THE HUMAN GENOME PROJECT

The Human Genome Project (HGP) is an international scientific research project with the goal of determining the sequence of chemical base pairs which make up human DNA, and of identifying and mapping all of the genes of the human genome from both a physical and functional standpoint.[1] It remains the world's largest collaborative biological project.[2] After the idea was picked up in 1984 by the US government the planning started, with the project formally launched in 1990, and finally declared complete in 2003.

Most of the government-sponsored sequencing was performed in twenty universities and research centers in the United States, the United Kingdom, Japan, France, Germany, and China.

The Human Genome Project was declared complete in April 2003. An initial rough draft of the human genome was available in June 2000 and by February 2001 a working draft had been completed and published followed by the final sequencing mapping of the human genome on April 14, 2003.[1]

Key findings of the project included:

1. There are approximately 20,50 genes in human beings, the same range as in mice.[2]
2. Only 2% of human DNA coded for proteins (contained instructions for making a specific protein)
3. The protein-coding genes are very similar in all animals.
4. We share 96% of our protein coding genes with a chimpanzee.

These findings were devastating to believers in intelligent design (creationists). If man and chimpanzee shared 96% of their protein coding genes then they must have a common ancestor. But man also shares 92% of his protein-coding genes with a mouse and 72% with an acorn worm, a deep-sea marine worm!

Biologically, cells are very similar in their biochemistry in all the animal kingdom. Cells produce similar proteins, so no wonder that the protein coding genes (blueprints for making proteins) are similar across the different phyla and families.

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[1]https://en.wikipedia.org/wiki/Human_Genome_Project

[2]Ibid

As an example, a bicycle has nuts and bolts and so does a car, and an aeroplane and even a ballistic missile. Can we interpret this that they all have a "common ancestor"?

Even more devastating was the fact that 98% of our DNA did not code for proteins which was quickly given the name "junk DNA" by evolutionists. This junk DNA was deemed to be the left over from the unregulated random mutations that evolutionists believe led to the evolution of the human Genome. An intelligent designer would not have left 98% of the DNA as junk. "Junk DNA" quickly became a strong argument for evolution among biologists.

The news were devastating to intelligent design advocates and some of them decided to accept the inevitable; that evolution has been proven and decided to believe in it. They became theo-evolutionists! People who believed that God created the world but followed the theory of evolution while doing so.

One of these is Dr. Francis Collins, the director of the Human Genome Project. His most recent book is "The Language of God: A Scientist Presents Evidence for Belief."

Encyclopedia of DNA Elements (ENCODE)

This is a public research project launched by the US National Human Genome Research Institute in September 2003. Intended as a follow-up to the Human Genome Project, the ENCODE project aims to identify all functional elements in the human genome.

The project involves a worldwide consortium of research groups, and data generated from this project can be accessed through public databases.

Humans are estimated to have approximately 20,000 protein-coding genes, which account for about 1.5% of DNA in the human genome. The primary goal of the ENCODE project is to determine the role of the remaining component of the genome, much of which was traditionally regarded as "junk."

In September 2007, National Human Genome Research Institute (NHGRI) began funding the production phase of the ENCODE project. In this phase, the goal was to analyze the entire genome and to conduct "additional pilot-scale studies".

At that time the project evolved into a truly global enterprise, involving 440 scientists from 32 laboratories worldwide. Once the pilot

phase was completed, the project "scaled up" in 2007, profiting immensely from new-generation sequencing machines. And the data was, indeed, big; researchers generated around 15 terabytes of raw data.

By 2010, over 1,000 genome-wide data sets had been produced by the ENCODE project. In September 2012, the project released a much more extensive set of results, in 30 papers published simultaneously in several journals, including six in Nature, six in Genome Biology and a special issue with 18 publications of Genome Research.

The most striking finding was that the fraction of human DNA that is biologically active is considerably higher than even the most optimistic previous estimates. In an overview paper, the ENCODE Consortium reported that its members were able to assign biochemical functions to over 80% of the genome. Much of this was found to be involved in controlling the expression levels of coding DNA, which makes up less than 1% of the genome.[1]

The 30 papers published by the 440 world renowned scientists turned the tables on evolutionists. Newspapers around the world had these headlines:

Junk DNA - Not So Useless After All
Researchers report on a new revelation about the human genome: it's full of active, functioning DNA, and it's a lot more complex than we ever thought[2]

Hidden Treasures in Junk DNA
What was once known as junk DNA turns out to hold hidden treasures, says computational biologist Ewan Birney[3]

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[1]https://en.wikipedia.org/wiki/ENCODE

[2]http://healthland.time.com/2012/09/06/junk-dna-not-so-useless-after-all/

[3]http://www.scientificamerican.com/article/hidden-treasures-in-junk-dna/

Evolutionists went wild, attacking the scientists that wrote the report and the media and the creationists and advocates of intelligent design. One of them published this rebuttal:

