

In the interim, our research team is releasing this report to focus on the 1677/157 RNA segment of mtDNA because it is easy to understand. Several other mtDNA comparisons have been carried out, each much longer than the one here, and three of those are depicted and analyzed in the Starchild Skull Essentials eBook.

Remember that the information found by comparing mtDNA segments cannot and should not be considered thoroughly verified, as some sequencing errors are undoubtedly present. Each mtDNA segment must be sequenced several times to establish exactly how many differences exist between the Starchild Skull and the human CRS, and this kind of targeted testing, rather than shotgunning at random, is time-consuming and expensive.

Nonetheless, based on the preliminary results now in hand, our research team is very confident that when the Starchild's entire genome is recovered and sequenced, the total number of confirmed differences will be so staggering that it can only lead to a conclusion that the Starchild represents an entirely new humanoid species, and that species is "alien."

How could an "alien" have any human DNA, or even survive on our planet? Surprisingly, the genomes of many animal species have certain similarities (or homology) with humans. Proteins are the building blocks of all animal life on Earth, and the DNA that guides the production of proteins is very similar across all species. The genome of chimps is $\pm 97\%$ the same as humans. Gorillas are 95% the same. Rats are 70% , mice 65% . Etc.

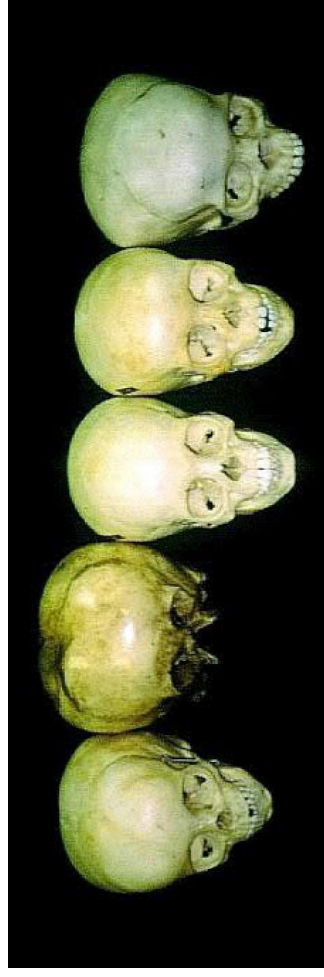
As mathematicians like to say, "Numbers don't lie." In this case, the 17 differences found in one short segment of Starchild Skull mtDNA makes it seem possible—even probable—that when the entire $16,570 \pm$ nucleotides in the Starchild's mtDNA are sequenced, they will contain far more than the $120 \pm$ variations shared by the 33 human haplogroups.

Add to those 17 the number of differences found in three much longer fragments discussed in the eBook, and the total is mind-boggling. That number convincingly indicates that the Starchild will carry far more differences than the $200 \pm$ of Neanderthals. It will carry far more than the $385 \pm$ of Denisova. Can it possibly, or conceivably, reach the $1500 \pm$ of chimps? Only further investigation will tell, but this is already a monumental discovery.

Collected from the writings of Lloyd Pye
www.starchildproject.com and www.lloydpye.com

Please write to contact@StarchildProject.com if you feel you could support this research financially – or just look at www.starchildproject.com to find updated information and find out how you can help more.

Spot the Difference...



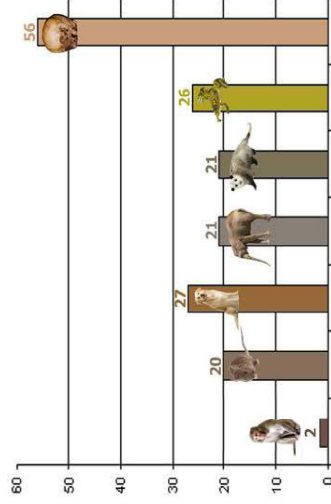
In one well-studied mutation in the section of the gene that influences speech development mechanisms in humans, those who inherit it will never be able to speak. This has led some to suggest FOXP2 is a language gene, or a speech gene, but that is not the case. Speech is much too complex an arrangement of working parts to be so simply controlled, although a properly functioning FOXP2 gene is an essential part of the speech-development equation.

