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Coronavirus Invasion and Neanderthal Retreat

Adrian Bejan
J. A. Jones Distinguished Professor
Duke University, Durham, NC 27708-0300, USA

An unexpected discovery of a new mental 'connection' between
two previously disconnected physical phenomena.

An avalanche of articles is asking why Africa was relatively untouched by the coronavirus. NBC News put it bluntly: Covid models predicted devastation in Africa, but 'the reality is starkly different' [1].

Last March 6, at the start of the pandemic, I predicted the African exception and I communicated it to three of my correspondents. In this article I share with you what I wrote then, and I conclude with the science developments that have just occurred, which support my prediction:

Coronavirus news dominates scientific publications and journalism. The news follows three threads: what the virus is, by what mechanisms it spreads, and how far it has spread on the day of the report.

This letter is about an aspect that appears to have escaped scrutiny, namely, the chronology and geographical directions of the spreading of the disease. This aspect jumped in my mind because in my new book [2] I illustrated based on the latest scientific literature [3-9] the chronology and geographical directions of another spreading phenomenon: humans, out of Africa.

First, let's look at the facts about the coronavirus, which can be viewed in summary every day, for example in Fig. 1 (note: data as of 5 March) [10]. The disease spread first in China (in all directions), and then it spread to the east (Korea, Japan) and south (Thailand, Singapore, Australia, etc.). Later, it spread to the west in this sequence: India, Iran, the Middle East, North Africa (Egypt), North America and now most of Europe.

Important is that except for a few spots that begin to emerge now (March 2020), the disease has not spread over the African continent. Why?

In science, explanations come easily when the data are available for examination. As I will show, more difficult is *to predict* the phenomenon that underpins the spreading flow architecture hidden in the data.

One easy explanation of the available data is that the spreading happened because Korea is next door to the source, and Iran, the Middle East and the rest are farther. Such an explanation may have been correct when long distance travel was by camel and boat, not today.

Today everybody flies 'instantly' all over the globe [11]. Many people were flying for several weeks before the Chinese government allowed news about the virus to seep out.

The conflict between the easy explanation and the pattern in the data (chronology, geography, spreading) means only one thing: people on the globe are not uniformly susceptible to the coronavirus. If not equally susceptible, then why?

The answer lies in a much older phenomenon that looks just like the virus spreading of Fig. 1, except that the older spreading happened in the opposite direction, and over the same latitudinal region of the globe. The older phenomenon is the spreading of humans [2].

Neanderthals and other hominids (Denisovans) populated Europe, the Middle East and Asia long before the *homo sapiens* migrated out of east Africa to the north and east. Along the way, on the world map and in time, humans lived through three sequential events of interbreeding with the hominids encountered in their path, Fig. 2.

