Coronavirus, Population Genetics, and Humanities[1]
Coronavirus, Genética de las poblaciones y Humanidades
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Coronavírus, *Genética das populações* e Ciências Humanas

Ángel GÓMEZ MORENO[2]

FORTHCOMING ARTICLE FOR A SPECIAL MONOGRAPHIC ISSUE OF MIRABILIA
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Antonio CORTIJO, Vicent MARTINES, Armando Alexandre dos SANTOS (orgs.).
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War and Disease in Antiquity and Middle Ages
Guerra y enfermedad en la Antigüedad y la Edad Media
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[1] This is an enlarged version of a talk delivered by the author to mark the Closing of the School Year 2019-2020 within the Institut Superior de Investigació Cooperativa IVITRA [ISIC-IVITRA] from the Universitat d'Alacant/Universidad de Alicante. The author wishes to thank in particular the help of Charles B. Faulhaber (UC Berkely), as well as that of Antonio Cortijo Ocaña (UC Santa Barbara), Hernán Sánchez Martínez de Pinillos (University of Maryland) and Vicent Martines Peres (Universitat d'Alacant).

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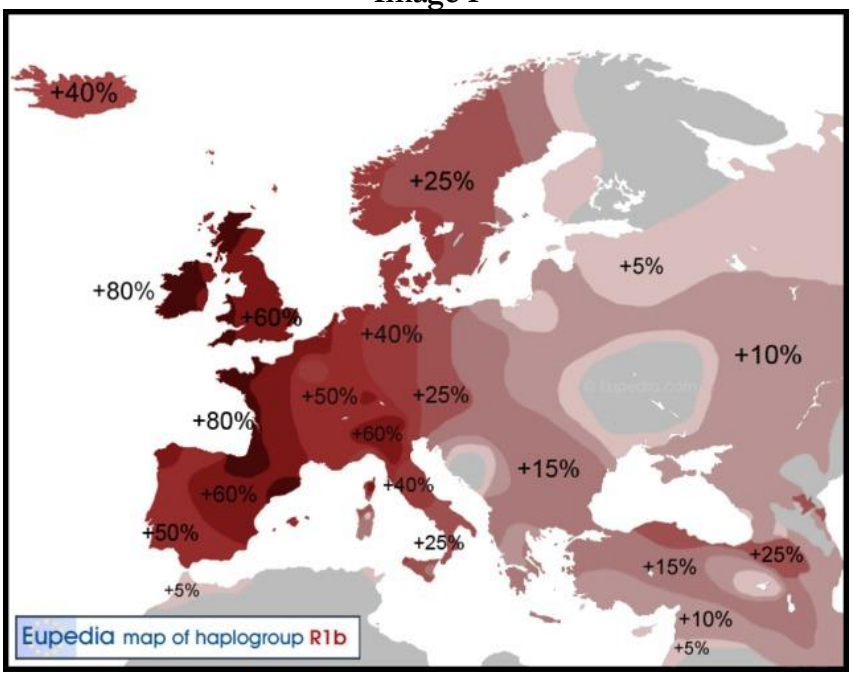
Coronavirus, Population Genetics, and Humanities[3]

Ángel GÓMEZ MORENO[4]

In this study, I should like to bring to your attention the correspondence between the distribution of the coronavirus (SARS CoV-2) and the resulting COVID-19 pandemic in Europe and the map of European genetics. It is noteworthy that the pandemic strikes most deeply in those human communities in which the R1b haplogroup, characteristic of Western Europe, predominates. However, it is even more noteworthy that this fact could have escaped the attention of the scientific community, which should take into account the hypothesis presented here because of its possible implications. [In this regard, see image 1, in which the percentage of haplogroup R1b is indicated by color intensity gradation.

Image 1



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From far-distant China, the coronavirus came to Europe in a way impossible to specify (its traceability is complex, as we know). The only certainty is that this minuscule and fearsome invader, of whose existence the Chinese authorities informed the WHO on December 31, 2019, had showed its face in Europe at least by the end of January. It was on January 31 when two Chinese tourists in Rome were hospitalized with suspicious and worrying clinical symptoms. In a matter of days, the virus had spread throughout Lombardy, Veneto, Emilia Romagna and, indeed, all of northern Italy, infecting many thousands of people.

In this region, the coronavirus struck deeply, far beyond what occurred elsewhere, including in southern Italy itself. The Italian map of the coronavirus assumed a profile from the very beginning and has remained almost unchanged: the pandemic ebbs as we move down the Apennine Peninsula, with its lowest frequency (in number of infections and deaths) in Calabria and Sicily (the geography and intensity of the coronavirus, updated regularly by experts of the Johns Hopkins University [Baltimore, MD, USA], are in the public domain. The numbers used here are those from April 19, 2020).

