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Preview of Single Nucleotide Polymorphism (Snp) and Potential Correlation between Human Genomes and Evolutionary History As Well As Religious Behaviors

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Introduction

The story of a race to unlock the Holy Grail of biology is a fascinating and an exciting one. It appears to be an impossible task to predict the final outcome of the quest while there are so much left to play for, but undoubtedly, the swift advances in decoding the human genome and the tools available to decipher the genetic information will likely forever alter the practice of medicine. It will definitely affect anyone on this planet that have access to modern health care and will subsequently improve the condition of the entire human race.

In 1953, ***Francis Crick*** and his American colleague, ***James Watson,*** discovered the double helix structure of DNA. For this breakthrough discovery, Watson, Crick, and their colleague Maurice Wilkins won a Nobel Prize in Physiology, or Medicine, in 1962. However, it is of paramount importance to remember that this discovery was dependent on many other scientists that came before them. Miescher, Hershey and Chase, Chargaff, Wilkins and Franklin, and others deserve to be acknowledged and recognized for their work in helping to unravel the fundamental role of DNA in biology. Rosalind Franklin, succeeded in taking an X-ray diffraction pattern from a sample of DNA that allowed researchers, Watson and Crick to work out the 3D structure of DNA which showed a clearly recognizable cross or helical shape. The story of DNA often seems to begin in 1944 with Avery, MacLeod, and McCarty showing that DNA is the hereditary material. However, the DNA story has already begun in 1869, with the young Swiss biochemist, Friedrich Miescher. He isolated a new compound from the nuclei of some white blood cells and called them "nuclein" (a term still preserved in today's name deoxyribonucleic acid). In 1950, Erwin Chargaff showed that the proportions of the bases included in the structure of DNA followed a certain law. He stated that in DNA of any given species, the ratio of adenine to thymine is equal, as is the ratio of cytosine to guanine. Two technologies transform genetics in the 1970s: gene sequencing and gene cloning.

Gene cloning includes the complete range of techniques used to extract genes from organisms, manipulate them in test tubes, create gene hybrids and produce million copies of such hybrids in living cells. In the 1980s, geneticists begin to use these techniques to map and identify genes linked to diseases, such as Huntington's disease and cystic fibrosis. The identification of these disease-causing genes heralds a new era of genetic management.

The transformation of genetics reached their peak in 1990. The U.S. Government approved a 15- year, 3 billion dollars plan to launch the Human Genome Project, whose goal was to map and sequence the entire human genome. In 2001, and President Clinton unveiled the human genome sequence. He said, "We are here to celebrate the completion of the first survey of the entire human genome. Without a doubt, this is the most important, most wondrous map ever produced by human kind." [1] This stunning achievement was brought about by the combined wisdom of biology, chemistry, physics, engineering, mathematics and computer science; it was also brought about by the combined effort of the best scientists in the global community. Through this revolution in medical science, we are witnessing the language in which God created life and we are more in awe of the wonder and complexity of God's most sacred gift.

In 2007, the first genome of a single and identifiable individual was published, it was Craig Venter's. [2] Venter is best known for founding the company Celera and leading the privately funded project to sequence the human genome. He launched the era of genomics by sequencing the first bacterial genome in 1995.

Several advances resulted from the Venter Genome Project. The significant one is that human cells contain two copies of our genome. Twin sets of 23 chromosomes: one from our mother and one from our father. Previous projects only sequenced one set to make matters simpler. The price tag of Venter's genome was US$100 million which was a bargain compared to US $3 billion Human Genome Project.

The price of the next genome sequence was a mere US $1.5 million. It was that of James Watson, a Nobel Laureate and co-discoverer of the double helix. [3]

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On the heels of the Human Genome Project, sequencing projects that are designed to uncover the associations between genetic signatures and key traits were initiated. The first large-scale collaborative project was the International Hap Map Project. It was an organization that aimed to develop a haplotype map (Hap Map) of the human genome and to describe the common patterns of human genetic variation. Hap Map is used to find genetic variants affecting health, disease and responses to drugs and environmental factors. The project focused on special sites in the genome called 'single nucleotide polymorphisms' or SNPs.

SNPs (Single Nucleotide Polymorphisms) are common DNA variations where a single base-pair has been mutated or deleted. SNPs are important because they will alter DNA function. Depending on where they are, this can potentially cause critical illness by altering an important genetic feature. At the other end of the spectrum, they may have no discernable impact. Genetic epidemiologists use SNPs as genetic markers to track disease with. Large studies called Genome-Wide Association Studies study the SNPs in tens to hundreds of thousands of people and find associations between particular SNPs and disease.

The role of SNPs to significantly advance our ability to understand and treat human disease looks promising. A lot has been written about DNA revolution but the aim of Part 1 is get an overview of what SNPs are. Part 1 will highlight on the meaning, distribution, application, functional importance, role as genetic makers, of Single Nucleotide Polymorphism (SNP). Nearly every technology, no matter how beneficial, brings with it the potential for misuse, Genomics provides us with better understanding of human disease and potential new cures, but its application is also raising questions about genetic selection of individuals with particular traits. We have unlocked the DNA from inside our cells and are reaping the extraordinary volume of information it contains, it is hard to predict where all of this knowledge will take us and what its impact on humanity will be. The personalization of medicine through genetics is near, and with it come many ethical questions that must be answered. How should genomic information be stored and shared? How far should scientists go in changing and controlling DNA? These ethical concerns must be addressed even as genetics is on the edge of revolutionary change. Evolution is the process by which modern organisms have descended from ancient ancestors and is responsible for both the remarkable similarities we see across all life and the amazing diversity of that life. We have seen the direct evidences that evolution occurs. We have seen the change that occurs in huge number of organisms and we understand the mechanisms by which evolution operates. All of evolution is based on genetic change and science has built up a large volume of knowledge about how the genetic material of living organisms works.