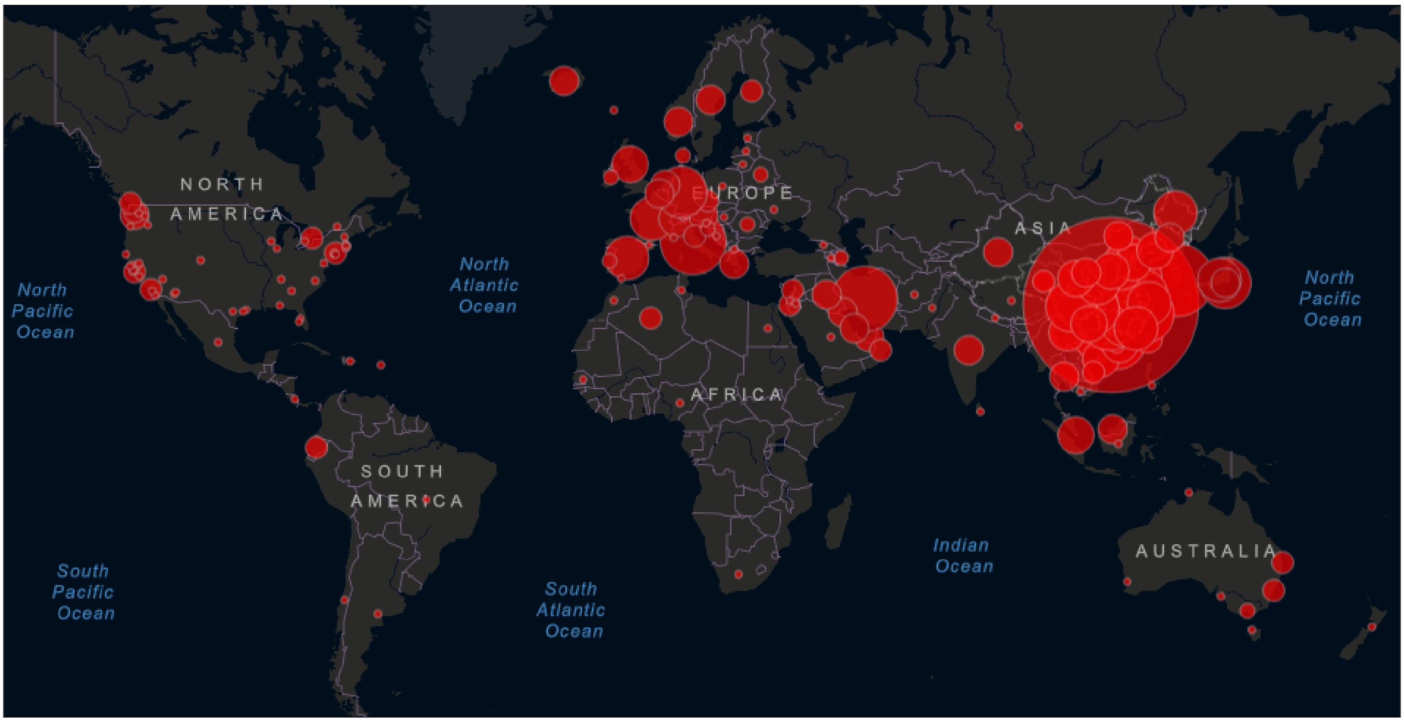

Figure 1 Coronavirus COVID-19 Global Cases by Johns Hopkins CSSE [10], accessed 5 March 2020.

The offspring from the first interbreeding were the Melanesians and Australoids, which spread eastward on land and water. Later, this first hybrid interbred with hominids for a second time, and gave birth to the Middle Eastern type, which spread east to the Indian subcontinent, and west to Europe and North Africa. Most recently, the Middle Eastern type interbred with hominids for a third time, and the result was the East Asian type.

The evidence that supports the chronological and geographical sequence of Fig. 2 is massive: some is invisible (in DNA), and most of it is in plain view. The evidence is presented in the book [2] and its sources [3-9]. Specifically, the percentage of Neanderthal DNA in humans increased stepwise through each interbreeding event, from zero in Sub Saharan Africans to roughly 4 percent in East Asians. In the same sequence, the center of mass of the human body moved lower, legs and arms became shorter and brain size increased.

Conclusions:

1. The nonuniform distribution of human susceptibility to the coronavirus corresponds to the nonuniform distribution of Neanderthal DNA.
2. The susceptibility to the virus was inherited from the Neanderthals, which is why those with zero DNA are less susceptible to the disease.
3. If the most susceptible to viruses were the Neanderthals themselves, then it stands to reason that the Neanderthals declined to extinction because of virus induced diseases, not because Darwinian competition with allegedly superior humans out of Africa.

Any new ‘connection’ such as 1-3 above is an opportunity for new scientific research. This means to take a fresh look at the available body of data on the coronavirus spreading. It means to ask new questions about the known facts. This new understanding would make it easier to track the spreading of the disease, and to offer greater help to people who are threatened the most.

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Many months after my correspondence of March 6, pandemic science publications showed that my DNA-based prediction was correct. For example, on September 30 in an empirical paper (and its references) in Nature magazine [12] we read, “the major genetic risk factor for severe COVID-19 is inherited from Neanderthals.”

In retrospect, it was fortuitous that I made this prediction very early in the pandemic, before the whole world became infected, and before governments intervened to control the spreading. Today it would be impossible to see the pattern that the early spreading revealed (Fig. 1).