The key point to understand is that while a tiny amount of survivable mutations are possible in FOXP2, every one that occurs presents debilitating or life-threatening consequences, so to this point in time none have been passed on to the general population of humans. Therefore, in the vast, vast majority of humans, the FOXP2 master gene is absolutely identical.

With that said, let's examine the fragment of Starchild Skull FOXP2 sequenced by our geneticist. Of the entire 2,594 base pairs of the normal FOXP2 gene, our fragment is 211 base pairs that come from a segment near the center of the gene. If the same 211 base pair section were isolated from any normal human, every base pair would be exactly the same as what is found in any other human. There would be no difference in any of them.

Okay, ready...brace yourselves. The Starchild's 211 base pair FOXP2 fragment has a grand total of 56 variations! Now, while extrapolating this 211 base pair fragment is a bit more of a stretch than extrapolating the four combined fragments of mtDNA we discussed earlier, doing so does provide something to think about. Divide 2,954 by 211, and you get 12.3. Multiply 12.3 by 56, and the range of total variations in the Starchild's FOXP2 base pairs would be 600 to 700! So let's be crazy conservative and say it's only 200 or 300. It is still astounding in a super highly conserved gene that in normal humans has no variations at all!

If we compare the same section from a rhesus monkey's FOXP2, only 2 of its 211 base pairs would vary from any human. If it were a mouse, it would be 20. If a dog, 27. An elephant, 21. An opossum, 21. A Xenopus (a kind of frog), 26. So dogs and frogs are the most different, at 27 and 26 base pairs respectively.



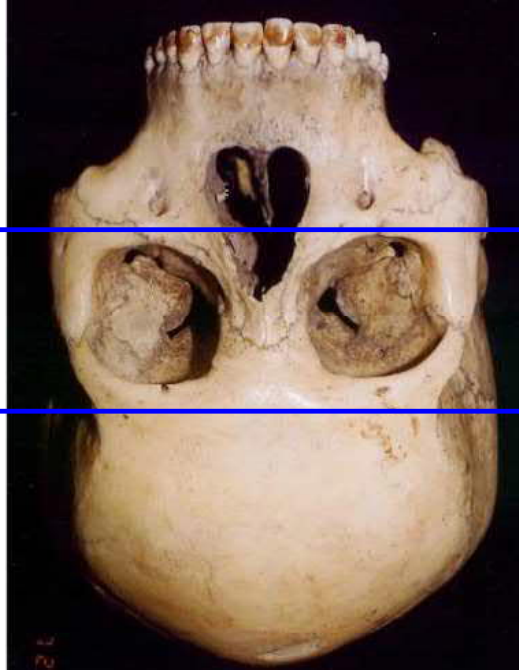
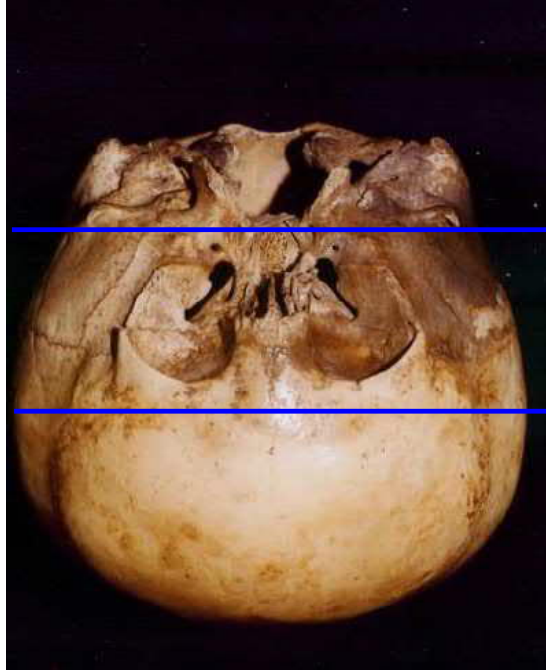
To put this in perspective, let's imagine that when alive, the Starchild was indeed some unknown humanoid. No matter how different from humans it might have been, to be in the humanoid family its FOXP2 gene would have to be in the range of 1 or 2 or at most 3 base pair variations from a normal human. To go past 5 or 10 would put it into another class of species. 20 to 25 would put it in the range of mice and elephants, and dogs and frogs. To have 56 is to put it in another realm, another dimension entirely. It is utterly unique.