Yet, there seems to be an inherent conflict between the Biblical creation narrative in Genesis 1-3 and the modern scientific theory of evolution. Do we have to reject the Christian faith to affirm modern science? Likewise, do we have to reject evolution and the modern scientific enterprise to affirm the Christian faith? Part 2 will explore in-depth the fundamental principle of creationism and biological evolution. As a person of faith, it would be uplifting to explore the reaction of the religious communities toward evolution. Can a man of science accept both creationism and evolution?

Most people can accept diseases or height and even weight being genetically heritable to some extent, but when it comes to our personal beliefs we tend to be more skeptical. For many, the idea that there is a genetic component to our faith--or lack of it--is a stretch too far.

The challenges of understanding the function of the billions of neurons in the brain, and all of their trillions of interconnections, makes an understanding of the human genome seem simple by comparison. There are complex neurological disorders whose inheritance cannot generally be so easily understood, though clearly genetic factors are involved. One of these is Parkinson's disease, another is Alzheimer's disease. Genetics influence our personality traits though upbringing should play a central role. Sexual orientation and intelligence is clearly influenced by heredity. As per Francis Collins, it may seem the height of wrongheaded genetic determinism that genetic influences could play a role in an individual's interest in spiritual matters. [4] He has evolved from being a committed atheist in his twenties to being a firm believer in his fifties. During his conversion, there is no evidence that his DNA changed. "Spirituality" is not a concept that can be quantified from a biological standpoint. The concepts of the "The God Gene" and "The Spirit Molecule" have only been recently presented to the general public. It is very intriguing to see the potential correlations between both concepts. In Part 3, this writer attempts to find the correlation between religion and spirituality by looking into the cutting-edge research that was done linking genes to one's openness to spiritual experiences.

Single Nucleotide Polymorphism (SNP)

Introduction to SNPs

The announcement of human genome in June of 2000 pleasantly sent shock waves throughout the scientific community and the general world population. It announced the completion of a draft of human genome, along with the arrival of post-genomic era. In fact, in the post-genomic era, we are focusing on DNA sequences, as these sequences in the human body determine the specific trait of an individual. To fully understand the significance of these sequences in the human body, we must first truly understand the "single nucleotide polymorphisms" (Single Nucleotide Polymorphism, SNP).

All human beings differ from one another; it can be their physical appearance, susceptibility to disease and response to medications. DNA and genes is the blueprint from which we are made. Therefore, differences between people are evident in the sequences of their DNA. Scientists have found that many of these differences are single nucleotide substitution in the DNA sequence. These are referred to as "single nucleotide polymorphisms" or SNP. For example, a SNP may replace the nucleotide cytosine (C) with the nucleotide thymine (T) in a certain stretch of DNA.

What are the so-called single nucleotide polymorphisms? Within the DNA lies the code that makes us human. DNA molecules look the same, yet they have different functions depending on the information they carry. The information in DNA is stored in the form of building blocks known as bases. The human genome is normally composed of about three billion base pairs of nucleotide bases: A, T, G, and C. The information content of DNA derives from the order of the bases. Every three bases specify one amino acid, a building block of protein. Proteins are structures that make each cell and organ distinct. Enzymes, hormones, and neurotransmitters are proteins. Therefore, what proteins we are made of depends on what DNA we have. Every human being has pretty much the same DNA, but there are subtle differences from one person to the next. There is a single nucleotide polymorphism in about every 500 bp - 1000 bp (bp: base pair), therefore, the chance of the appearance of single nucleotide polymorphisms in the human genome is quite high. [5]

Single Nucleotide Polymorphisms or SNPs (pronounced "snips") are variations in a DNA sequence that occur when a single nucleotide in the sequence is different from the norm in at least one percent of the population. When SNPs occur inside a gene, they create different variants, or alleles, of that gene.

Types of Nucleotide Base Substitution

Mutation is a change in the nucleotide sequence of a gene or a chromosome. Mutations may be small-scale mutations or large scale mutations depending on the effect of mutation on the gene structure. Small-scale mutations are a type of mutation where one or few nucleotides of a gene are affected.

They are further classified as follows:

(1) Substitution mutations

(2) Insertion mutations

(3) Deletion mutations

Substitution mutations

A type of mutation in which a single nucleotide is substituted with a different nucleotide. Transition substitution which accounts for nearly two-thirds of all SNPs, occurs between purines (e.g. A > G) or pyrimidines (e.g. C > T).

Transversion substitution occurs between purines and pyrimidines (e.g. A > C and G > T).

One example of a substitution mutation is Sickle Cell Anemia. It causes a single nitrogen base in a codon for one amino acid in the protein called glutamic acid to instead code for the amino acid valine.

Insertion mutations

Insertion mutation is the addition of one or more nucleotide base pairs into a DNA sequence. Huntington's disease is an example of insertion mutation wherein trinucleotide repeats are inserted into the DNA sequence leading to this disease

Deletion mutations

Deletions are mutations in which a section of DNA is lost, or deleted. 22q11.2 deletion syndrome is caused by the deletion of some bases of chromosome 22. This disease is characterized by cleft palate, heart defects, autoimmune disorders etc.

Scientific Approaches to identify and characterize SNP

The **genomic** approach is used by scientists who want to see the big picture. Many institutions participated in several large-scale projects to identify and catalog all of the SNPs in the 3-billion-base pair human genome. Each project involves hundreds of scientists, who compare the genomes of numerous individuals to identify the differences. These comparisons require a lot of computer-powered data analysis. As they work, scientists sort and catalog their results in databases that are available to anyone who are interested. The first large scale project is the International Hap Map Project. Its goal is to identify common genetic variations among people. This project represents a collaboration of scientists from public and private organizations in six countries. Data from the project is freely available to researchers worldwide. Researchers can use the data to learn more about the relationship between genetic differences and human disease.