> I am sort of sick to see junk DNA being buried, dismissed, rendered obsolete, eulogized, and killed twice a week. After all, your findings have no bearing on the vast majority of the genome, which as far as I am concerned is junk. Turning the genome into a well oiled efficient machine in which every last nucleotide has a function is the dream of every creationist and IDiot (intelligent designer), so the frequent killing of junk DNA serves no good purpose.[1]

Evolutionist web sites came up with their own headlines:

Most of what you read was wrong:
How press releases rewrote scientific history
Repeating myths may make good stories,
but it breeds confusion.[2]

In a presentation given by Dan Graur at the 2013 meeting of the Society for Molecular Biology and Evolution in Chicago he said:

> If the human genome is indeed devoid of junk DNA as implied by the ENCODE project, then a long, undirected evolutionary process cannot explain the human genome. If, on the other hand, organisms are designed, then all DNA, or as much as possible, is expected to exhibit function. If ENCODE is right, then Evolution is wrong.[3]
> Long stretches of DNA previously dismissed as "junk" are in fact

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[1]Dan Gruar's response to Axel Visel (ENCODE member)

[2]http://arstechnica.com/staff/2012/09/most-of-what-you-rea d-was-wrong-how-press-releases-rewr ote-scientific-history/

[3]http://www.evolutionnews.org/2014/07/junk_dna_darwin08 8361.html

crucial to the way our genome works, an international team of researchers said on Wednesday. It is the most significant shift in scientists' understanding of the way our DNA operates since the sequencing of the human genome in 2000, when it was discovered that our bodies are built and controlled by far fewer genes than expected. Now the next generation of geneticists have updated that picture.

Dr Ewan Birney, of the European Bioinformatics Institute near Cambridge, one of the principal investigators in the Encode project, said: “In 2000, we published the draft human genome and, in 2003, we published the finished human genome and we always knew that was going to be a starting point. We always knew that protein-coding genes were not the whole story.”

For years, the vast stretches of DNA between our 20,000 or so protein-coding genes - more than 98% of the genetic sequence inside each of our cells - was written off as “junk” DNA. Already falling out of favour in recent years, this concept will now, with Encode's work, be consigned to the history books.[1]

In January, Francis Collins, the director of the National Institutes of Health, made a comment that revealed just how far the consensus has moved. At a health care conference in San Francisco, an audience member asked him about junk DNA. “We don't use that term anymore,” Collins replied. “It was pretty much a case of hubris to imagine that we could dispense with any part of the genome - as if we knew enough to say it wasn't functional.” Most of the DNA that scientists once thought was just taking up space in the genome, Collins said, “turns out to be doing stuff.”[2]

A new book from Columbia University Press, Junk DNA: A Journey Through the Dark Matter of the Genome, by virologist Nessa Carey provides a detailed review of the vast evidence being uncovered showing function for “junk DNA.”

For years, scientists had no explanation for why so much of our DNA

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[1]https://www.theguardian.com/science/2012/sep/05/genes-genome-junk-dna-encode

[2]http://www.nytimes.com/2015/03/08/magazine/is-most-of-our-dna-garbage.html?_r=0

doesn't code for proteins. These non-coding parts were dismissed with the term "junk DNA." But gradually this position has begun to look less tenable, for a whole host of reasons.[1]

Let's imagine we visit a car factory, perhaps for something high-end like a Ferrari. We would be pretty surprised if for every two people who were building a shiny red sports car, there were another 98 who were sitting around doing nothing. This would be ridiculous, so why would it be reasonable in our genomes? A much more likely scenario in our car factory would be that for every two people assembling a car, there are 98 others, doing all the things that keeps a business moving. Raising finances, keeping accounts, publicizing the product, processing the pensions, cleaning the toilets, selling the cars etc. This is probably a much better model for the role of junk in our genome. We can think of proteins as the final end points required for life, but they will never be properly produced and coordinated without the junk. Two people can build a car, but they can't maintain a company selling it, and certainly can't turn it into a powerful and financially successful brand. Similarly, there's no point having 98 people mopping the floors and staffing the showrooms if there's nothing to sell. The whole organization only works when all the components are in place. And so it is with our genomes.[2]

The other shock from the sequencing of the human genome was the realisation that the extraordinary complexities of human anatomy, physiology, intelligence and behaviour cannot be explained by referring to the classical model of genes. In terms of numbers of genes that code for proteins, humans contain pretty much the same quantity (around 20,000) as simple microscopic worms. Even more remarkably, most of the genes in the worms have directly equivalent genes in humans.