To verify this radical statement, below is the actual comparison of the Starchild's FOXP2 fragment with the same gene segments of some of the species listed above. In each case, imagine it as a string of 211 base pair nucleotides, although to fit into this format it must be broken into two segments, top and bottom. Notice the steady blue of the human nucleotides that make up its base pairs, and the stark red of each variation in the other species.

In the 211 base pair fragment from the FOXP2 gene in normal humans, no variations occur among the amino acid sequence in the FOXP2 protein, and the coding pattern for Gln (using either CAA or CAG) is exactly the same not only in humans, but essentially in all primates. (Compare only 2 amino acid variations in a rhesus monkey, which is not even a great ape.)

In the Starchild Skull, we find 16 amino acid variations in this fragment, which despite all those differences unmistakably resembles the human FOXP2. Yet it demonstrates a coding pattern that is wildly different from all species shown above. This is an astounding contrast!

Human female (HF) found with Starchild Skull (SC). Both size of a small adult or 12-year-old. SC has no brow ridges, no dip from brow to nose. Nose widths equal. Human's eye sockets 2" deep; SC 1/2" deep. SC optic foramina (slits) lower by 1/2". SC eyeballs—if present—rest in middle of nose, require huge upper eyelid. SC eye socket surfaces amazingly symmetrical, not deformity. Zygomatic arches (cheeks) of Human folds into eye socket as part of the socket. SC cheeks snapped off in a way improbable in Human. Human chewing muscles attach high up sides of skull. SC chewing muscles reach just above top line, cover less than 1/2 normal area. Dark area on SC right cheek is due to staining from soil in which it was buried for 900 years.



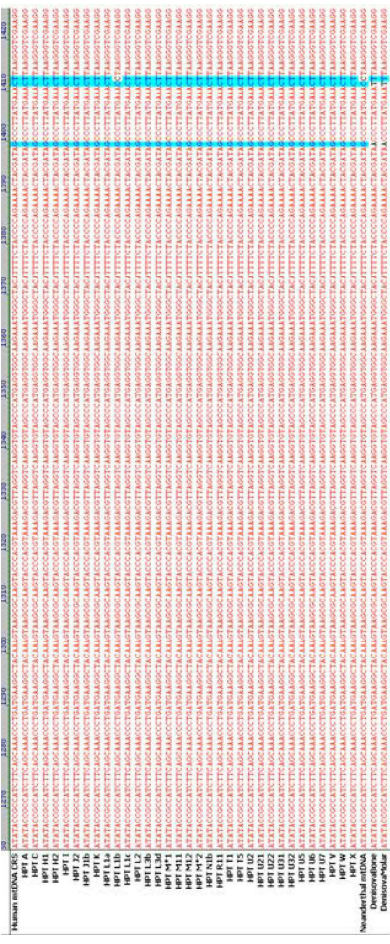
Front View

Rear View



SC occipital stretched high and flattened, though not as flat as if cradle-boarded. It lacks an inion (bump at back of human skulls). HF inion (at bottom) has wide fossa (depressions) on sides. SC inion should be at circle of dark flecks in mid-occipital. Only slight fossa remains. HF neck muscles sweep from inion to mastoids (bones behind ears, at edge of frame). SC neck attaches 1/2 inch from foramen magnum (where spine enters skull). SC neck 1/2 size HF neck, if that. Note stark difference in crowns. SC has uniform, symmetrical "crease"; thus, no upward pressure from hydrocephaly. Robust and numerous Wormian bones along SC's left lambdoid suture (against left parietal) is indication of an age at death beyond childhood.