For those acquainted with Population Genetics, the coronavirus map shows us that the illness it causes, COVID-19, has a higher incidence in areas where haplogroup R1b predominates. For those who are not familiar with genetics, I should clarify that a "haplogroup" is defined by DNA variations that individuals share with other members of the human community to which they themselves belong in the present and / or to which their ancestors belonged to in the past. I shall add that alleles, alternate forms of a gene that arise by mutation, determine DNA and that many illnesses and hereditary syndromes are caused by allele alterations.

While the geneticist is usually a research physician or a molecular biologist, the expert in population genetics may be a linguist (for instance, someone devoted to the study of Indo-European) or an archeologist or historian (someone interested in Prehistory or later periods, whose instruments are found not in a laboratory but in a library) and who routinely works with statistics. Population genetics is used for research on the Middle Ages as well as on even more recent periods.

In such cases population genetics allows us to reconstruct the past in a way no one could have foreseen even a few years ago. Thus, the current genetics of La Mancha region (South Central Spain) allows us to delve into a thousand years of history, to the

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1085 Toledo campaign, when King Alphonse VI conquered the city of Toledo with thousands of Gascon and Basque soldiers (I devoted attention to this event in a recent book on Basque toponyms in the region). In exactly the same way, population genetics confirms the origins (Empordà, the Pyrenees, and Languedoc) of those who repopulated the Balearic Islands after their conquest by James I (1229-1235).

Susan M. Adams *et al.*, "The genetic legacy of religious diversity and intolerance: paternal lineages of Christians, Jews and Muslims in the Iberian Peninsula", *The American Journal of Human Genetics*, 83 (2008), 725-36 is also based on population genetics. The authors point out that in the Iberian Peninsula, together with a European majority (different branches of the R1b haplogroup and, specifically, with the mighty R1b1b2a1b*, also known as R1b1b2a1a2, P312 or S-116), there are two important non-European genetic minorities: North African (10.6%) and Sephardic (19.8%). For this international group modern Spanish genetics reflects centuries of contact and conversion processes.

This study was based on a total of 1,140 individuals. In the resulting map, the total correspondence of haplogroups with ethnic groups or races is noteworthy, although the automatic identification of haplogroups with ethic-cultural groups is not a little suspect. For example, it is excessive to identify as Jews all those individuals who carry haplogroups J or K; similarly, one must also take into consideration the fact that R1b ranges between 7% and 8% in the Ashkenazi community of eastern Europe, while in the case of the Sephardim, or Hispanic Jews, the percentage varies between 13% and 14% [*see the results of the study in the map of graphs in image 2*.]

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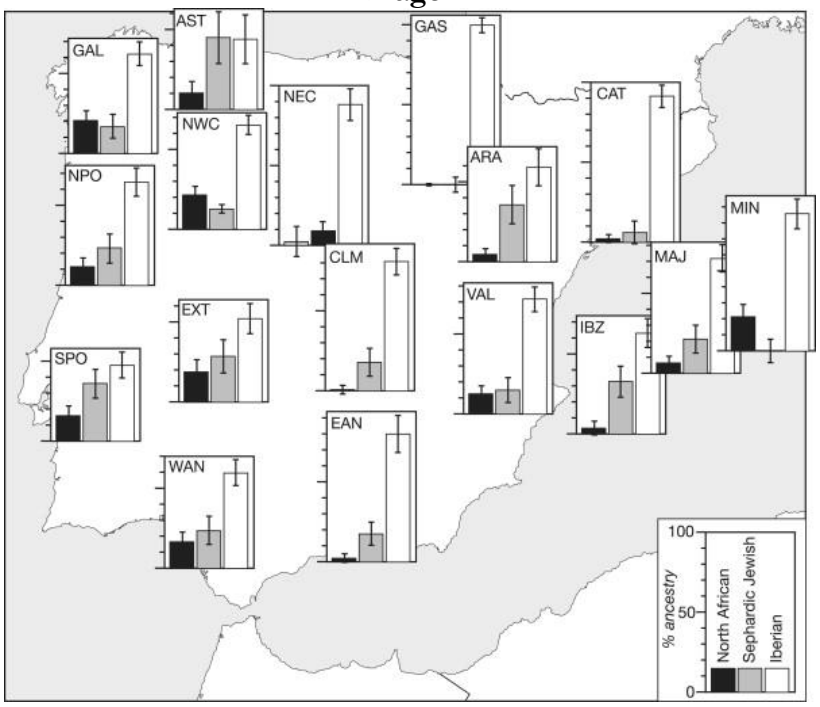
Image 2



Now we shall examine in detail how the formula "to a greater frequency of R1b corresponds a greater incidence of proven or probable (or, if one prefers, real or potential) COVID-19" proves valid in almost all cases. In this sense, its abundance is just as eloquent as its low frequency or even total absence. Let us begin with Italy. First, we must take into consideration that the highest percentages of R1b are found between the Alps and Tuscany, in some areas it is present in more than 60% of the male population. On the contrary, in the South, where the incidence of COVID-19 is much lower, R1b reaches at most 25% in Calabria and some 20% elsewhere (Sicily).