It was fortuitous to connect the virus susceptibility to the chronology and geography of the interbreeding with Neanderthals, because this shed a new light on the extinction of Neanderthals, in addition to the spreading of future pandemics.

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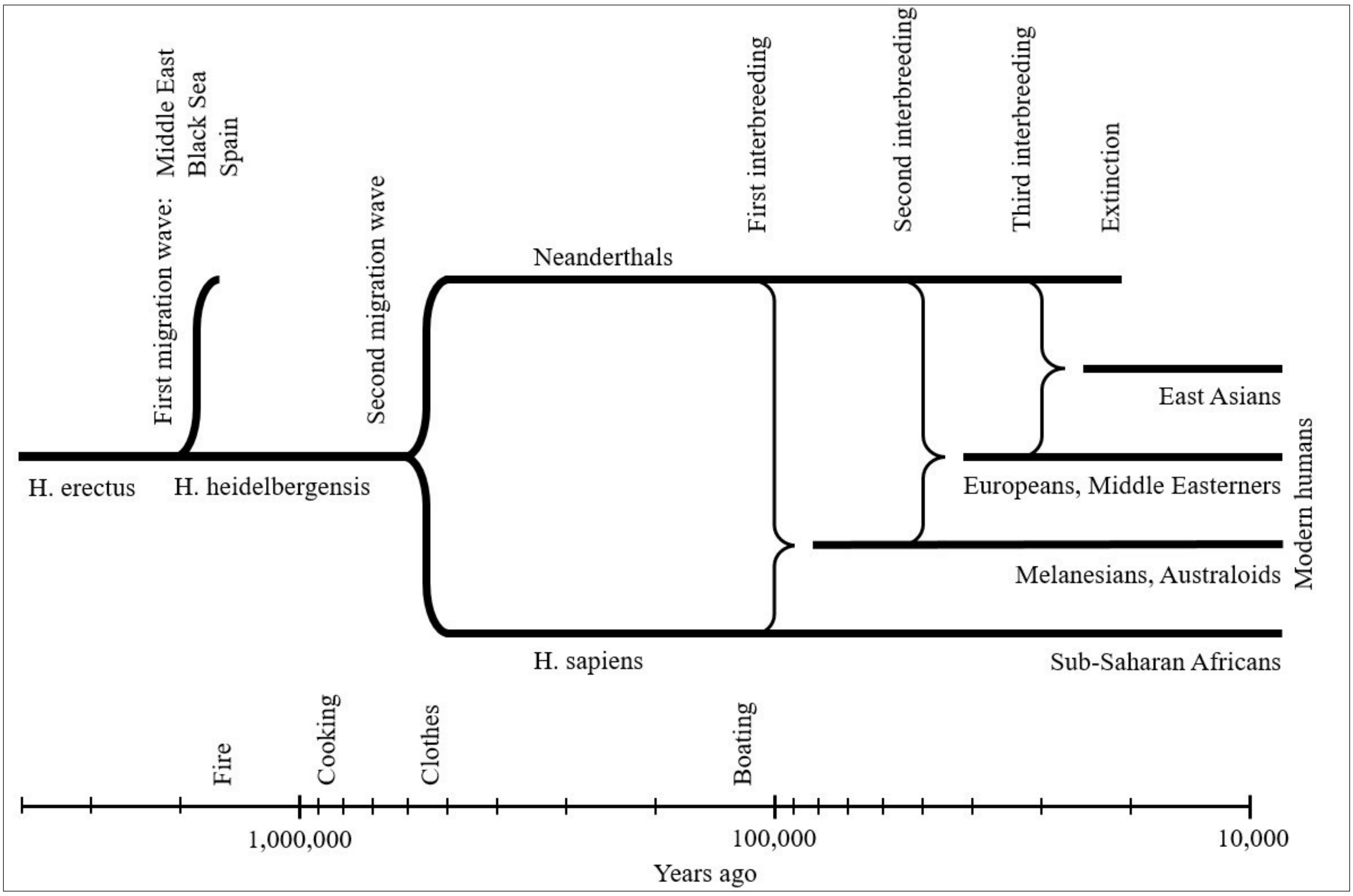

Figure 2 The spreading and mixing of humans on the globe [2]. The time scale is logarithmic.

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