

Genomic SETI Initiative identifies potential DNA 'Wow! Signal' hidden in non-coding regions

Evidence of Genetic Anomalies Found

Swansea, UK – An international team of SETI researchers have identified anomalies in the human genome that they speculate is an indication of an extraterrestrial 'message'. The potential signal, encoded into highly conserved regions of non-coding DNA, emerged from the Wales-based Genomic SETI Initiative, a big data analytics project spearheaded by Anglia Ruskin University Information Systems graduate, Bruce Fenton.



This finding, which emerged from a process of cross-referencing specific target patterns against existing genetic studies, highlights dozens of short DNA sequences displaying currently inexplicable differences from expectation, which can be interpreted as an intervention in normal evolutionary processes. The anomalous genomic regions in question are not well studied, but have been implicated as having key roles in controlling gene expression. These segments of DNA are designated Human Accelerated Regions (HARs) and their origination dates to the Middle Pleistocene (2.580 to 0.773 million

years ago).

The full results of the Genomic SETI Initiative are to be published on the 1st of June in the book *Exogenesis Hybrid Humans: A Scientific History of Extraterrestrial Genetic Manipulation*.

Expanding the Search

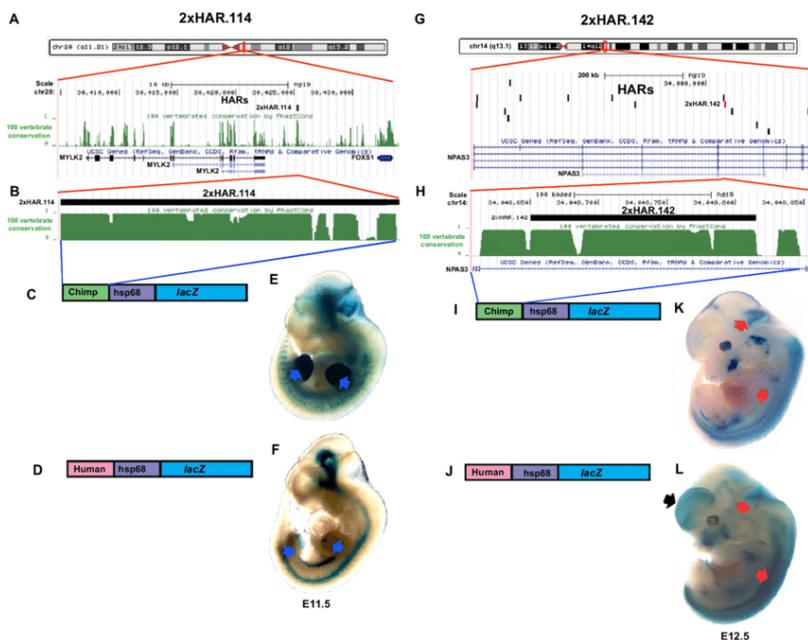
The Genomic SETI research began at the suggestion of noted astrophysicist Professor Paul Davies, chairman of the SETI Post Detection Task Force.

"If there were alien technology in the solar system, when did it arrive? A hundred million years ago? What would last a hundred million years? Not much but there are some things, like nuclear waste. Or any sort of biotechnology that has knock-on effects: If you tinkered with genomes a hundred million years ago, the traces of that would still be with us today," said Arizona State University physicist Professor Davies.

Professor Davies highlighted the potential for a suitably skilled graduate student to run a low cost, short duration, genomic data mining project that could complement the better-known search for alien radio signatures. Davies explains, "... it seems to me we could, in addition to scouring the skies for radio waves with a message encoded, we could scour terrestrial genomes which are being sequenced anyway to see if there is a message from ET encoded in it."

The senior SETI Institute astronomer, Dr Seth Shostak, expressed open-minded scepticism about the idea but offered the opinion that it was not a bad idea and required little time investment. "I think it's a two-week project actually," said Dr Shostak.

Formulating the Protocols



The project's research parameters were formulated with guidance from the mathematician, and complexity scientist, Samuel Arbesman. One central hypothesis was that any viable signature of alien genetic manipulation would be discovered in the DNA regions most essential to an organism's survival: those that ensure one generation can pass on genes to the next.

If a hidden message resided in anything other than the most essential, very highly conserved, genetic code it would likely be swept away by the constant mutations which occur over evolutionary timescales.

Human Accelerated Regions a Glaring Anomaly

Most of the Human Accelerated Regions (HARs) appeared long after the split between hominins and their primate relatives but prior to the divergence of Neanderthals, Denisovans and the direct ancestor of modern humans. Various well studied HARs have profound impact on gene expression, especially in respect to foetal brain development.