Eupedia allows us to verify that in Southern Italy R1b gives way to two other haplogroups combined: Eastern Mediterranean J1 and J2n (23%) and North-African E1b1b (20.5%). This diversity explains such extreme figures as the 5,561 cases per million inhabitants in Lombardy as opposed to the 457 in Sicily. Let us look at other countries or regions, in Europe or on other continents, where the figures are more illustrative.

The case of Greece, where the coronavirus has shown its friendliest face, is an absolute revelation: it has caused just 187 SARS-CoV-2 infections per million inhabitants (as compared to the 6,882 cases per million in Madrid). How can we

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explain this? Although we cannot discard the explanation offered by the media (for instance, Cristina Losada refers to "El 'milagro' griego frente al coronavirus", *Libertad Digital*, 6 April 2020), this fact agrees with an indisputable reality: the genetics of the Greek population differs profoundly from that of populations of other Western European countries. Concretely, in Greece, the dominant haplogroups are of North-African (E1B1B) and Eastern Mediterranean (J1 and J2) origin; while on the other hand the R1b haplogroup appears in only some 15% of the Greek population. [*See the genetic map from the Eupedia Project in image 3*.]

Image 3

Let us now turn our attention to Germany, whose impressive results to date are due—and this opinion is almost unanimous—to the country's economic resources, its enthusiastic investment in research in the health sciences, and a unique network of laboratories in the medical and pharmaceutical industries. To these almost unmatchable means we should add the efficiency and speed of Germany's political reaction against the virus. However, in my opinion, and without underestimating the Geman health system, the genetics of the German population may also play an important role. It is likely that the SARS-CoV-2 and COVID-19 figures in Germany, so envied by Spaniards, have to do with the fact that Germany is a genetic transition zone.

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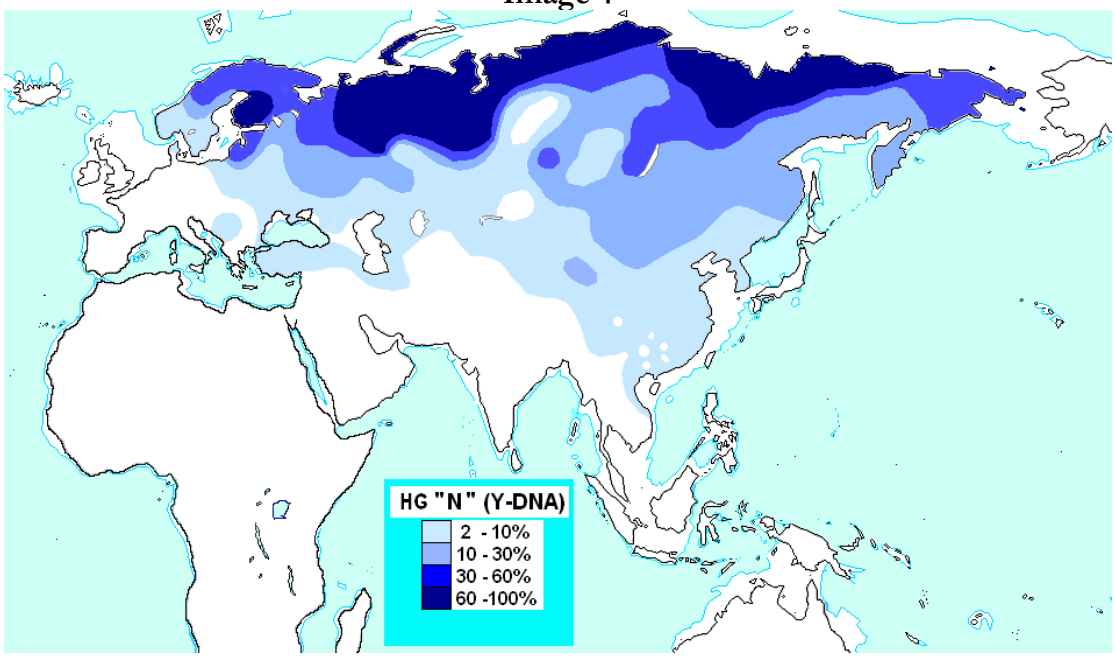
It is the case that the decrease in the frequency of the haplogroup R1b (44%) and the increase in R1a (16%), characteristic of the Slavic peoples, moves eastward from Germany; the Scandinavian haplogroup I1 is present in roughly the same proportion, followed by a pot-pourri of low-frequency haplogroups. This proportion is identical in Austria, although two facts stand out: Austria's genetic diversity and, the comparatively low frequency of R1b (32%), surpassed by the sum of the Scandinavian I1 (12%), the Slavic R1a (19 %), and the Slavic-Balkan I2a-b (9%) haplogroups; and secondly, the not inconsiderable presence of the African haplogroup E1b1b (8%). By the way, ironically, according to some analyses, this seems to be the haplogroup of Adolf Hitler.