See www.starchildproject.com for more information



This chart goes from #1262 to #1426 (164 nucleotides). Now imagine a line added across the top labeled "Starchild Skull" containing 167 nucleotides, but covering only 157 of the human mtDNA nucleotides to which it matched. Discrepancies like this (167/157) occur because the computer program is designed to find matches between two or more DNA fragments, in this case the human CRS and the Starchild Skull's mtDNA. If it calculates that a sequence would match if more or fewer letters were in either code, it inserts gaps containing dashes to produce better aligned results, as seen in the diagram below:

Human CRS	A	G	T	C	G	T	A	C	C	A	G
XXXX Sample	A	G	T	C	-	T	A	C	C	A	G

In the comparison above, the first four letters match. However, at the fifth space a jumble would begin within the sample if the gap (containing a dash) was not inserted where it is. This is how the computer program works; it seeks to record the highest possible number of matches between two samples, so it inserts gaps, and each gap provides a negative penalty score as the program calculates the highest total of matches.

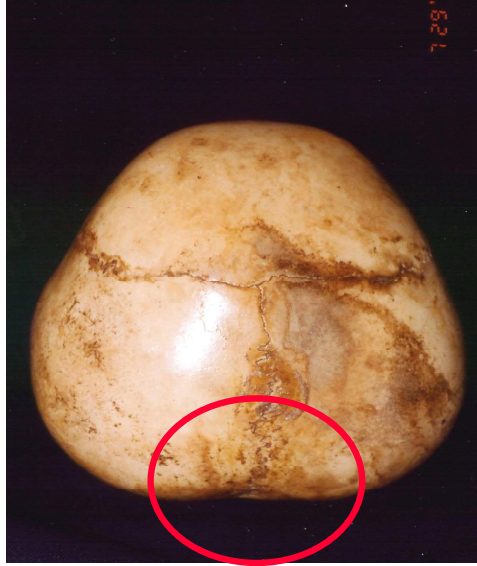
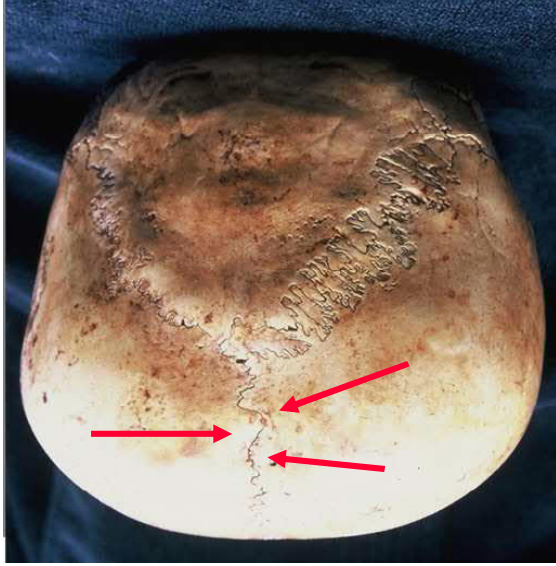
To make the Starchild's mtDNA match the human CRS, the program added gaps marked as dashes either to the Skull's mtDNA or to the CRS to obtain the highest matching score between them. Adding spaces to such misalignments in both samples provides a total cumulative difference, which in this case is a 10-gap differential (167 - 157 = 10). It is important to distinguish that adding gaps is not the same as outright changes in the nucleotides, as was seen earlier with the single C found in a row of Ts. Such changes are only one of three ways that differences are recorded when samples are being compared.

(1) The SNP just referenced is a *substitution*, when one nucleotide is replaced by another; (2) an *insertion* is when an extra nucleotide is found in a sample and the program has to introduce a gap into the other sequence to accommodate the extra nucleotide; and (3) a *deletion*, which is when a nucleotide is missing from one of the samples, and once again the program introduces a gap into the sequence to align it with the other sequence.

In the latter two cases, insertions and deletions, the program makes no distinction between which is the cause of the gap. All it does is insert the gaps into either sequence to keep the matching count as high as possible. Those gaps are called *insertion-deletions*, or *indel(s)*. Indels are clear points of variation between samples, but not all of them can be considered ironclad. All DNA testing requires multiple "runs" to be certain of every result. When the same sample is sequenced again and again, any of the three possibilities above might be corrected. Several runs will establish which variations can be catalogued as confirmed.

Now return to the Starchild's 167 mtDNA nucleotides compared to 157 nucleotides of the human CRS in a highly conserved region where only one single variation is found among 33 human

Is The Starchild Hydrocephalic?

