Virol Curr Res
Volume 5:4, 2021

Virology: Current Research

Review Article

Open Access

Footprints of Past Pandemics in the Human Genome

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Abstract

Viral pandemics over centuries and millennia have left indelible signatures on our genomes. Deciphering these signatures could give us profoundly important information on our evolutionary history that appears to have been directed by the arrival of new viruses from the deep cosmos. A recent study that shows a residual signature of SARS-CoV-2 (in the form of multiple generational expression of host-specific SARS-CoV targeting viral interacting proteins known as VIPs) in the genomes of a South Asian population suggests that a major COVID-19 type infectious episode may have occurred about 25,000 years ago. The need to monitor the stratosphere for the arrival of new pathogenic viruses, or even the return of old viruses such as Small Pox, is stressed.

Keywords: SARS-CoV-2 • Footprints • Pandemic infectious episodes • Evolutionary history

Introduction

In this article we discuss the growing evidence to support the view that at least some of the viruses that cause diseases in plants and animals including humans are of extra-terrestrial cosmic origin. This was raised first specifically for the fully-sequenced human genome by Wickramasinghe [1], and expanded to review evidence for the range of integrated full-length viral genomes and their fragments, of DNA and RNA viruses, both retro-viral and non-retroviral, by Wickramasinghe and Steele [2]. This is but one part of the body of evidence that is pointing towards an extra-terrestrial origin of life on our planet, in contradiction to the conventional view that life originated de novo on the Earth from a primordial soup of organics. This alternative viewpoint argues that life is unequivocally a cosmic phenomenon, and one that takes root on every habitable planetary abode throughout the cosmos.

Nearly four decades ago Hoyle and Wickramasinghe, from their studies of interstellar and cometary dust, arrived at the startling conclusion that a large proportion of cosmic dust is comprised of bacteria and viruses, a fraction of which must exist in viable form Hoyle and Wickramasinghe. It was argued that the origin of life on habitable planets like Earth inevitably involved the arrival of microorganisms in viable form, thereby circumventing the concept of small-scale planet-bound abiogenesis, an issue which is fraught with both inconsistencies and extreme statistical improbabilities [3,4]. As a consequence of these ideas, it was further proposed that the occurrence of pandemic diseases of viral origin in plants and animals is an anticipated corollary that in turn would have a crucial impact on the evolution of life. Indeed, the several stages of human evolution must have been profoundly affected by these myriad viral genetic integration signatures. They are the most striking feature of the human genomic DNA sequence structure-"the forest rather than the trees against which protein-coding genes are conventionally embedded."

In the book "Living Comets" published in 1985 Hoyle and Wickramasinghe wrote [5]. Thus:

"An illusion was put about widely a few years ago that it would be impossible for viruses from space to mount pathogenic attacks on terrestrial plants and animals with the specificity that is actually observed, for example with measles being a specifically human disease. But this was merely an expression of opinion. Worse, it was untrue. Human viruses attack tissue-cell cultures of other primates, and most human viruses can be cultured even in chick embryo, a taxonomic class apart from humans.

The specificity does not come therefore from individual cells or from the viruses themselves, but from our immune systems. This should really be no surprise because our immune systems can be specific even to the extent of rejecting tissue from close relatives of our own species.

It appears very likely that our very genetic make-up has an origin external to Earth. As well as causing pathogenic attacks, viruses can simply add themselves to our chromosomes, placidly multiplying only as our cells divide. In this way we derive new genes as a matter of fact, not conjecture. Since it needs only an elementary mathematical calculation to show that genes are so astonishingly complex that they could never be produced by random internal shuffling of bases on our DNA, it is then but a short step to the realisation that all of our genes are of external origin, added by viruses [1-4]. Complete immunity to viral invasion can therefore be seen to be impossibility for an evolving biological system."