Finally, in Russia, the haplogroup R1a is dominant, with 46% of the total, well ahead of N (23%), second in frequency, which is of Eurasian origin, and also of I2 (11%), third in frequency and also of Eurasian origin. This genetic mixture, where R1b (no more than 6%) is almost absent, corresponds perfectly to the number of SARS CoV-2 infections: only 92 cases per million inhabitants. [*Distribution of haplogroup N, common in Russia and, above all, in China, in image 4.*]

Image 4



As we have seen, in Europe the R1b haplogroup spans from Northern Italy to Finisterre in northwestern Spain, with a very high frequency in the Basque Country

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(90%), Ireland (81%) and in two French regions: Brittany (80%) and Normandy (76 %). After Ireland, the largest reservoirs of R1b by country are, in order, Spain (69%), Great Britain (67%), Belgium (61%) and France (58.5%). Italy comes next, although the incidence of R1b varies greatly by region, as we have seen. In R1b Europe, COVID-19 has had devastating effects.

For a time, Britain and France were thought to be—at least relatively—safe from what was happening in Italy and Spain; however, in the first week of April, the death toll figures shot up to record highs. The same day I finished the first version of this article (April 15) the media began to spread terrible news: once again an increase in the number of deaths in France (1,427) and Great Britain (761). The authorities of these countries, as well as those of others in which R1b is predominant, must realize that the key to these figures lies in genetics.[*Addenda 1*º: The daily magnitudes show a rise and fall, since only one day later (April 16) the number of deaths fell by half, to 753 in France.

Let us continue our journey. With regard to Belgium, its incidence of COVID-19 corresponds to the haplogroup data, since R1b is found in 61% of its population. Thus, the number of infections (3,226 per million, above Italy, with 2,920) is what one would expect. It is surprising that the numbers should be practically the same for Walloons, the French-speaking population (3,078), as for Flemish (3,288).

Although the proportions are not exact, one can say of the Netherlands, with 49% of R1b and 1,324 cases per million inhabitants, that it departs from the formula minimally. But we do have to deal with a couple of partial exceptions to the rule: one is Switzerland, whose incidence (3,168 cases per million) is higher than would be expected, given the fact that R1b is found in 50% of the population; and the other is Ireland, which leads the list in R1b (81%), but only 2,998 cases per millon. However, in the last week the Irish situation has worsened considerably, with an astonishing boost from 1,814 on April 16 to the current figure.

Sooner or later in all countries or regions where R1b is dominant, COVID-19 incidence and death reach an intensity unknown in other countries where RB1 is low or virtually non-existent: almost all of Africa and a good part of Asia, but also the European countries of the old Iron Curtain (R1) or of the South, of which Greece is emblematic, where R1b almost does not exist.