The Hap Map (short for "haplotype map") is a catalog of common genetic variants called single nucleotide polymorphisms or SNPs (pronounced "snips"). Each SNP represents a difference in a single DNA building block, called a nucleotide. These variations occur normally throughout a person's DNA. When several SNPs cluster together on a chromosome, they are inherited as a block known as a haplotype. The Hap Map describes haplotypes, including their locations in the genome and how common they are in different populations throughout the world. The human genome contains roughly 10 million SNPs. It would be difficult, time-consuming, and expensive to look at each of these changes and determine whether it plays a role in human disease. Using haplotypes, researchers can sample a selection of these variants instead of studying each one. The Hap Map will make carrying out large-scale studies of SNPs and human disease (called genome-wide association studies) cheaper, faster, and less complicated.

Scientists who are interested in a particular disease or drug response use the **functional** approaches. The biological processes involved in diseases and drug responses are controlled by the activities of many genes. Scientists interested in a particular process will select genes known to be involved in the process and examine them in people who have a response or disease, as well as those who don't. By comparing people's DNA sequences, scientists can identify SNPs that correspond with a particular function or response.

The difference between a SNP and a Mutation

The new definition of genetic polymorphism was proposed by Cavalli-Sforza & Bodmer in 1971. It is defined as the occurrence in the same population of two or more alleles at one locus, each with appreciable frequency and widely accepted at arbitrary threshold of 1%. [5a]

SNP and Mutation are both single-nucleotide differences in a DNA sequence, but SNPs should not be confused with disease-causing mutations.

First, to be classified as a SNP, the change must be present in at least one percent of the general population. No known disease-causing mutation is this common.

Second, most disease-causing mutations occur within a gene's coding or regulatory regions and affect the function of the protein encoded by the gene. Unlike mutations, SNPs are not necessarily located within genes, and they do not always affect the way a protein functions.

Distribution of SNPs

SNPs are not uniformly distributed over the entire human genome, neither over all chromosomes and neither within a single chromosome. There are one third as many SNPs within coding regions as non-coding region SNPs. Within a single chromosome, SNPs can be concentrated about a specific region, usually implying a region of medical or research interest. For instance, the sequence that encodes proteins that present antigens to the immune system in chromosome 6 displays very high nucleotide diversity compared to the other areas of that chromosome. [5b]

Future Prospects

Analysis, diagnosis and prevention against diseases

Once the human data of single nucleotide polymorphism become more complete, we can accomplish the distribution pattern study of single nucleotide polymorphism in association with the data study of bioinformatics with the comparison between normal controls and patients. With such an intensive study, thereby, one can identify the cause of many genetic diseases, a prior diagnosis of some latent ethnic and vulnerable factors can hopefully be gotten under control.

Successful integration of pharmacogenomics and bioinformatics

In light of the abundance of new potential therapeutic drug targets that have emerged from the extraordinary progress of human gene sequencing, selection of novel molecular targets have become of great importance. This can be realized by the pharmaceutical industry, through the successful integration of clinical, genomics, molecular phenotype data partnered with the use of informatics. Though bioinformatics and pharmacogenomics are facing some hurdles, they show enough potential to help drug development in the future. The most appropriate drug for an individual could be determined and used for treatment by analyzing a patient's SNP profile. The ability to target a drug to those individuals most likely to benefit, referred to as 'personalized medicine' would allow pharmaceutical companies to bring many more drugs to market and allow doctors to prescribe individualized therapies specific to a patient's needs.

Genetics will help crack the history of human migration

In 2002, from 15th to 18th of October, the U S National Geography Club conducted a global human gene (DNA) genetic program that was led by internationally renowned geneticist, Dr. Spencer Wells. Wells is the Project Director of the multi-year Genographic Project that use DNA samples in tracing human migration from Africa over 60,000 years ago, a discovery that has broken grounds all over the world. The work of an Asian DNA sampling was carried out in Taiwan and Hong Kong. Rapid advances in genetic sequencing have opened up a whole new window into the past, allowing scientists to use genetic markers to trace the migration routes and origins of modern human populations, therefore providing us with an increasingly sophisticated view of human history.

The establishment of so called 'household' record would need to transfer maps or so called 'Atlases' after applying as a marker. When a SNP is adjacent to the coding sequence of a gene, the SNP would very likely linked together with the hereditary gene; the researchers then can compare the atlas with that of its counterpart from the control group. Hence, it will be essential to further study any individual pattern change, or to track any difference that may be related to genetic factors. To draw atlases of the effective SNP requires an estimated number between 100,000 to 1,000,000 SNP, with the ideal number ranging between 600 thousands and100 million. [6]

Diagramming of SNPs on biological networks with the intention to assimilate information about SNPs and protein arrangement mutations in biological networks. There are some developed node characteristic files for Cytoscape that permit the conjuring up of such information in the background of networks. The utilization of such node attribute files encompassing protein annotations permits the ID of the nodes in the network that have mutations and/or natural disparities. Such information on all the annotations existed for each SNP in the attribute files; these annotations can be castoff to visualize, screen and search the network. As aforesaid, in the pathway representation all dissimilar states of a protein appear as different nodes. Hence, the information about the protein mutation and ordinary variation of a given protein, on top of all the consistent nodes in the pathway. The UniProt identifier was used for this mapping and hence any pathway, protein-protein interaction network or network model containing UniProt identifiers can be prolonged with the attribute files, according to Masaru Katoh (2007) Dysregulation of stem cell signaling network due to germline mutation, SNP, helicobacter pylori infection, epigenetic change, and genetic alteration in gastric cancer, Cancer Biology &Therapy.