As researchers deepened their analyses of what differentiates humans from other organisms at the DNA level, it became apparent that genes could not provide the explanation. In fact, only one genetic factor generally scaled with complexity. The only genomic features that increased in number as animals became more complicated were the regions of junk DNA. The more sophisticated an organism, the higher

[1]Nessa Carey: A Journey Through the Dark Matter of the Genome, Columbia University Press, pg2

[2]Ibid pg3

the percentage of junk DNA it contains. Only now are scientists really exploring the controversial idea that junk DNA may hold the key to evolutionary complexity.[1]

Nessa mentions in her book that evolutionists are angry about these discoveries:

The most forthright responses were mainly from evolutionary biologists. This wasn't altogether surprising. Evolution is the biological discipline where emotions tend to run highest. Normally the bullets are targeted at creationists, but the Gatling guns may also be turned on other scientists. ... The angriest critique of ENCODE included the expressions "logical fallacy," "absurd conclusion," "playing fast and loose" and "used the wrong definition wrongly." "The ENCODE results were predicted by one of its lead authors to necessitate the rewriting of textbooks. We agree, many textbooks dealing with marketing, mass media hype, and public relationships may well have to be rewritten"... She finally comments on this fury by saying: "There are interesting scientific arguments on both sides, but it would be disingenuous to believe that the amount of heat and emotion generated by ENCODE has been purely about the science. We can't ignore other, very human factors."[2]

Orphan Genes:

Orphan genes are genes without homologues in other lineages. Orphans are a subset of taxonomically-restricted genes, which are unique to a specific taxonomic level (e.g. plant-specific). In contrast to non-orphan TRGs, orphans are usually considered unique to a very narrow taxon, generally a species.

The classic model of evolution is based on duplication, rearrangement, and mutation of genes with the idea of common descent. Orphan genes differ in that they are lineage-specific with no known history of shared duplication and rearrangement outside of their

[1]Nessa Carey: A Journey Through the Dark Matter of the Genome, Columbia University Press, pg4

[2]Ibid, pg198

specific species or clade.[1]

Orphan gene" was coined to designate protein-coding regions (that is, genes) in an animal that were not found in any related animal type. In other words, there were no similar "ancestral genes" the orphan gene could have evolved from. It is just there, doing a task unique to that animal, like allowing a honeybee to make honey.With continued research the total number of orphan genes identified and recognized has continued to increase, and at present may be as high as 10 to 30 percent of all known genes. More than 1,000 orphan genes are recognized in humans. At least some of these orphan genes are very important; one of them is responsible for the large brain in humans.[2]

A group of scientists[3] performed in-depth sequencing of the transcriptomes of four mammalian species—human, chimpanzee, macaque, and mouse—and subsequently compared the assembled transcripts and the corresponding syntenic genomic regions. This has resulted in the identification of over five thousand new multiexonic transcriptional events in human and/or chimpanzee that are not observed in the rest of species.[4]

We have found thousands of transcripts that are human and/or chimpanzee-specific and which are likely to have originated de novo from previously non-transcribed regions of the genome.

(We) identified 634 human-specific genes (1,029 transcripts), 780 chimpanzee-specific genes (1,307 transcripts), and 1,300 hominoid-specific genes (3,062 transcripts). Taken together, the total number of candidate de novo genes was 2,714 (5,398 transcripts)[5]

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[1]https://en.wikipedia.org/wiki/Orphan_gene

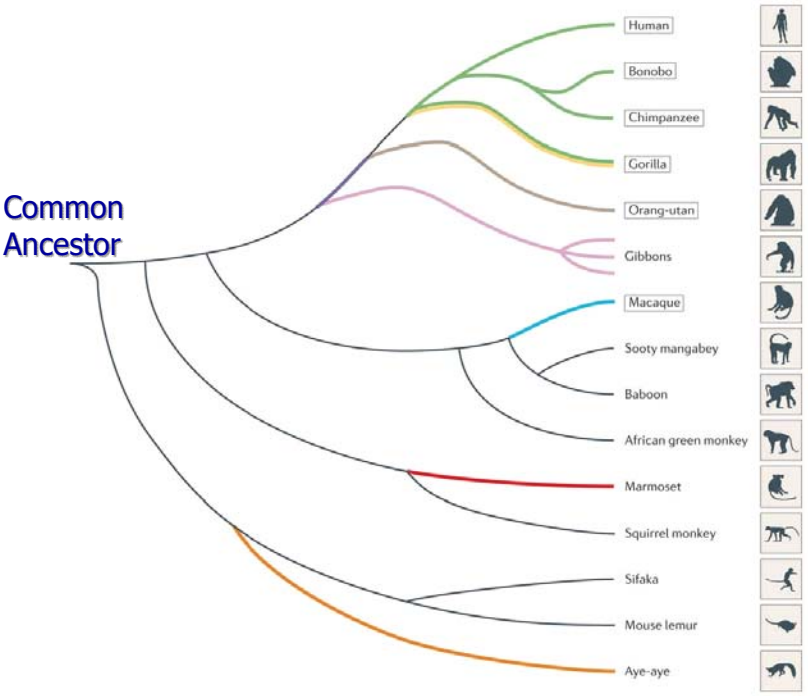
[2]http://thenewwalk.org/m/members_articles.php?title=63#sthash.mFr4004U.dpuf