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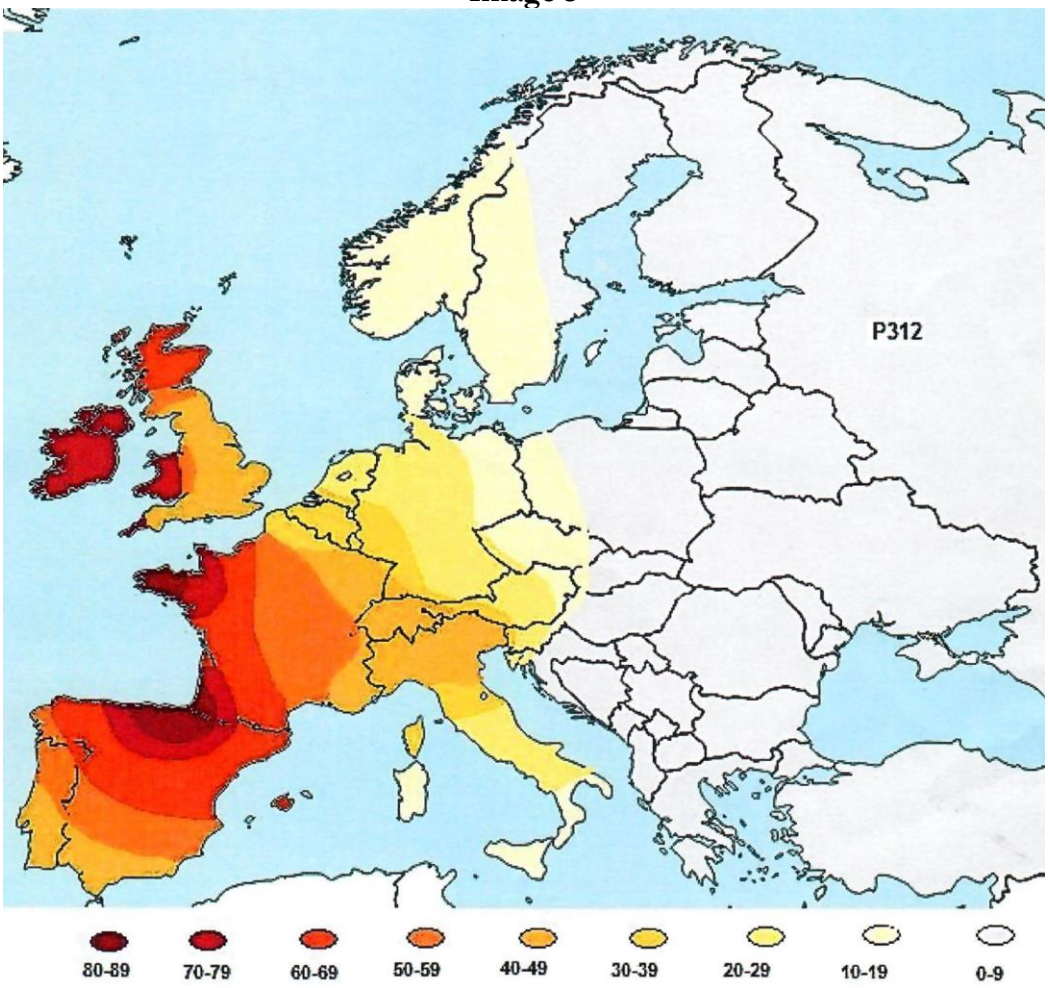
Because it is so frequent in the most developed countries, R1b has been intensely studied by population geneticists, who have segmented this haplogroup into branches or clades (a group of organisms descended from a common ancestor). Among them, the most frequent and widespread is P312, S116, or R1b1b2a1b (my own haplogroup). The *italo-celtic* label has been attached to this subclade because, in the past the center of its radiation was thought to lie in the Italian Alps. In recent years, new theories have emerged about the genesis and expansion of these sub-haplogroups and subclades. Special attention has been paid to the Basque Country and its role as a center of radiation. In any case, I stress again he importance of P312 for this analysis, since it is present in all of the large R1b communities [*Distribution of P312 in image 5*.]

Image 5



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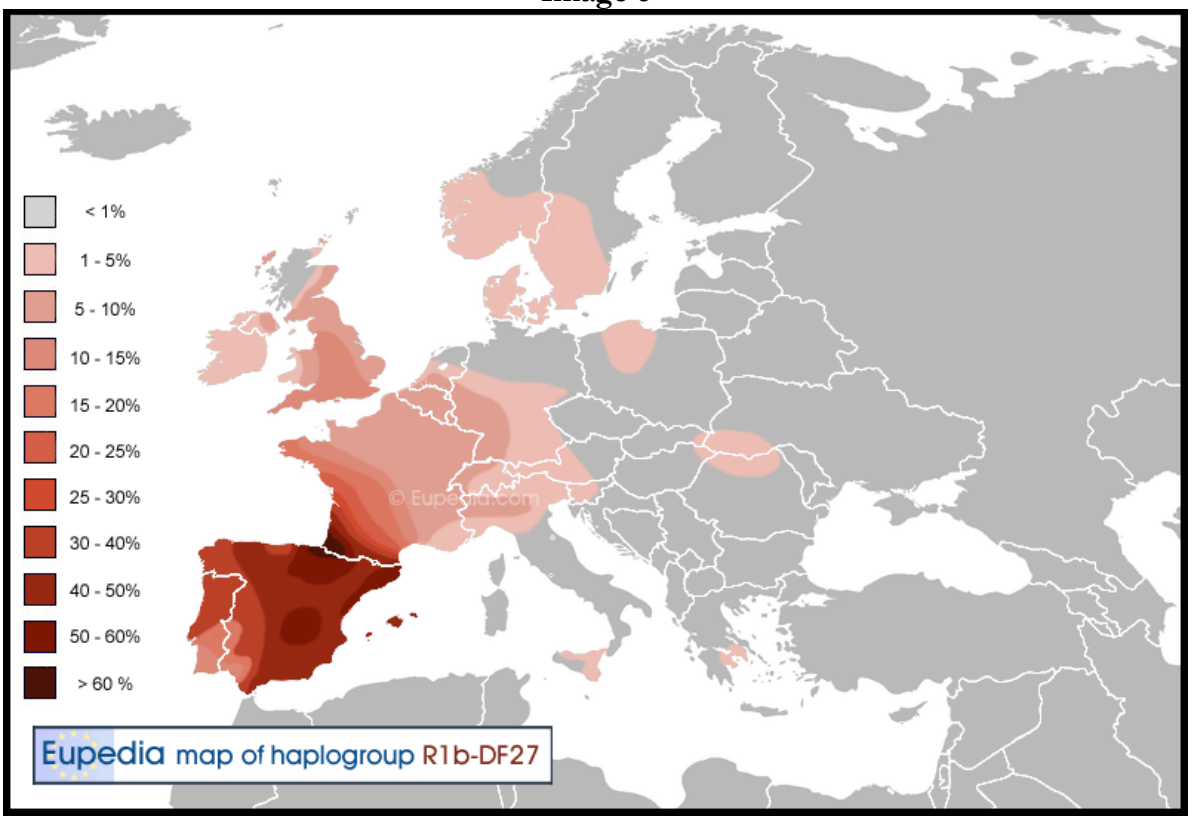
On the other hand, some branches or subclades of R1b are linked almost exclusively to a given country or region. For instance, DF27, characteristic of the Iberian Peninsula, reaches its highest density in the Basque Country and the Pyrenees. This helps to explain why the highest percentage of COVID-19 cases in Spain (as of 19 April), 11,556 per million inhabitants, is found precisely in La Rioja, a region bordering the Basque Country with universally renowned wines.