Mitochondrial aldehyde dehydrogenase 2 (ALDH2) in the liver removes toxic aldehydes including acetaldehyde, an intermediate of ethanol metabolism. Nearly 40% of East Asians inherit an inactive ALDH2*2 variant, which has a lysine-for-glutamate substitution at position 487 (E487K), and show a characteristic alcohol flush reaction after drinking and a higher risk for gastrointestinal cancers. There has been a report on the characterization of knocking mice in which the ALDH2 (E487K) mutation is inserted into the endogenous murine Aldh2 locus. These mutants recapitulate essentially all human phenotypes including impaired clearance of acetaldehyde, increased sensitivity to acute or chronic alcohol-induced toxicity, and

reduced ALDH2 expression due to a dominant-negative effect of the mutation. When treated with a chemical carcinogen, these mutants exhibit increased DNA damage response in hepatocytes, pronounced liver injury, and accelerated development of hepatocellular carcinoma (HCC). Importantly, ALDH2 protein levels are also significantly lower in patient HOC than in peritumor or normal liver tissues [3]. Our results reveal that ALDH2 functions as a tumor suppressor by maintaining genomic stability in the liver, and the common human ALDH2 variant would present a significant risk factor for hepatocarcinogenesis. The aforesaid study proposes that the ALDH2*2 allele-alcohol interaction may be an even greater human public health hazard than previously. [7]

In the post-genomic sequencing era, one of the exciting directions to fully understand the meaning that underlying the genomic sequences is deciphering the epigenetic codes, including 5meC/5 hmeC DNA methylation, protein/histone post-translational modifications and expression/splicing of non-coding transcripts. For instance, single nucleotide polymorphisms (SNPs) play a critical role in the study of imprinted genes. Imprinted genes refer to the mono-allelic expression of some genes according to their parent-of-origin, and the differentially existed SNPs on either maternal or paternal allele facilitate the investigation of the transcriptional origin at the imprinted loci. In mammals, as normal expression of imprinted genes is directly regulated by the DNA methylation that presents at the imprinted control regions (ICRs), 3 it is interesting to investigate the relationship between the establishment of DNA methylation and the variability of SNPs [4]. Strikingly, recent observation revealed that apart from DNA methyl transferases (DNMTs), some histone modifiers are also involved in the maintenance of imprinted DNA methylation, 4 which suggested that the differentially existed SNPs might also influence the deposit of histone modifications. Taken together, investigation of the link between SNPs and epigenetic markers might create a novel direction towards the fully understanding of human genetic codes.

Interim conclusion

This time,, we live in a world full of health problems and disease. The truth is that as population increases along with technology, we have a growing number of people suffering from obesity, cardiovascular disease and diabetes among other health issues. With the rapid advance in biotechnology, a variety of life experiences has gradually and has at least partially unraveled the mystery of creatures, but SNP is still the key to unlock such mystery. If this mystery can be totally unlocked, it will bring more understanding in the prevention of disease in human body, the treatment of various diseases, and ultimately the development of a variety of drugs that can extend the life span of human being.

The development of biotechnology vastly improves the longevity of human life. The improvements of daily diet and living environment also have significant benefits. We are expecting to seeing further advancement in the field of biotechnology and also have a high degree of anticipation that the development of a safe and effective cancer drug therapy will not remain elusive in the near future.

Biological determinism or genetic determinism is the belief that human behavior is controlled by an individual's genes or some component of their physiology, generally at the expense of the role of the environment, whether in embryonic development or in learning.[8] Is it still around in this 21st century? Some scientists and social critics may have severely criticized much of the work in human behavior genetics. E. G. Steven Rose, a professor of Biology and Neurobiology and a frequent critic of human behavior genetic research, recently wrote his brief critique of "genetic determinism." He argued that trying to explain social problems like violence, alcoholism, or homelessness by genes is bad science and a bad guide for social policy (1995). Social responsibility does not lie in our DNA. Hundreds of other studies have come to the same conclusion, showing a clear genetic influence on intelligence. But that doesn't mean that intelligence is determined by genes merely.

It seems to be bad science because if it tries to reduce complex social problems to things like brain chemistry, for instance.. Shyness in early infancy. It, as well, is a bad guide for any social policy because it can result in blaming victims for their problems, in diverting scarce rssuesources from effective solutions, and in suggesting genetic engineering solutions for social issues.

In 1980, religious leaders from Protestant, Catholic, and Jewish communities wrote a letter to Jimmy Carter, then president of the United States, to express their concerns about the risks of genetic engineering to humanities. They all assert that human beings are created in the image of god, from which they derive power and responsibility over creation. Technology is viewed as part of this power as derived from the sovereign creator and, therefore, should be harnessed with discretion, to achieve goods for individuals and society.

Genes and Evolution

Introduction

The question of whether life was intelligently designed or evolved over billions of years has been a major point of contention since Darwin's On the Origin of Species was first published in the mid-19th century. In Origin, Darwin strongly makes the case for evolution. He says the ability or lack of ability to adapt to changes and challenges in the natural environment are a key factor in the evolutionary process. Certain aspects of the theory were debated, doubted, and even rejected by the scientific community in the late 1800s and early 1900s. However, the advent of the scientific discipline of genetics strengthen the Darwin's Theory, it even amplify Darwin's vision of evolutionary change.

Genes are the portions of an organism's DNA that carry the information responsible for building that organism in a very specific way. Genes and the traits they code for are passed from parent to offspring. From generation to generation, well-understood molecular mechanisms reshuffle, duplicate, and alter genes in a way that produces genetic variation. This variation is then the raw material for evolution.

