current global minimum of solar activity. It is possible that the conditions for the favorable development of local epidemics into a global pandemic at the maximum or minimum of 11-year cycles of solar activity depend not only on the place of the 11-year cycle in the quasi-centenary cycle, but are also determined by the interaction of longer cycles.

The coincidence of the dynamics of morbidity and mortality in countries with a similar genetic composition was revealed. The success of individual vaccination in each country also depends on the dominant haplogroup of the population. For countries with haplogroup R1b, universal vaccination lowered the relative mortality rate by 5–8 times. However, for countries with haplogroup N and R1a + N, by mid-2022, relative mortality increased by 2–4 times compared to 2020. The effect of vaccination decreases with increasing solar activity for all countries from mid-2021. The influence of these multidirectional processes on the coronavirus pandemic at the maximum of the 25th cycle of solar activity requires further study.

References

1. Ragulskaya M.V: Space weather and COVID-19 pandemic genogeography. *J Nov Physiother Phys Rehabil* 7(1), 031(2020).
2. Atri D, Melot A.: Cosmic rays and Terrestrial Life: a Brief Review. *Astroparticle Physics* 53, 186–190 (2014).
3. Obridko V, Nagovitsyn Yu.: Solar activity, cyclicity and forecasting methods. VVM, Saint Petersburg (2017).
4. Obridko V, Ragulskaya M, Khramova E.: Young Sun, galactic processes and origin of life. *Journal of Atmospheric and Solar-Terrestrial Physics* 208, 105395 (2020).
5. Ragulskaya M., Tekutskaya E. : Solar activity global minimum and genogeographic features of the COVID-19 pandemic. *IOP Conference Series: Earth and Environmental Science* 853 012002 (2021).
6. Güdel M.: The Sun in Time: Activity and environment. *Living Reviews in Solar Physics* 4(3), 137–237 (2007).
7. Belisheva N, Lammer H, Biernar H, Vashenuyk E.: The effect of cosmic rays on biological systems. *Astrophysics and Space Sciences Transactions* 8, 7–17 (2012).
8. Nasirpour M. H., et al.: Revealing the relationship between solar activity and COVID-19 and forecasting of possible future viruses using multi-step autoregression. *Environmental Science and Pollution Research* 28, 38074 (2021).
9. Ragulskaya M.: Solar activity and COVID-19 pandemic. *Open Astron.* 30 (1), 149–158 (2021).
10. Nguyen, A. et al: Human leukocyte antigen susceptibility map for SARS-CoV-2. *Journal of Virology* 94(13), e00510-20 (2020).
11. Souilmi, Y. et al: An ancient viral epidemic involving host coronavirus interacting genes more than 20,000 years ago in East Asia. *Current Biology* 31(16), 3504–3514 (2021).