The highly irregular nature of Human Accelerated Regions is best highlighted with the example of HAR1. Consisting of just 118 letters, HAR1 is almost identical in both chickens and chimpanzees, displaying just a two-letter difference despite 300 million years of divergent evolution.

When we contrast the same HAR1 code segment in the chimpanzee with that of modern humans, we find an 18-letter disparity after only 6 million years of separation. This code segment in humans is now understood to play a crucial role in the development of the cerebral cortex, both in respect to its pattern and the layout.

Dr Katherine Pollard, bio-statistician at the Gladstone Institute and discoverer of HAR1, explained in an article for *The Scientist* discussing the discoveries her team made in 2006, "The fact that HAR1 was essentially frozen in time through hundreds of millions of years indicates that it does something very important; that it then underwent abrupt revision in humans suggests that this function was significantly modified in our lineage."

Despite considerable research into the origins and functions the causal mechanisms remain unknown; several hypotheses have been considered but each has fallen short of consensus scientific acceptance due to the astonishing and unprecedented speed of mutation required.

"Statistically speaking, the probability that a highly conserved DNA sequence will change multiple times over six million years of evolution is close to zero—that is, unless the forces that have been selecting against mutations in its sequence suddenly change," said Dr Pollard. Fenton notes that Dr Pollard's comments in 2016 were what led him to his current hypothesis that an intelligent agent might be specifically targeting these regions.

Dr Pollard has more recently suggested that HARs might be the result of biased gene conversion, a slight favouring of the DNA letters G & C during the unidirectional exchanges occurring as a part of recombination events. The biased gene conversion explanation has however already considered and rejected by other genomic researchers ([Levchenko et al 2018](#)) who found that, 76%, of HARs appeared to be driven by positive selection while at most 14–19%, might potentially be explained by this molecular mechanism.

"Our study provides the first comprehensive cataloguing of potential indications of intelligent extraterrestrial contact with terrestrial lifeforms at the level of biological processes. Incredibly, of all Earth's organisms, we have found the strongest potential signatures exist only in the human genome. Human Accelerated Regions are of particular note

being that they are currently inexplicable DNA sequences hidden in the most highly conserved non-coding regions of the genome,” said Bruce Fenton, lead author of the study results.

Directed Panspermia

Questions remain as to how exactly an extraterrestrials intelligence might go about engineering changes in the genomes of any terrestrial organisms. If HARs resulted from some form of intelligent intervention it would imply a level of understanding of hominin genome organization that is far in excess of current human knowledge.

“An interesting speculative scenario is one in which an alien probe imbued with advanced artificial intelligence visited the planet in prehistory, while here it used yet unknown advanced technologies to specifically modify these regions and redirect hominin evolution. Already human development of genome editing tools such as the recently announced prime editing, which combines CRISPR-Cas9 and a reverse transcriptase, might well provide a framework to suggest how something much more advanced than us might carry out such an astonishing intervention,” said Fenton.

Professor Davies, who was not directly involved in the research, has previously speculated on how a DNA message might be transmitted saying that, “A typical virus contains thousands of bits of information encoded in either RNA or DNA – enough for a decent message. So why not engineer trillions of viruses, package them in pea-sized microprobes, and spew them around the galaxy?”

It should be noted that while a virus might be an instrument to deliver a message, the virus would still need to be customized locally by a suitably advanced artificial intelligence that understands the local ecosystem and species to modify.

“If human accelerated regions can be shown to have resulted from external manipulation it will certainly have a profound impact on our understanding of Earth’s place in the cosmos. We can’t state this to be the case, but we can say that HARs represent an intriguing anomaly without current explanation. These segments of DNA are unique to humans among all mammals studied and are situated in precisely the highly conserved non-coding regions where any message or signs of manipulation would be preserved if any exist,” notes Fenton.

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Media Contact

Bruce Fenton

Senior Editor for Ancient News

T: +44 (0)7902 697 587

E: bruce@ancientnews.net

Notes to editor:

1. Book Title:

Exogenesis: Hybrid Humans: A Scientific History of Extraterrestrial Genetic Manipulation

Bruce & Daniella Fenton

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The book details are available at the [publisher's website](#).

Please name the book in any story you write. If you are writing for the web, please link to the book's page on the publisher's website.

2. The Genomic SETI Initiative is an independently funded research project founded by the Ancient News Network and based in the UK.