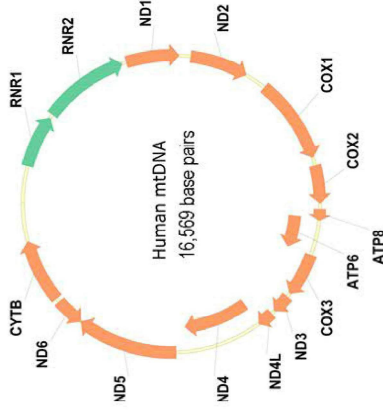


See www.starchildproject.com for more information

Human mtDNA contains 37 genes, 15 of which are larger and depicted above, and 22 of which are tiny bits of transport RNA (tRNA) not included. Of the 15 larger, 2 encode for mitochondria-specific RNA (ribonucleic acid) that constitutes a crucial component of mtDNA's protein-making machinery (called ribosomes), but does not actually encode proteins. That is carried out by the 13 other large genes in the mtDNA, which do encode proteins for the production of energy and other critical functions of the mitochondria.

Mitochondria are the power plants of all cells that contain them, with a similar function in the biology of all species on Earth. MtDNA is one of the most thoroughly researched and well-understood aspects of human genetics. The coding capacity of mtDNA is used very efficiently, having exactly enough genes to carry on its job of producing proteins.

Since the beginning of eukaryotic cells (those with a nucleus) around 2 billion years ago, the mitochondria in them have carried out the most fundamental aspects of sustaining life. This has been true from yeasts to dinosaurs to humans. Their critical functioning is why very few differences are found between the mtDNA sequences of closely related species.



The primary genes within human mtDNA

Mutational change in the human mtDNA nucleotide sequence is exceptionally rare (only 120 ± among all humans), and each mutation is well documented. The chart below is a screen capture of the output from a computer program that compares the entire mtDNA sequences of 33 different human haplogroups, one sequence for Neanderthal, and two for the recently discovered Denisova type of hominid. This output is called DNA alignment.

At the top, highlighted in dark blue, is the Human mtDNA Control Reference Sequence (CRS), which represents the sequences of one particular individual chosen as a reference, so everything else can be compared to that standard. The sequence depicted here starts at nucleotide #1255 (out of 16,569) and continues across to #1350. Notice this block of 95 nucleotides contains no variations in any haplogroup. Every base pair nucleotide is identical across all 33 groups of humans, the Neanderthal, and the two Denisova.

Human mtDNA CRS	1255	1260	1270	1280	1290	1300	1310	1320	1330	1340
HPT A	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT B	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT C	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT D	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT E	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT F	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT G	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT H	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT I	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT J	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT K	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT L	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT M	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT N	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT O	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT P	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT Q	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT R	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT S	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT T	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT U	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT V	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT W	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
HPT X	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
Neanderthal mtDNA	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
Denisova1 mtDNA	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									
Denisova2 mtDNA	TCAGCCTATATACCCGCAATTTTCAGCAACCCCTGTAAGGCTTCAAGTATAGCCGAGAGTACCCACCGTAAAGAGGTTAGGTCAGAGGTTAAGCCCA									

The comparisons were conducted using a sophisticated computer program called the Basic Local Alignment Search Tool (BLAST), an NIH application that can analyze nucleotide sequences of any length, short or long, and attempt to match them to any of the millions of sequences in the database that represent essentially every living species on Earth.

All of the sequenced fragments recovered from the Starchild Skull DNA sample were run through the BLAST program. As anticipated, a large percentage of recovered fragments were matched perfectly with DNA catalogued from various species of bacteria.

Also anticipated were the results for several fragments like the one seen below. That fragment was 265 base pairs in length, and it was found to correlate with a segment on human chromosome #1. This proves some of the Starchild's nuclear DNA is analogous with segments of human DNA, and those parts of its genome are human or human-like.