Evolutionary theory has weathered many storms. It has been hit repeatedly by the winds of creationism and its cousin,

intelligent design (ID) and has shown no signs of disappearing. Most recently, creationists have resorted to notions of intelligent design that is, there must be an intelligent designer behind organisms who frequently display intricate anatomies and behaviors to perform certain functions. A natural process like natural selection would be inadequate to perform such functions of intricate complexity.

Creationism versus Evolution

Evolution is a change in the gene pool of a population of organisms over time. The mechanisms of evolution operate at the genomic level. Changes in DNA sequences affect the composition and expression of our genes, the basic units of inheritance. To put it simply, our evolutionary history is written into our genome and the foundation of evolution is not just our working DNA but changing DNA. Creationism is based on a literal reading of the Bible's Book of Genesis, which describes the creation of the world and all the life in it over a period of six days.

The key area of disagreement between creationists and evolutionists regarding genetic operation is that the creationists claim genetic change cannot go beyond a certain point. Usually, there is no support offered for this position. Evolutionists, in contrast, can point to empirical mechanisms that can allow organisms to survive with mutations. First, severely detrimental mutations would kill an organism or prevent it from passing on its genes. Second, currently living organisms do carry genes with detrimental mutations, and yet these organisms thrive.

Evolution meets the criteria accepted by scientists as defining science, and the vast majority of scientists accept evolution as science. Scientific theories must be, at least, as following:

1. Empirically Testable & Falsifiable

Science requires the testing the theories of the natural world against nature itself and discarding those theories that do not work. Although any theory may be modified, the core ideas of science have been tested so many times that we are confident that there is an extremely low probability of their being discarded. The three elements of evolution – descent with modification, pattern of evolution and the mechanism of evolution can all be tested through the methods of science. The heart of creationism, that God created the universe, is not testable by Science.

2. Consistent

The idea of common descent is still overwhelmingly supported by both historical and contemporary evidence as well as our understanding of how changes occur in living organisms, although there are gaps in our knowledge, disagreements as to how evolution occurred,

3. Useful

Much of what is done in the biological and medical sciences could not occur without the background premise of evolution.

4. Correctable and Dynamic

Evolutionary theory today is not quite similar as the evolutionary theory which Charles Darwin originally devised and wrote about, though he was correct enough that much of what he discovered continues to be valid. Evolution is based solely on the evidence, thus if the evidence changes so will the theory.

5. Progressive

A new scientific theory should build on earlier scientific theories. In other words, a new theory must explain what previous theories explained at least as well as they did while providing a new understanding for additional material — something which evolution does.

Is creationism a scientific theory? Let us go through each scientific criteria:

1. Empirically Testable & Falsifiable

Creationism relies on supernatural entities which are not only not testable but are not even describable. Creationism provides no model that can be used for making predictions and provides no scientific problems for scientists to work on. The question of whether God created the universe is outside the abilities of science to test.

2. Consistent

Creationism is usually internally consistent and logical within the religious framework in which it operates.

3. Useful

To be "useful" in science means that a theory explains and describes natural phenomena, but creationism is not able to explain and describe events in nature.

4. Correctable & Dynamic

The only real changes which have occurred in the creationist movement is to try and push the biblical arguments further and further into the background to make creationism look more and more scientific.

5. Progressive

Creationism is not progressive: it does not explain or expand upon what came before and is not consistent with established accompanying theories.

Leading creationists basically admit that creationism is not testable and clearly state that biblical revelation is the source of their ideas. If Creationism is not considered scientific by the movement's leading figures, then how can anyone we take it seriously as a science?

Evidence/Arguments for Creationism

Two popular forms of evidence/arguments cited by creationists are as follows:

Intelligent Design

Creationists claim that some system could not possibly have arisen naturally and therefore, it must have been designed by some Designer. However, the skeptics say that belief in an intelligent designer is a religious theory that has no basis in

science. Six scientific disciplines that point toward the existence of an intelligent designer [9]

In a study in the journal Science, Anderson, Roth and their colleagues demonstrate the process in lab-grown Salmonella enterica. [10] They grew one strain that missed a gene key for expressing the essential amino acid tryptophan. The strain needed to rely on another gene, which had a primary job but also a weak ability to take on the missing gene's work. The researchers encouraged the bacteria to duplicate the overworked gene, and its copies gathered mutations—some of which enhanced tryptophan production. At the end of a year's time (3,000 generations later) the bacteria had one gene that did the original job and a second that had evolved a new primary function—manufacturing tryptophan. If this model holds, it can give researchers insight to harnessing evolution's power—as bioengineers coax microbes to gobble oil spills, for example.

Basic Mechanisms of Evolutionary Changes

Natural Selection Natural selection is a process that is fundamental to evolution. This theory was described by Charles Darwin. By natural selection, any characteristic of an individual that allows it to survive to produce more offspring will eventually appear in every individual of the species, simply because those members will have more offspring. For example, those individuals who are better able to find and use a food resource will, on average, live longer and produce more offspring than those who are less successful at finding food. Inherited traits that increase individuals' fitness are then passed to their offspring, thus giving the offspring the same advantages.

Mutation

Mutation is a change in DNA, the hereditary material of life. So a change in an organism's DNA can cause changes in all aspects of its life. Mutations can happen when DNA fails to copy accurately. It can also be caused by exposure to specific chemicals or radiation.

Migration

Migration is any movement of individuals, and/or the genetic material they carry, from one population to another. For example, some individuals from a population of brown beetles might have joined a population of green beetles. That would make genes for brown coloration more frequent in the green beetle population than they were before the brown beetles migrated into it.

Genetic drift

Imagine that in one generation, two brown beetles happened to have four offspring survive to reproduce. Several green beetles were killed when someone stepped on them and had no offspring. The next generation would have a few more brown beetles than the previous generation . but just by chance. These chance changes from generation to generation are known as genetic drift.