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Received: June 30, 2020; **Accepted:** July 14, 2021; **Published:** July 21, 2021

The Role of Viruses-Evidence from DNA

After the human genome was fully sequenced in 2001 our cosmic ancestry was laid bare and many of the predictions of the cosmic theory of the 1980s were verified. The discovery that only 25,000 genes exist to code for all our proteins left the origin and the role of the vast majority of our seemingly redundant DNA unexplained. There seems now little doubt that much of this genetic inheritance is comprised of DNA whose origin is viral in nature. This DNA shows up as LINEs (Long Interspersed Nuclear Elements) (21%), and SINEs (Short Interspersed Nuclear Elements) (13%). The LINES are directly functionally related to retroviruses as reverse transcriptase encoding elements which assist the integration and retro-transposition of other shorter SINE elements (e.g. Alu elements). The HERVs (Human Endogenous Retroviruses) and LTRs (Long Terminal Repeats) comprise about 9% of the human genome (see Ref.6 Appendix B). These are all relics of viruses that have infected our ancestral lineage over the past millions of years and have left their footprint in our DNA. During the past 4.2 billion years of terrestrial evolution of life on this planet viruses have played a key role. When a virus invades and productively infects a cell it multiplies with the "assistance" of the invaded cell. In other instances viruses can instead insert genetic (viral) elements which can alter the previous cell program without causing any overt deleterious changes to the cell. Such program insertions by viruses may have been responsible for many stages of evolution over millennia for the vast ensemble of life forms (species) both on Earth and elsewhere in the cosmos.

In general, it will not happen that a virus on entering a cell will have precisely the right elements for insertion of genetic material into the life-form in question at its current stage of evolution. During evolution there will thus necessarily have been a multitude of "abortive trials", likely with massive viral replication and cell death, before a successful program insertion is accomplished and evolutionary advances occur. It is our hypothesis that a cosmic imperative is for viruses to act as a driver of evolution, in which viruses seek cells, not vice versa.

Viral sequences added through the mechanism of pandemic disease could provide evolutionary potential that leads to new genotypes and new species at one end of the scale, and to new traits and the capacity to express our genes in novel ways at the other. It is becoming clear that our entire existence on this planet is contingent on the continuing ingress of cosmic viruses, which we had hitherto thought were merely the vehicles for death and disease. Their positive role in evolution that was predicted in the 1980's may only just be beginning to be seen. Major evolutionary steps in the development of complex life forms leading to Homo sapiens are thus all externally derived, and evolution is essentially driven from the universe outside. If this is so the overall impression will be of a pre-programming in the higher levels of development of intelligence that is manifest in biology.

Evidence from Geology

The facts relating to the evolution of life on the Earth progressing through a long series of punctuated steps have been available for several decades [7]. Long periods of slow and tedious evolutionary progress are frequently interrupted by sudden bursts of evolution and innovative speciation, with or without accompanying episodes of extinctions, which we can often attribute either to comet collisions or climatic catastrophes of one form or another [8]. It is this process of speciation that Hoyle and Wickramasinghe already discussed in the 1980's and attributed to viral additions [9] (Figure 1).

A recent observation in the field of geology that is inconsistent with the standard theory that life emerged in a primordial soup on the Earth is the discovery that the very first evidence of microbial life on Earth was found locked away within crystals of zirconium in rocks that formed 4.1-4.2 billion years ago now exposed in the Jack Hills outcrop in Western Australia [10]. This discovery lies to rest the possibility of the origin of life in a primordial soup brewing on Earth at a time when the planet was being relentlessly bombarded by comets and meteorites. The evidence is in favour of the alternative viewpoint that the first life on Earth in the form of bacteria came from impacting comets.

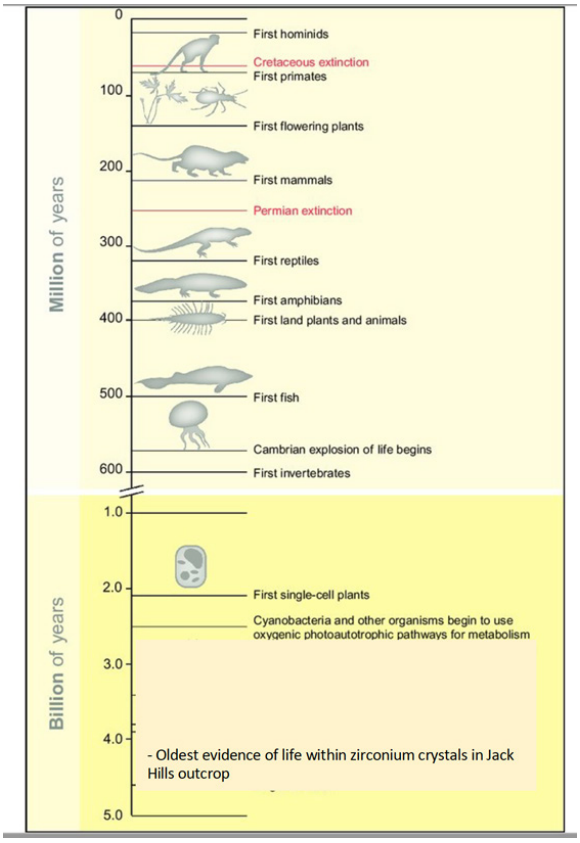

Figure 1. Evolution of plants and animals, from the time of the first introduction of life 4.2 billion years ago.