BLAST Basic Local Alignment Search Tool

Database Name: 3 databases
Description: P-585-05525
Program: BLASTN 2.2.24+ - Citibion

Nucleotide Sequence (265 letters)

Query ID: ICI14929
Description: None
Accession: NC_001328.2.1
Query Length: 265

Accession	Description	Max Score	Total Score	Query Coverage	Max E-Val	Max Identities	Links
NC_001328.2.1	Homo sapiens chromosome 1 genomic contig, GRCh37 (bp)	432	432	99%	4e-136	100%	
NC_001328.2.1	Homo sapiens chromosome 1 genomic contig, alternate1 (bp)	432	432	99%	4e-136	100%	

Sequence producing significant alignments:

Legend for links to other resources: UniGene, GEO, Gene, Structure, Map Viewer, PubChem BioAssay

Homo sapiens chromosome 1 genomic contig, GRCh37

Homo sapiens chromosome 1 genomic contig, alternate

These results were not surprising since the 2003 Trace Genetics test concluded that the Starchild had a human mother. However, these were not the only results. Other BLAST results, like the one below for a 342 nucleotide fragment, gave a very different answer.

BLAST Basic Local Alignment Search Tool

Database Name: 3 databases
Description: P-585-05525
Program: BLASTN 2.2.24+ - Citibion

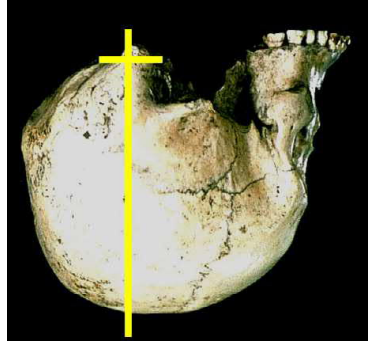
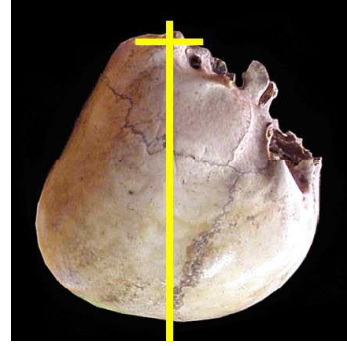
Nucleotide Sequence (342 letters)

Query ID: ICI14933
Description: None
Accession: NC_001328.2.1
Query Length: 342

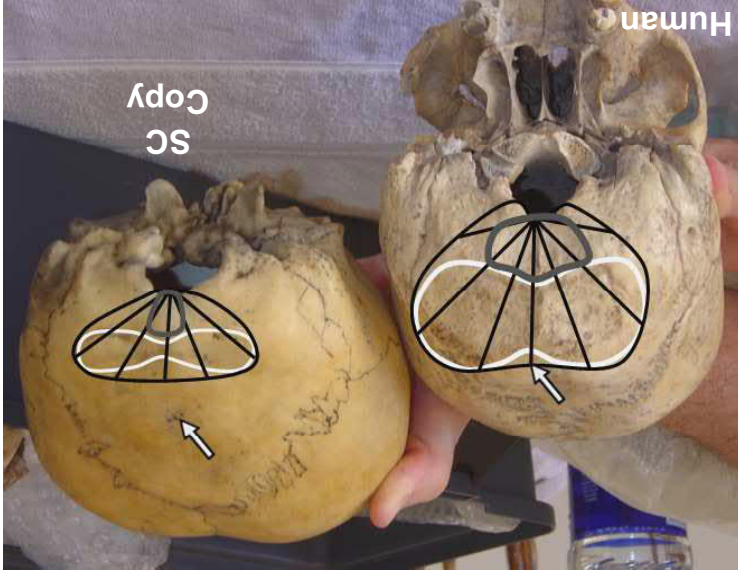
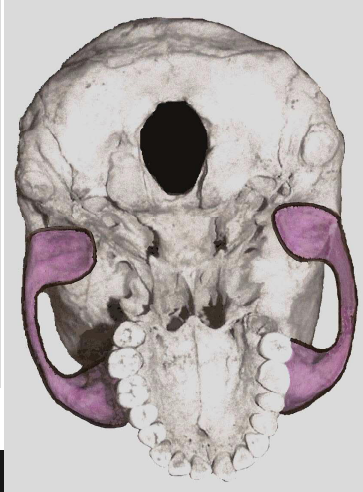
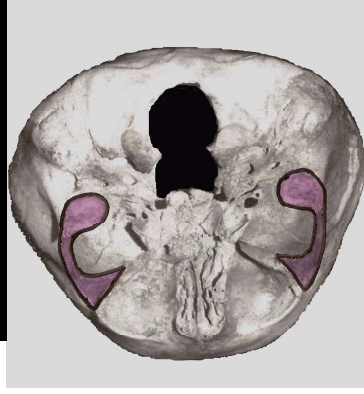
No significant similarity found.