Different types of evolution

Convergent evolution

In evolutionary biology, convergent evolution is the process whereby organisms not closely related, independently evolve similar traits as a result of having to adapt to similar environments or ecological niches.

For example, flying insects, birds and bats have all evolved the ability to fly, but independently of each other.

Co-evolution

When two (or more) species reciprocally affect each other's evolution. For example, flowering plants and pollinating insects such as bees. Co evolution is likely to happen when different species have close ecological interactions with one another. These ecological relationships include Predator/prey and parasite/host, Competitive species, and Mutualistic species.

Adaptive radiation

In evolutionary biology, adaptive radiation is a process in which organisms diversify rapidly from an ancestral species into a multitude of new forms, particularly when a change in the environment makes new resources available, creates new challenges, or opens new environmental niches. [11] Information essential to the understanding of evolutionary mechanisms. But much is in doubt and much remains to be learned. This is heartening and inspiring for any scientist. For those that are still unknown, the answers must be pursued authentically. Christians should be willing to listen to any new ideas but not jump to conclusions nor be restricted by any doctrines except whatever already the Bible. Both science and history attest to the accuracy of the Bible.

Are Religious Behavior Governed by Genes?

Introduction

Stephen Hawking, in his book "A Brief History of Time", says, "**If we discover a complete theory, it would be the ultimate triumph of reason – for then we should know the mind of God.**"Obviously, Hawking has always looked at God metaphorically, in much the same way as Einstein. "**I cannot believe that God plays dice with the cosmos**" was Einstein's famous quip about his discomfort with quantum mechanics. He also declared, "**I want to know how God created the world."**

Baroness Susan Greenfield, one of England's most distinguished scientists, was asked to comment on Haw king's musings about God. Was she worried by scientists making claims about other areas of life? "Yes I am," she said. "**All science is provisional and therefore to claim to have the definitive answer to anything is a hard-line view. It would be very great shame if young people think that to be a scientist you must be an atheist.**"

There are plenty of scientists who have Christian faith. Francis Collins, a genome researcher, has led the effort to decode human DNA. He stands by his faith in the existence of God and

positions science not as a substitute for theology, but as a subset of it. In an essay written to CNN, Collins wrote:

"**I have found there is a wonderful harmony in the complementary truths of science and faith. The God of the Bible is also the God of the genome. God can be found in the cathedral or in the laboratory. By investigating God's majestic and awesome creation, science can actually be a means of worship**". [12]

Gregor Mendel, known as the "father of modern genetics, who discovered the basic principles of heredity through experiments in his garden. His observations became the foundation of modern genetics and the study of heredity, and he is widely considered a pioneer in the field of genetics. He spent his entire adult life as a monk in an Augustinian monastery.

Nicolaus Copernicus, who was a canon in the cathedral of Krakow, celebrated astronomy as "a science more divine than human" and viewed his heliocentric theory as revealing God's grand scheme for the cosmos.

Isaac Newton, perhaps the greatest scientist of all time, viewed his discoveries as showing the creative genius of God's handiwork in nature. "This most beautiful system of sun, planets, and comets," he wrote, "could only proceed from the counsel and dominion of an intelligent and powerful being."[13] All of the leading scientists saw their scientific vocation in Christian terms. Their Christian conviction was the scientists' guiding inspiration. Religious motivation can sometimes result in breakthrough discoveries that change the course of scientific history. Are their devotion driven by their genes?

The Double Helix that is DNA

Within DNA is a biological code that is simply composed of only four letters: A, C, G, and T, the first letters of their chemical names. The bases are not hooked directly to each other. Instead, a long backbone structure runs the length of the DNA molecule, and each base is connected to the backbone. Though simple, it is embedded in us all and in our culture. Every human being has pretty much the same DNA, but there are subtle differences from one person to the next. These variations are sometimes called polymorphisms. Polymorphisms occur about once every 1,000 bases between unrelated humans. Of the 35,000 genes present in the human genome, the function of only about one-third is known. Another one-third of the genes are similar genes in other species. The remaining one-third of genes- more than 10,000 of them- are complete unknowns. William James, an American philosopher and psychologist, says, "There is very little difference between one person and another, but, what little there is, is very important." Our genes play such a pivotal influence in human behavior that scientist now estimates that gene determine about 50 percent of child's personality. [14] Therefore, is not it possible that our genes might play a determining role in an individual's spiritual development? According to recent genetic studies, they do play a significant role.

Spiritual Instinct or Human Faith

Any physical characteristic that is universally shared by every individual of a given species represents a genetically inherited trait. For example, all monarch butterflies share the same color pattern on their wings suggests that this specific color and design must be written into this species' genes.

This rule also applies to universal functions as well. For example, all human grow hair, all fish have gills, and all cats have whiskers. For every inherited function, there must exist some specific physiological site of set of sites from which that function is generated. Also, there must exist some underlying gene or set of genes responsible for the emergence of those physiological sites that perform that function. Consider another example, all honeybee colonies construct their honeycombs in the same hexagonal fashion, regardless of whether they've ever been exposed to another honeybee colony. When bee larvae are removed from their colonies and raised under artificial conditions, they still emerge as adults to construct their hives with the same hexagonal fashion. Take a kitten away from its mother, and raise it in total isolation, and it will still meow, suggesting that meowing is an inherited reflex.

Does this biological principle apply to Homo sapiens? All human cultures communicate through a spoken language, because we all possess this linguistic capacity. This would suggest that we must possess the "language genes". Like all cognitive capacities, ours for language originates from within the brain.

Within the human brain, there exist specific structures responsible for our language Capacities. They include Broca's area, Wernicke's area, and the angular gyrus. The angular Gyrus receives sensory information such as scent of a flower or the sound of the bell and then link the sensory input to its verbal "word". For example, when we smell a rose, our angular gyrus recall the word "rose" prompted by the scent. The Wernicke's area plays an essential role in linguistic comprehension, retrieves the recalled word from the angular gyrus and then processes it in such a way that we can grasp that word's meaning. The Broca's area, which controls the muscle of the face, jaw, palate, and larynx, allows for our words to be physically spoken.