The delivery of micro biota from comets to the Earth would of course have continued from that early moment 4.2 billion years ago to the present time, bringing the set of microbial genes from a vast cosmic ensemble that directed the evolution of life on our planet in the manner first proposed by Hoyle and Wickramasinghe in 1981 [9] and all the relevant supportive evidence recently reviewed by Steele et al. [4,6] The existence of virus-related DNA in vast quantity in our genomes testifies to the operation of such a process taking place over billions of years of evolutionary history [1,2].

Deep History of Ancestral Pandemics

DNA sequence studies over the past decades have clearly shown that the evolution from early primates leading up to Homo sapiens was marked by a long series of viral pandemics, each of which could well have represented a "brush with extinction", but the evolving line survived through eventually to reach us today. The branching points in the evolutionary lineage are marked by the discovery of HERVS and ERVS as shown schematically in Figure 2.

Viral inserts via direct viral-encoded reverse transcription as for the retroviruses is clear. In the case of non-retroviral RNA infections this would require host cellular-derived reverse transcription, such as for the single-stranded coronaviruses like COVID-19. Such inserts appear involved at the branching points in the evolutionary tree depicted in Figure 2 are arguably also implicated in a long sequence of pandemics of disease. In each postulated pandemic of disease [11]. In each postulated pandemic of viral disease over the past 45 million years a surviving cohort of our ancestral line would have directly acquired the retroviral genes indicated (Figure 2).

A recent study of the genomes of an East-Asian population group has shown evidence of multiple generational human gene signatures of strong positive genetic adaptations which occurred in these populations, in multiple genes that interact with coronaviruses, including SARS-CoV-2. These signatures of viral-interacting proteins show up as a strong peak after retracing mutational steps generation-by-generation through 900 generations in the past [11]. This evidence is reproduced from Souilmi et al [11]. below indicating a major Covid-19 type pandemic some 25,000 years ago (Figure 3).

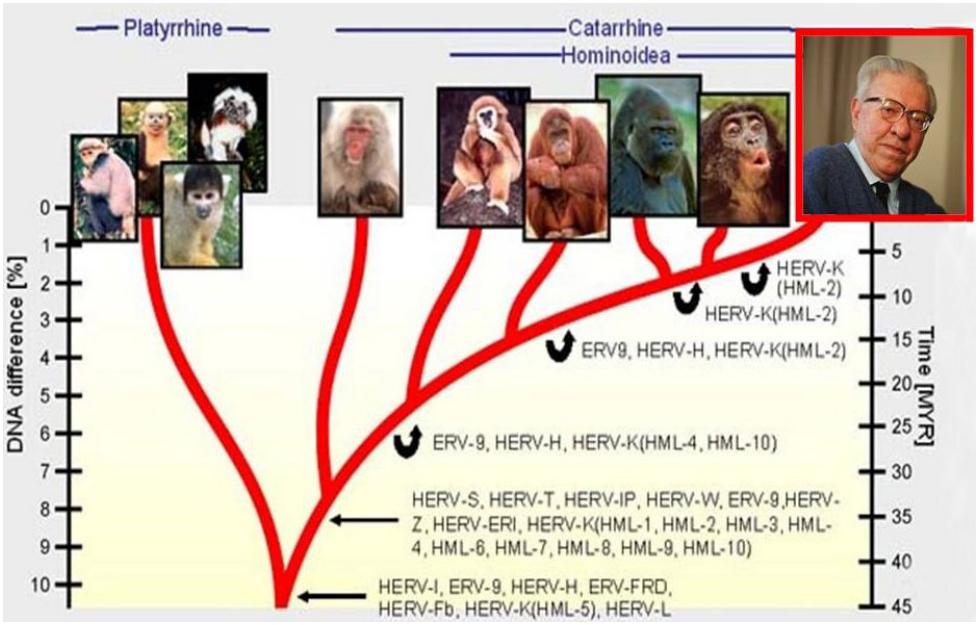

Figure 2. Schematic evolution of the hominid line leading up to Homo sapiens.