Moreover, DF27 presents very high figures in La Mancha (Central Spain) as well as in the Balearic Islands. This distribution is closely related to the history of Spain, as I pointed out at the beginning of this paper [*DF27, according to the Eupedia Project in 2017, in image 6*.]

Image 6



The genetic border of the Strait of Gibraltar is virtually absolute; although only 10 km wide it completely separates the European haplogroup R1b and the North African haplogroup E1b1b. If the available information is reliable, the indigenous population of North Africa seems to be much more resistant to the virus, since Morocco has

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only 42 cases per million. In this regard, it is important to have reliable information about COVID-19 in Ceuta and Melilla, the Spanish enclaves in Morocco. I have been able to gather information only about the first (April 11), Ceuta, where about 87% of those infected are Caucasian Europeans, while 13% are North African. Keep in mind, however, that Europeans represent 52% of the city's total population and North Africans 48%. Nevertheless, the official numbers do not coincide with the real ones, which speak of a North-African population of 70-75% in Ceuta. This brings the proportions of infected persons closer to 90-95% for Caucasian Europeans and 5-10% North African. Completing and updating the information about these Spanish enclaves in Africa is fundamental.

Counting and fixing percentages are vital tasks needed to confirm, revise or refute my hypothesis regarding the relationship between the coronavirus and the R1b haplogroup, which I am defending here. This analysis (or any other based on genetics) may be able to throw light on the diverse incidence of COVID-19 in Europe and the rest of the world as well as to suggest strategies for its eventual containment. [*See image 7, a map of the prevailing haplogroups in Europe and neighboring areas in Africa and Asia, and image 8, The incidence of COVID-19 in Europe, as reflected on a map of April 5*]