If any one of these sites has incurred physical damage, it has been shown to have a direct effect on some specific part of that's person's language abilities. For example, damage to Broca's area will cause impairment so that articulation may be slowed and labored, depending on the extent of the injury.

Therefore, cognitive traits are no different from all other physical traits that they are passed from generation to generation through the transmission of genetic material. Just as every culture has perceived the world linguistically, every culture also has perceived the world spiritually. Is it possible that humans inherit their inclinations to perceive spiritual reality? If we possess such instincts, then there must be some physiological site in us, what we call a "God" part of our brain.

Human have had maintained a belief in the existence of unseen spirit guardian we refer to as gods since the dawn of our

species. The fact that all human cultures, no matter how isolated they are, have believed in the existence of a spiritual world. Every culture has erected sites of worship through which members of its community can gather to pray to its gods. It can be a Muslim mosque, a Catholic church, a Jewish synagogue, a Shinto shrine, Egyptian temple. Such sites of worship are physical evidence that all cultures have believed in the existence of a spiritual reality.

All cultures have expressed a belief in an afterlife. This is manifested in burial ritual. The deceased's body is buried with a rite that anticipates sending that individual's spirit on to the next or some other realm. In addition, every culture has possessed some form of a priesthood whose role is to act as the community's intermediary between the material and spiritual worlds. They can be a shaman, priest, rabbi, pope, psychic, medium or imam. Furthermore, sacred status has also been ascribed to various objects. Totems, relics, icons, amulets, charms, as they are called by their respective cultures, all represent examples of physical objects believed to contain some essence of spiritual realm within them.

In summary, all of our "spiritual" cognitions, perceptions, and behaviors are the manifestations of inherited impulses generated from neural connections in the brain. Though we all possess the same regions in the brain from which our spiritual impulses are generated, based on its unique set of historical and environment circumstances develop its own spiritual identity called religion.

Why do people believe in things they cannot see, smell, taste, hear, or touch? Why do some people believe in God, while others do not? Why do some people hear the divine word easily while others remain spiritually tone-deaf? Ask true believers of any faith to describe the most important thing that drives their devotion, and they'll tell you a feeling of a higher power far beyond us. So, is the person's religious behavior guided by her choices or simply divine will? Is it God or DNA?Over the last few years, scientists attribute spirituality, religious behavior to genes.

Early Studies on God-Genes

Most people can accept diseases or height and even weight being genetically heritable to some extent, but when it comes to our personal beliefs we tend to be more skeptical. For many, the idea that there is a genetic component to our faith--or lack of it--is a stretch too far.

Sir Francis Galton, a 19th century English scientist, was the first to recognize the potential of twins to answer quantitative questions about the origins of behavior. He uses his twin method to examine many different aspects of human development, health, and behavior. Galton guessed correctly that the twins appeared so similar because the identical twins had the same inherited makeup. Galton was also fascinated by spirituality and religion. He was the first modern scientist to study objectively the effectiveness of prayer and belief. The one thing that Galton did not do in his studies of twins was to explore whether belief and spirituality has an inherited component.

In 1970, a group of scientists at the University of Minnesota conducted a study on twins separated at birth. In the first published study of its kind, the researchers examined 53 pairs of identical twins and 31 pairs of fraternal twins, all reared apart, for five different scale of religiousness. Some of the scales looked at how much important religious faith was to the twins' lives. Others asked how much time they spent in religious activities such as attending church services. There were questions about their interest in religious occupations and their belief in God. The studies showed that genes do indeed play an important role in what they called "intrinsic religiousness." All of the twins grew up in different environments, but the identical twins, who share matching DNA, were much more likely to have similar levels of spirituality than fraternal twins, who share only half of their DNA. The measures for intrinsic religiousness were clearer. The correlation for identical twins was 37, about double the correlation of 20 for fraternal twins. Since these twins were raised by different parents, in different neighborhoods, and sometimes even in different religions, their similarities seemed to be the result of their DNA rather that their environment.

In 1999, Nicolas Martin and Lindon Eaves teamed up with Australian scientist Katharine Kirk to pursue the correlation between self-transcendence and heritability. This unlikely research partnership was formed between two academic twin experts--Nick Martin, an extrovert atheist Australian, and Lindon Eaves, a British lay preacher originally from Birmingham. The study focused on twins over 50 years of age who were mailed a health and lifestyle questionnaire. The response rate was 71 percent. The subjects had an average age of 61, with a range of 50 to 94 years. There are twice as many women as men. The subject has also different educational and socioeconomic backgrounds. Self-transcendence was assessed using Cloninger's Temperament and Character Inventory test. To assess spirituality, the twins were asked about their religious affiliations and church attendance. The studies also included questions about health, depression, optimism, and various aspects of personality. The result was striking. The self-transcendence scores of identical twins were more alike by far that those of fraternal twins. They estimated the heritability of spirituality to be around 40 to 50 percent, which is quite high considering how tricky it is to measure. These studies demonstrate our variable but innate inherited sense of spirituality, which affects how we perceive the world, ourselves and the universe. This is independent of our formal religious beliefs and practices and, strangely, largely independent of family influence.

Difference between Spirituality and Religiousness

Spirituality and religiousness are fundamentally different. The twins' studies strongly support the distinction. Religiousness, as measured by church attendance, is learned from parents, teachers, religious leaders, and peers. On the other hand, spirituality, as measured by self-transcendence, is more inborn and comes from within. The evidence suggests that spirituality is within us from the beginning and has to be developed like any other talent.