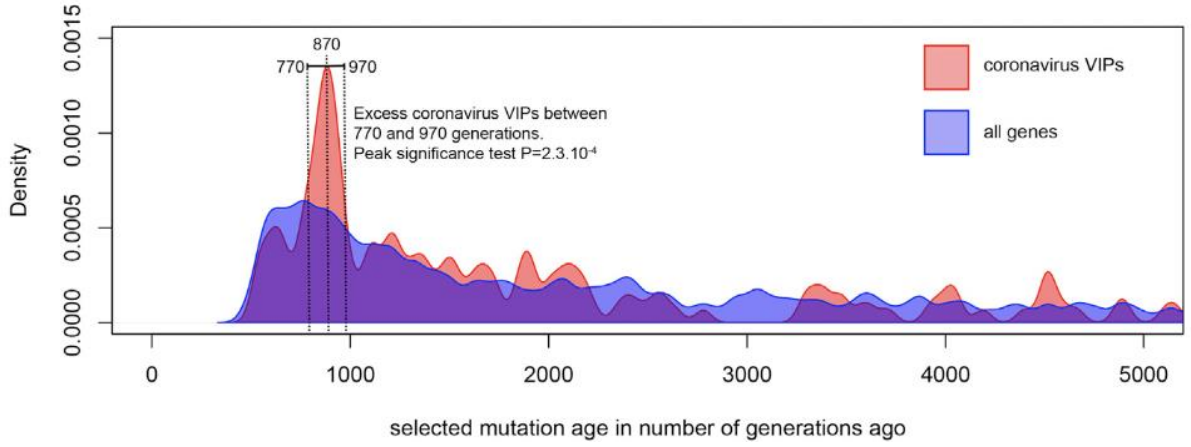

Figure 3. Evidence of COVID-19 pandemic 870 generations ago in the form of multiple generational expressions through the genome of SARS-CoV specific proteins known as VIPs. From Figure 2 in Souilimi et al [11].

Reports of the sudden spread of plagues and pestilences have punctuated human history throughout the centuries [12]. The various epidemics, scattered through time and across the world are sometimes in a few instances recognisable as similar to modern diseases, a striking example being smallpox. Skin lesions strongly suggestive of smallpox have been found in the Egyptian mummy of Ramses V (1145 BCE). Furthermore, clinical descriptions consistent with smallpox are described in medical writings both from ancient India and China at around the same time. The absence of any comparable descriptions of pandemics in classical Greece and throughout early Christendom in Europe suggests an absence of the disease from human populations for over 1500 years, until it reappeared in China possibly in the 5th century of the Common Era. Thereafter it remains endemic in the world's human population until its final deliberate eradication in the 20th century. A major puzzle for understanding the re-emergence of smallpox after an absence for 1600 years is the lack of an animal reservoir into which the virus might have receded, humans being the only known host of the Variola major virus. An alternative viewpoint considers the data to make a prima facie case for a comet with period 1600 years-if the last episode of infection is assumed to have happened in 500 AD in China (vide supra), a return of the same comet is alarmingly imminent.

The identifiable recurrence of smallpox (Variola major) through history is an exception. More often, from written descriptions alone, ancient epidemics bear little or no resemblance to either modern disease or to one another. However, they all share the common property of afflicting entire population centres, countries or even widely separated parts of the Earth in a matter of days or weeks.

The Greek Historian Thucydides said of one such isolated event, the plague of Athens of 429 BC [12,13], thus:

"It is said to have begun in that part of Ethiopia above Egypt. On the city of Athens it fell suddenly and first attacked the men in Piraeus; so that it was even reported by them that the Peloponnesians had thrown poison into the cisterns."

Thucydides writes further that many families were simultaneously struck by a disease with a combination of symptoms hitherto unknown.

The prevailing orthodoxy that viruses responsible for all major pandemics have their origin in animal reservoirs (birds, pig, bats) is a conjecture with no substantial evidential backing. The fact that both influenza viruses and corona viruses both represent broad viral families with counterparts in animals does not imply a plausible mechanism of transfer. Indeed, it has been argued that for the COVID-19 virus to be transferred from a bat, via a pangolin to a human requires random mutations that would far exceed the available probability space in the whole universe [14].