Image 7

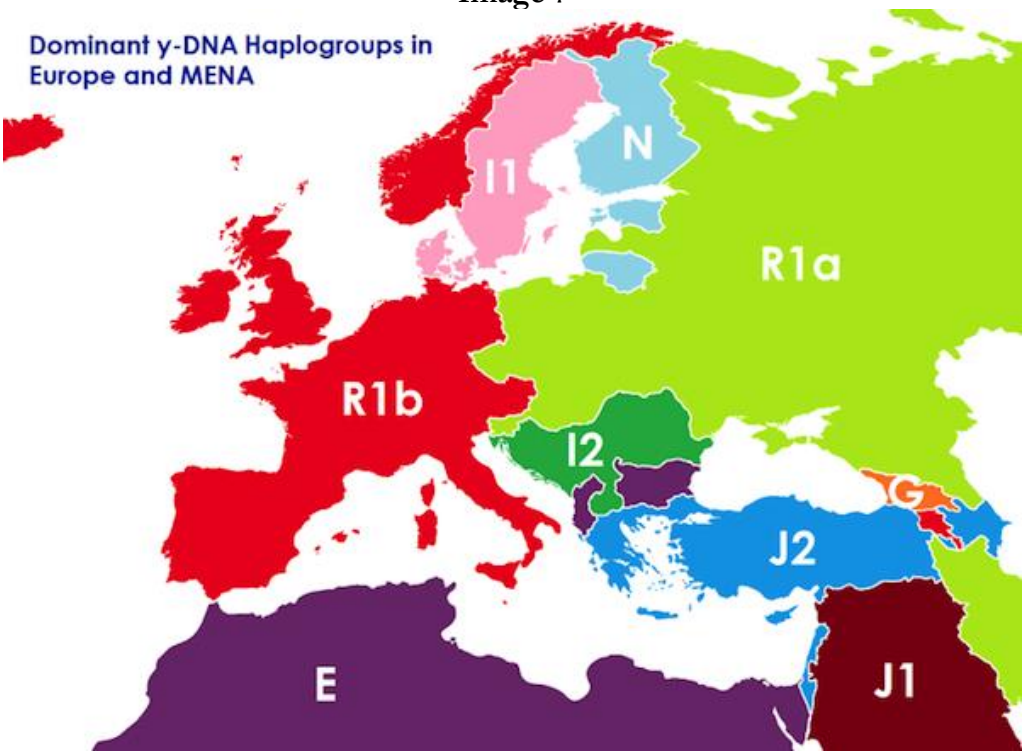

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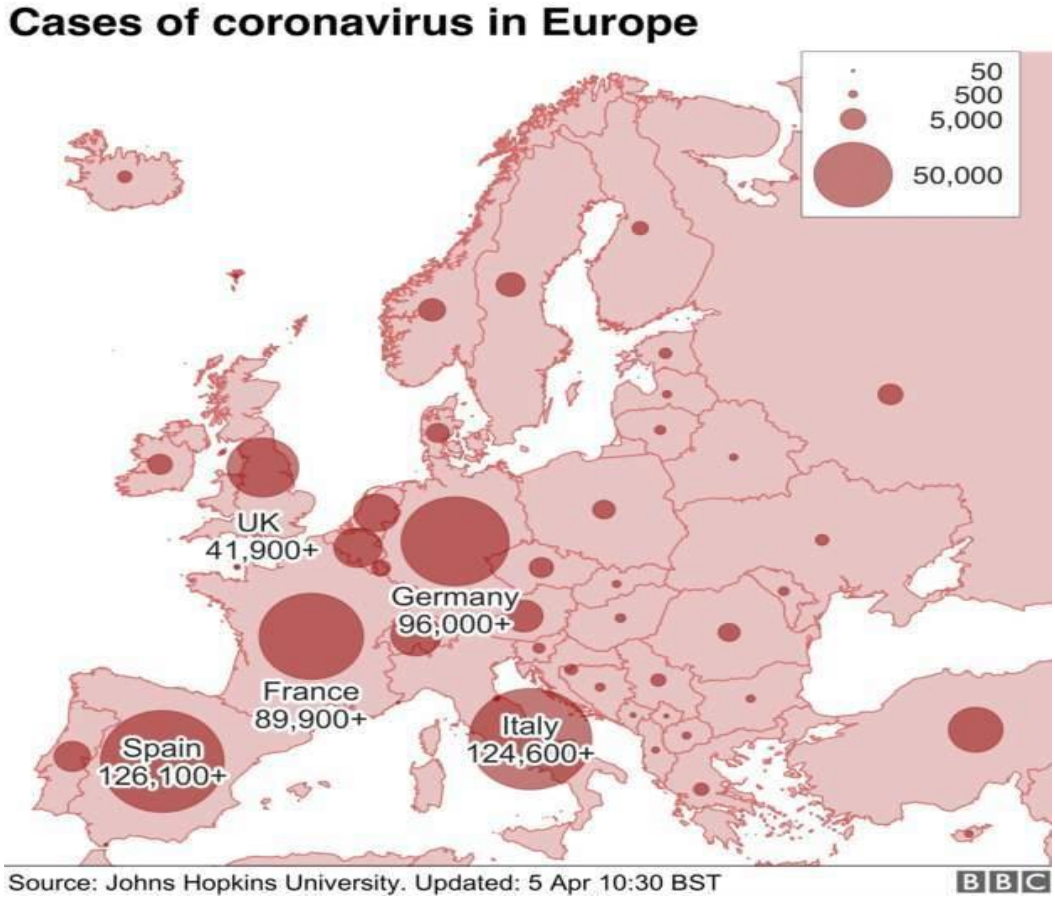
Image 8



Special attention should be paid to Australia, where the R1b haplogroup is the most dominant by far. The percentage of R1b compared to other haplogroups and the number of cases per million are also relevant, but these data must also take into account Australia's special circumstances: its geographic isolation reinforced by the closure of borders and the rigorous control established by the authorities of what is a nation-continent.

Now, let us return to the extremely low incidence of COVID-19 in Morocco. But in neighboring Spain, which counts itself among the nations with the highest quality of life and almost equals Japan in life expectancy, is living a drama: the current drama of Western Europe. Morocco is not an exception in its relative immunity: most countries in Africa and Asia share that immunity as well as a role as mere witnesses to this drama. Even in countries with a large population, a health system that does not deserve the name, and with an extremely low per capita income, SARS CoV-2 is not

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feared as much as the measures taken to defeat it. I refer to India, with 1,352 million people and a contagion rate of 11.5 per million; Nigeria, a population 196 million and little more than 2.5 case per million. Similarly, it is shocking that Egypt (with 98 million inhabitants and 30 cases) and Indonesia (264 million inhabitants and 23 cases) are light-years away from the figures of Europe or America.

