What Do Our Got hacking Genealogies Tell Us?

Human Genealogy:

We need to chart our genealogies and understand our origins. By sequencing our genomes, we can trace our roots back to our ancestors and understand our genetic history. This knowledge is crucial for understanding our evolution and our place in the world. It also helps us understand our relationships with other species and our potential for future evolution.

The Human Genome Project, which began in the 1990s, was a major endeavor to sequence the human genome. This project was successful in 2003, and it has provided us with a wealth of information about our genetic makeup. This knowledge has been used to develop new treatments for diseases and to understand the evolution of our species.

In recent years, the field of genomics has grown rapidly, and we have gained a deeper understanding of our genetic history. This knowledge has been used to develop new treatments for diseases and to understand the evolution of our species. We have also learned that our genetic history is not just about our species, but also about our interactions with other species.

In conclusion, understanding our genealogies is crucial for our understanding of our place in the world. By studying our genetic history, we can better understand our evolution and our potential for future evolution. This knowledge is crucial for our development as a species and for our ability to adapt to changing environments.

References:


Appendix:

A summary of the key findings from the Human Genome Project.

Table 1: Comparison of Genomes

<table>
<thead>
<tr>
<th>Species</th>
<th>Genome Size (Mbp)</th>
<th>Chromosome Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>Human</td>
<td>3,000,000,000</td>
<td>23</td>
</tr>
<tr>
<td>Mouse</td>
<td>2,198,000,000</td>
<td>24</td>
</tr>
<tr>
<td>Dog</td>
<td>3,140,000,000</td>
<td>39</td>
</tr>
</tbody>
</table>

Figure 1: The Human Genome Project.

This figure shows the timeline of the Human Genome Project, from its inception in 1990 to its completion in 2003.

Figure 2: The Genome of E. coli.

This figure shows the genome of the bacterium E. coli, which is small and compact compared to the human genome.

Figure 3: The Genome of S. cerevisiae.

This figure shows the genome of the yeast S. cerevisiae, which is much larger than the genome of E. coli.

Figure 4: The Genome of D. melanogaster.

This figure shows the genome of the fruit fly D. melanogaster, which is even larger than the genome of S. cerevisiae.

Figure 5: The Genome of H. sapiens.

This figure shows the genome of the human species, which is the most complex and diverse of all.

Figure 6: The Genome of M. musculus.

This figure shows the genome of the mouse species, which is smaller than the genome of H. sapiens but similar in complexity.

Figure 7: The Genome of C. elegans.

This figure shows the genome of the roundworm C. elegans, which is one of the smallest genomes studied.

Figure 8: The Genome of A. thaliana.

This figure shows the genome of the Arabidopsis thaliana, which is one of the smallest genomes studied.

Figure 9: The Genome of T. brucei.

This figure shows the genome of the trypanosome T. brucei, which is one of the smallest genomes studied.

Figure 10: The Genome of B. subtilis.

This figure shows the genome of the bacterium B. subtilis, which is one of the smallest genomes studied.

Figure 11: The Genome of M. genitalium.

This figure shows the genome of the bacterium M. genitalium, which is one of the smallest genomes studied.
circumstances and habitats allowed (Bucher et al., 2003).

Phenomenal progress in genome science and DNA sequencing technology has enabled scientists in the last few years to determine complete or partial genomic sequences of more than 1,000 species from diverse groups of organisms (Madigan & Martinko, 2006). Computer analysis of DNA sequences now allows scientists to compare genes and their encoded proteins from both closely-related and distantly-related species. Not only are humans and chimpanzees 98% identical; 60% of fruit fly genes, 43% of the genes of a nematode worm, and 46% of baker’s yeast genes are similar to human genes (Rubin, 2001). Even genes for basic metabolic functions (such as fermentation, respiration, cell growth, and protein synthesis) found in primitive bacteria are retained in higher organisms including humans (Bucher et al., 2003). Structural and functional similarities of organs such as liver, lung, eye, etc., between other mammals and humans are the result of their genetic similarities and make animal experimentation relevant to human functions and diseases, as well as life-saving procedures such as organ transplants. Such genetic similarities allowed us to use pig insulin protein, almost identical to human insulin, to treat diabetes for 50 years until the 1980s. At that time human insulin was finally produced by cloning a gene for human insulin into E. coli, thus having a bacterium produce genetically-engineered human insulin (Riggs et al., 1984).

The relatedness among diverse species is not limited to genes and proteins. Cells of all species from bacteria to humans are composed of the identical chemical elements, carbon, hydrogen, oxygen, nitrogen, phosphorus, sulphur, and trace elements. Also, the capacity to synthesize proteins (the signature of life), using DNA, messenger RNA, transfer RNA, ribosomes, and a universal triplet genetic code have remained intact in all species from our earliest ancestors to the present (Gregg et al., 2003).

All available scientific evidence, some of which is reviewed in this piece, points to the fact that genes in the DNA determine the heritable characteristics of all organisms from bacteria to humans. It also establishes the fact that genes may occasionally mutate (change the nucleotide sequence of a gene), either spontaneously or from exposure to various natural or man made mutagens in the environment. Gene mutations along with recombination, gene duplications, and exon shuffling provide genetic variation for natural selection to act on, resulting in, over millions of years, the species diversity that exists today. The antibiotic resistance of pathogenic bacteria, insecticide resistance of insects, herbicide resistance of plants and changes in host specificity (as in the cases of West Nile virus, Asian bird flu virus, and SARS [severe acute respiratory syndrome] virus now shifting to humans) are examples of rapid, relatively minor evolutionary modifications and diversities that we can observe today (Springael & Top, 2004). These kinds of changes in response to strong selection are especially easy to observe in bacteria and viruses with their small genome sizes, short generation times, and huge populations. But similar genetic adaptations have also been observed in more complex organisms, such as insects and plants. These kinds of changes accumulating over millions of years underlie the species diversity we see today.

The scientific evidence summarized here, in addition to the fossil, anatomical, morphological, and developmental evidence widely published in the scientific literature, demonstrates clearly that all species from bacteria to humans are related and the root of relatedness is contained in the universal genetic blueprint of DNA. It can therefore be concluded that since all species have a common genetic basis and are genetically related, they must have arisen from a common ancestor and not have been independently created in random times and places (Gregg et al., 2003). Thus human genealogy (genetic relatedness) is much deeper and wider than only ape-like ancestors. It goes back to the very early single-celled organisms. Scientific curiosity about human genealogy should be encouraged to spark students’ minds to engage in further scientific investigation and understanding of genomic science and genealogy for the construction of a complete “genetic atlas” of all species on Earth.

In view of the importance of science in the modern world it is essential to realize that the United States is losing its preeminence in science. The first heart transplant was performed in South Africa, the first “test-tube baby” was produced in England, and the major hub of information technology is in Bangalore, India. American school boards have the clear choice to regain the lead in high school science and math education and encourage teens to finish their math homework if they do not want students from other countries to take their jobs away (Friedman, 2005). While we continue to lower standards by introducing pseudo-science such as intelligent design, into the science curriculum, we complain about jobs in the fields of science, medicine, and technology going to more qualified foreign-born individuals. It is time to re-establish our global leadership in science and technology education; sharing our science classrooms with pseudo-science is not the way to achieve this goal.

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References
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