The orthodox narrative asserts that pandemics of viral or bacterial origin throughout human history were all initiated with the advent of farming and animal husbandry, thus allowing zoonotic viruses from wild and domestic animals systematically to access and infect humans. As we have already mentioned the cross-over from zoonotic variants to humans in the case of the COVID-19 pandemic involved an insurmountable probability barrier, and similar impediments may apply to other instances throughout history. In addition, the claim that the 2012 MERS-CoV outbreak was caused by viral jumps to humans in the Middle East via infected camels is not supported by existing evidence [15]. Indeed the evidence of a COVID-19 pandemic in a South Asian group of humans 25,000 years ago [11] already highlights the inconsistency in this idea. At this late stage of the Iron Age human populations were still thinly scattered across the globe and agriculture had barely been discovered.

The recent discovery by Zhang et al. in 2021 [16] is very significant in regard to COVID-19 genomic sequences eventually appearing as significant germline signatures in the human genome. These authors have shown that the fragments of the COVID-19 genome, particularly the highly expressed coding region for the nuclear capsid protein (NC) at the 3' end of the genome, are directly fused to multiple different protein-coding gene segments at many exon sites across the entire human genome. This provides molecular underpinning for the findings of Souilmi, et al. [11]. About two thirds of all integrated sequences appear to have been mediated at endonuclease site motifs that allow target site reverse transcription (RT) by the RT enzyme encoded by LINE1 elements. We can only speculate that the other 33% of integrants have been target site reverse transcribed and integrated by the other known dominant cellular reverse transcriptase, the DNA repair enzyme DNA Polymerase-Ι] (eta) [17,18] and assisted by recently discovered RT activity also in the DNA repair enzyme DNA Polymerase–Θ (theta) [19]. At this stage all reported integrations have been into the nuclear DNA of somatic cells, and germline integrants have not been searched for, but given the sheer number of humans of all races infected with COVID-19, running into the many tens of millions, we should anticipate that significant germline human genomic sequences of COVID-19 and its many protein coding segments (fused in many cases to different human genetic coding exons) may appear in human genomes of future generations-these in turn may be associated with inborn genetic errors as mankind's legacy of the 2020-2021 COVID-19 pandemic.

Conclusion

As discussed by Hoyle and Wickramasinghe in many places the Earth interacts with the debris streams of comets that carry bacteria and viruses; and such comets have periods ranging from a few years to tens of thousands of years. In one particular instance, Comet Encke with a period of 3.3 years, a case was made to argue for a close correspondence with the appearances of this comet and cycles of Whooping cough from 1940 until routine vaccinations essentially eliminated the disease in 1980 [13]. As for longer period comets, the best known is Comet Hyakutake which reached its last perihelion in 1996 and which has an orbital period of 70,000 years. The putative comet responsible for the COVID-19 virus would be estimated to have a period of between 20,000 and 25,000 years, and a smallpox virus bearing comet a period of 1600 years.

Bacteria and other biological entities down to viral sizes have been isolated from the stratosphere over several years and the only reasonable explanation in our view is that they are of extra-terrestrial origin. From the stratospheric sampling carried out by Harris et al and others [20-23] we have estimated that some 10^8 bacteria and 10^{10} viruses per square metre arrive from space at the Earth's surface every day. Very recently the startling report of bacterial DNA discovered by PCR techniques on the outside of the International Space Station (ISS) orbiting at 400 km above the Earth has been reported [24], but has largely gone unnoticed.

In an unrelated project carried out by a team of international scientists the total flux of bacteria and viruses falling through the atmosphere on the tops of the Sierra Nevada Mountains has recently examined by Reche et al. [25]. The average downward flux of viruses from this height, presumably mainly lofted from the ground, was discovered to be 800 million per square metre per day close to the estimate that we made earlier from stratospheric sampling. If both the space-incident microorganisms and terrestrial microbes are mingled into this latter estimate their genetic differences could turn out to be difficult to detect. Efforts to separate these components are clearly of paramount importance, and after our current experience of COVID-19 this should be considered an international scientific priority [26]. The evidence that comets continue to bring bacteria and viruses including COVID-19 [26] to the Earth, and routinely thus contribute to the microbiomes of all life forms, aiding evolution in the long term, and sometimes cause pandemics, is still regretfully being ignored by mainstream science.

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How to cite this article: Wickramasinghe, N Chandra, Gensuke Tokoro, Daryl H. Wallis and Milton Wainwright et al. "Footprints of Past Pandemics in the Human Genome." *Virol Curr Res* (2021) 5: 134.