[3]Jorge Ruiz-Orera, Jessica Hernandez-Rodriguez, Cristina Chiva, Eduard Sabidó, Ivanela Kondova, Ronald Bontrop, Tomàs Marqués-Bonet, M.Mar Albà

[4]Origins of De Novo Genes in Human and Chimpanzee

[5]Ibid

What is the importance of this? Let us look at the evolutionist "tree of life"



The researchers found 634 human Genes that were not found in chimpanzee or Macaque, 780 genes that were specific to chimpanzee, not found in humans or macaque and 1300 genes specific to the macaque and not found in either humans or chimpanzee. How on earth could humans, chimpanzee and macaque have a common ancestor?

This study led to headlines like this one:

Orphan Genes Defy Evolution Theory

In a recent research paper, published in Trends in Genetics, scientists describe a new set of 1,307 orphan genes that are completely different between humans and chimps. In fact, the chimp-specific genes are not found in any other supposed chimp ancestor. These orphan genes are unique to the chimps just like the human orphan genes are

unique to humans.

The research team only analyzed genes that were spliced, meaning complex genes that have coding and noncoding regions. Many other genes in the genome are not spliced and were not included in this study.

Another point is that they examined tissues from the brain the testes and the stomach only. If other tissues were examined the numbers would have increased.[1]

Orphan genes are the biggest news in Genetics currently and is very embarrassing to evolutionists who are trying to explain it away:

- De novo genes are most likely involved in the response to a rapidly changing environment.
- The problem is that it's hard to prove that a potential de novo gene is really a gene
- In spite of what you might have read in the popular literature, there are not a large number of newly formed genes in most species.
- The gene prediction software tilts toward false positives in order to minimize false negatives.
- Further investigation and annotation reduces the number of potential genes.
- The human genome has a number of duplicated genes that aren't found in our closest relatives but, for the most part, these are transient duplications and the extra gene will soon be deleted or disabled YOU WISH!!!!

These are taken from a staunch evolutionist website of a professor of Biochemistry in the University of Toronto!

Horizontal gene transfer:

Horizontal gene transfer (HGT) refers to the transfer of genes between organisms in a manner other than traditional reproduction.[2]

[1]http://www.franklincountyvapatriots.com/2016/02/17/orphan-genes-defy-evolution-theory/

[2]https://en.wikipedia.org/wiki/Horizontal_gene_transfer

You're not completely human, at least when it comes to the genetic material inside your cells. You—and everyone else—may harbor as many as 145 genes that have jumped from bacteria, other single-celled organisms, and viruses and made themselves at home in the human genome. That's the conclusion of a new study, which provides some of the broadest evidence yet that, throughout evolutionary history, genes from other branches of life have become part of animal cells.[1]

This is the latest theory to explain away these orphan genes, they belong to microbes and viruses and some how the human genome welcomed them! If this is the best they can do then God help us.

So, is this the end of the story? I think not! In a few months another study will favour evolution and then a more recent study will refute it and things will go on till kingdom come. The important lesson to be learned is that faith does not depend on science. Science is fallible while the word of God is infallible. A believer does not change his mind because of a new study in a journal.

I finally would like to quote Francis Collins who was head of the Human Genome project, who was atheist but became a believer:

I had to admit that the science I loved so much was powerless to answer questions such as "What is the meaning of life?" "Why am I here?" "Why does mathematics work, anyway?" "If the universe had a beginning, who created it?" "Why are the physical constants in the universe so finely tuned to allow the possibility of complex life forms?" "Why do humans have a moral sense?" "What happens after we die?"

I had always assumed that faith was based on purely emotional and irrational arguments, and was astounded to discover, initially in the writings of the Oxford scholar C.S. Lewis and subsequently from many other sources, that one could build a very strong case for the plausibility of the existence of God on purely rational grounds. My earlier atheist's assertion that "I know there is no God" emerged as the least defensible. As the British writer G.K. Chesterton famously remarked, "Atheism is the most daring of all dogmas, for it is the assertion of a universal negative."[2]

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[1]http://www.sciencemag.org/news/2015/03/humans-may-harbor-more-100-genes-other-organisms

[2]http://www.cnn.com/2007/US/04/03/collins.commentary/