The God-Gene Theory

Geneticist Dean Hamer in his 2004 book, The God Gene: How

Faith Is Hardwired into Our Genes, links spirituality to genetics. According to Hamer's hypothesis, spirituality is a "biological mechanism" that is imprinted on our DNA. "We have a genetic predisposition for spiritual belief that is expressed in response to, and shaped by, personal experience and the cultural environment. These genes, I argue, act by influencing the brain's capability for various types and forms of consciousness, which become the basis for spiritual experiences" writes Hamer. To prove that there is a genetic component to spirituality is not a simple task. It is not like hair or eye color which is passed from generation to the next in a very obvious way.

Hypothesis

Human spirituality is influenced by heredity and that a specific gene, called vesicular monoamine transporter 2 (VMAT2), predisposes humans towards spiritual or mystic experiences.

Methods

Hamer decided to use the data he gathered in the smoking and addiction survey to conduct a little spirituality study on the side. First he ranked the participants along Cloninger's self-transcendence scale, placing them on a continuum from least to most spiritually incline.

More than 1000 individuals took the standardized Temperament and Character Inventory test which includes questions that measure self-transcendence (the ability to get entirely lost in an experience, transpersonal identification, and a feeling of connectedness to a larger universe) and mysticism (an openness to things that one cannot actually).After conducting the test, Hamer ranked the participants in terms of their spirituality, and then analyzed their genes to look for a correlation between spirituality and genetic codes. With over 35,000 genes and 3.2 billion chemical bases in the human genome, he limited his search for the "spiritual gene" to nine genes known to produce monoamines (brain chemicals that regulate mood and motor control).Monoamines appear to influence spirituality by altering consciousness, our awareness of ourselves including our thoughts, memories and perceptions. Studying the nine candidate genes in DNA samples provided by his subjects, Hamer quickly hit the genetic jackpot. A variation in a gene known as vmat2 for vesicular monoamine transporter seemed to be directly related to how the volunteers scored on the self-transcendence test. Those with the nucleic acid cytosine in one particular spot on the gene ranked high. Those with the nucleic acid adenine in the same spot ranked lower. "A single change in a single base in the middle of the gene seemed directly related to the ability to feel self-transcendence," Hamer says.

Potential limitations and flaws of the theory

1. Self-transcendence scale is a valid, robust, and fairly general yardstick for spirituality, but the scale is not comprehensive and spirituality is too multi-faceted to be captured in its entirety by a single measure.
2. Human traits often involve the interplay of hundreds or even thousands of genes, so it is doubtful that our sense of spirituality is dictated by cytosine alone. Other genes or chemical bases are likely to be involved.
3. If cytosine is related to spirituality as a contributing cause, it speaks nothing concerning the reality of God's existence. Hamer said, "My findings are agnostic on the existence of God. If there's a God, there's a God. Just knowing what brain chemicals are involved in acknowledging that is not going to change the fact."

Criticisms of God Genes Theory

Hamer's hypothesis has been widely criticized both in the scientific circles and in the theological world. Critics in the scientific community argue that Hamer's conclusions rely too much on anecdotal evidence and too little on testing of the VMAT2 gene to determine other possible connections to behavior. His findings were also criticized by many in the religious establishment who say that the research undermines a fundamental tenet of faith - that spiritual enlightenment is achieved through divine transformation rather than the brain's electrical impulses. "God is not something that can be demonstrated logically or rigorously," says Neil Gillman, a professor of Jewish philosophy at the Jewish Theological Seminary in New York City. John Polkinghorne, a physicist who is also Canon Theologian at England's Liverpool Cathedral, agrees: "You can't cut [faith] down to the lowest common denominator of genetic survival. It shows the poverty of reductionist thinking."

Brick John stone, a professor of health psychology at the University of Missouri, is one of the latest to throw cold water on the idea of a single part of the brain being able to explain spirituality. His 2012 study of 20 people with traumatic brain injuries affecting the right parietal lobe found that those with more severe damage reported feeling closer to a higher power. He also found that those who attended church more often showed increased activity in the frontal lobe. That suggests fascinating connections between the brain and spirituality but it also disrupts a simplified notion of a single "God spot."

Conclusion

Can so slight a variation in our DNA incline us toward religion? The Bible provides an authoritative explanation for our capacity to know God. As Genesis 1:26 makes clear, human beings are made in the image of God, therefore we are the only creatures able to know God consciously and intimately. Any effort to create a genetic explanation for a generic experience of self-transcendence will both fall far short of scientific credibility and will fall tragically short of providing an adequate theological explanation for how human creatures can know our Creator. That explanation is revealed to us by our Creator within the Bible.

If behavioral basis of faith is hardwired into our DNA is true, why Hamer's God gene or any of the others that may eventually be discovered is distributed so unevenly among us. Most believers will resist any attempt of "reductionistic" and "materialist" science to see religion as anything other than supernaturally inspired.

Establishing the existence of a spiritual gene, and establishing a causal relationship between that gene and religious faith are two different things. It remains to be determined whether Godcaused the gene, or the gene caused "God."

These days there seems to be a new openness to studying the brain and spirituality. The last decade in particular has brought a steady stream of research locating aspects of spirituality in the brain. Various scientists have claimed to have discovered a "God spot," a "God gene," or a "God circuit."Geneticists will continue to explore the newly sequenced human genome, we will surely hear more about links between genes and behaviors, including religious behaviors.

We should keep in mind that the chemistry of gene expression has been shown to be enormously complex and is deeply connected with the individual's environment. Thus, the deterministic theory ("It is all in the genes") does not suffice anymore. No wonder, 'thus it fits the definition of a living system that I have given. Like a biological virus, it is a rather degenate form, because it contains only instructions or genes, and does not have metabolism of its own [15]. .

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