Especially revealing is the case of Zambia, a country in which half of the population became infected with HIV during the worst years of AIDS. But now, with only 3 cases per million, it seems that COVID-19 hardly affects it, in line with the rest of Black Africa. This fact can only be qualified as "amazing", but it is a reality we must somehow explain. My hypothesis explains it. African peoples, from the Mediterranean border down to the cold waters of Cape Point, have the same shield: their genes and the absence from them of R1b.

A simple glance at the Johns Hopkins University map confirms that little has changed since the media noted the advent of the virus. Even in those early moments some commentators claimed that Africans were somehow immune to the virus. On February 27, *Le Monde* emphasized that Africa resisted the threat better than any other continent. One month later (March 24), BBC Africa said: «L'épidémie de coronavirus n'est plus une menace pour l'Afrique»; or this one: «le nombre relativement faible de cas en Afrique a déconcerté les experts».

The journalists have a reliable source in the electronic pages of Johns Hopkins University. The misinformed populace, in cities or villages, the savanna or the tropical forest, says "The coronavirus disease is a white man's disease"; or "The coronavirus is triumphing in Africa because of white people." Authorized voices, however, warn that no one has a 100% guarantee of escaping from COVID-19. In South-Africa, where the risk of getting infected is much higher than in the deepest Africa, Landon Myer, Head of the School. of Public Health at the University of Cape Town, says: "There is no evidence whatsoever that any particular group of people are immune from the SARS CoV-2 virus that is causing the Covid-19 epidemic." I agree with this expert as much as I disagree with those misinformed people who consider themselves protected by melanin in their skin or by some special climate conditions, supposedly inimical to SARS CoV-2.

As we have already seen, the haplogroup R1b offers the best lodging for SARS CoV-2 as well as an optimal home for the development of the associated illness. And since

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R1b is present everywhere in the U.S., we can understand why the number of infections and deaths grew exponentially before adequate social distancing measures were implemented. To repeat, the R1b haplogroup is the most frequent among North Americans, with a total of 87 million people of Irish, British and Scottish descent who bear it. Though no more than a survey based "on astoundingly unreliable data," Richard Morrill adjudicates, in "Race, Ancestry, and Genetic Composition of the US" (*Newgeography*, 9/22/2015) R1b to 188 million people in a total of 328 million in the country. And we should remember that autosomal R1b is also frequent in African Americans and still more so in those of Hispanic ancestry. Since both Africans and African Americans, share Mt-DNA U6, which is dominant in North Africa where COVID-19 has had little penetration, we conclude that the ease with which the virus enters bodies is not determined by this haplogroup.

In Central and South America, R1b is present in many people who look Amerindian. A study coordinated by the Centro de Investigación Genética y Genómica of the Universidad Tecnológica Equinoccial (UTE) of Ecuador concluded that in comparison with the Amerindian purity of Mt-DNA (mitochondrial or maternal DNA), Y-DNA (paternal), reflects a mixture of 60% European DNA, 30% Amerindian DNA, and 10% African DNA. Because the European ancestors were Spanish, the most frequent haplogroup is, by far, R1b.

Conclusion

Let us conclude: Population genetics show that the invisible, silent, and terrible enemy that faces us today inflicts more damage on some countries than on others and shows itself to be crueler to some groups or individuals than others. For this reason, Spain and other western countries where the frequency of R1b is very high, have become the principal target of COVID-19.

More than a single battle: we need a long-lasting campaign of epic proportions against such a powerful enemy ("little more than a flu", according to some politicians). But instead of the lonely struggle of a single epic hero—a Roland or a Cid Campeador—we need thousands of fearless men and women who are willing to risk their lives by dealing directly with COVID-19 patients, although conditions can be improved. In my opinion it was impossible to anticipate what has occurred in western Europe. Moreover, at this early stage in our knowledge, we still lack fundamental tools, principles, and strategies to understand, control, and neutralize the virus. One of

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these, perhaps the main one, may well be genetics, which must be used in a new way, skillfully and fruitfully, to understand the relationship between SARS-CoV-2, haplogroup R1b, as well as the less susceptible haplogroups: it is time to follow this path until it has yielded the knowledge that may be able to save us, or at least put us on the road to safety.

R1b is defenseless against SARS-CoV-2. This fact can provide vital information or simple but valuable clues showing how to approach the virus and how to destroy it. Getting acquainted with our haplogroup (my haplogroup) may focus the kind of research that could help to design the long-sought vaccine. Special attention must be paid to the way in which SARS-CoV-2 and P312, the most frequent and widespread of all R1b branches and clades, are interrelated.

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