It states that within the millions of DNA base pair strings catalogued in the NIH database, none were even "similar" to this section of the Starchild Skull's DNA! And please note that this astonishing result was obtained with the search parameters set to the broadest match criteria that seeks even a "somewhat similar" match, not only an exact match.

For all of the Starchild's DNA fragments, a wide net was cast into the NIH database with the hope there would be minimal doubt about results. Indeed, they were unequivocal: *Some of the Starchild's nuclear DNA is different from anything previously found on Earth!*



Balance Points of Craniums



Neck Muscle Attachments & Zygomatic Arches

CAT Scan, Braincasts (Done in 2013)

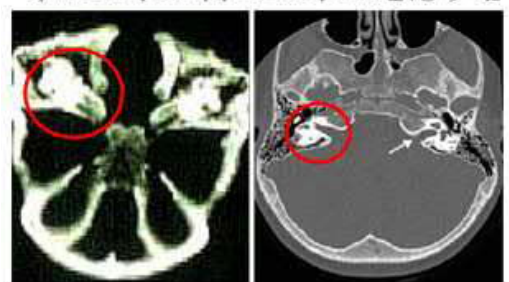


Fig. 6. CAT scan shows much larger inner ears in the missshapen skull (right) as compared to the human skull (left)



Starchild Skull CT Scan Image showing open, healthy suture lines

If the Starchild's nuclear DNA responded positively to primers designed to recover human nuDNA, that would establish its nuDNA as also human, confirming it as an astoundingly bizarre deformity, but 100% human. However, if its nuclear DNA proved to be other than entirely human, the Starchild Skull would represent a new type of humanoid—period.

In six full attempts (above), Dr. Eshleman and Dr. Malhi could not detect the Starchild's nuclear DNA by PCR. Given that nuDNA was easily recovered from the control skull with the same level of DNA degradation, and the Starchild's mtDNA was also easily detectable by PCR, the failure strongly indicated its nuclear DNA was present, but too different from human DNA to be detected by human-specific primers.

Though compelling, this result was not absolute proof that the Starchild had a non-human father. Also, if it were some kind of human-alien hybrid, the presence of mtDNA inherited from a human mother would suggest that a large portion of its nuDNA should also come from the mother. So, why wasn't this clearly human counterpart more easily detectable?

With only PCR-based detection techniques at their disposal in 2003, Dr. Malhi and Dr. Eshleman had no way to address the critical question of exactly *how far* the father was from human. Was it a razor-thin margin, barely enough to avoid detection by primers? Or was it a substantial margin, enough to confirm that he had an alien genetic heritage? (In this context, "alien" can mean anything from "foreign to normal human genetics within the framework of that subject as it is currently understood," to "definitely not from planet Earth" ... or anything in between.)

With Trace Genetics unable to determine how different the father's DNA was from human, the Starchild Project could offer no conclusion that would stand up to the intense scrutiny certain to descend on a claim that the Starchild's father might be of non-terrestrial origin.

The upside was that the mtDNA result proved the Starchild Skull's DNA was viable (not degraded to a point where nothing could be recovered from it), leaving open the possibility that later, using improved technology, its all-important nuclear DNA could be recovered.

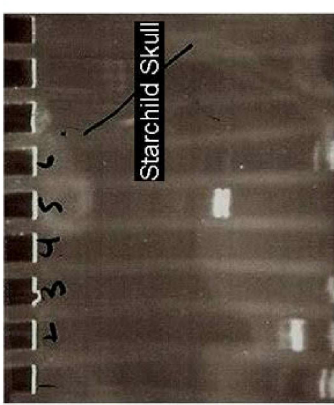
454 Life Sciences Technology:

In 2006, a company called 454 Life Sciences of Branford, Connecticut, announced they had developed a new DNA analysis methodology that enabled sequencing of any unknown DNA sample without prior knowledge of any of its sequences. The only requirement was that the sample to be sequenced had to actually be DNA (in a chemical sense).

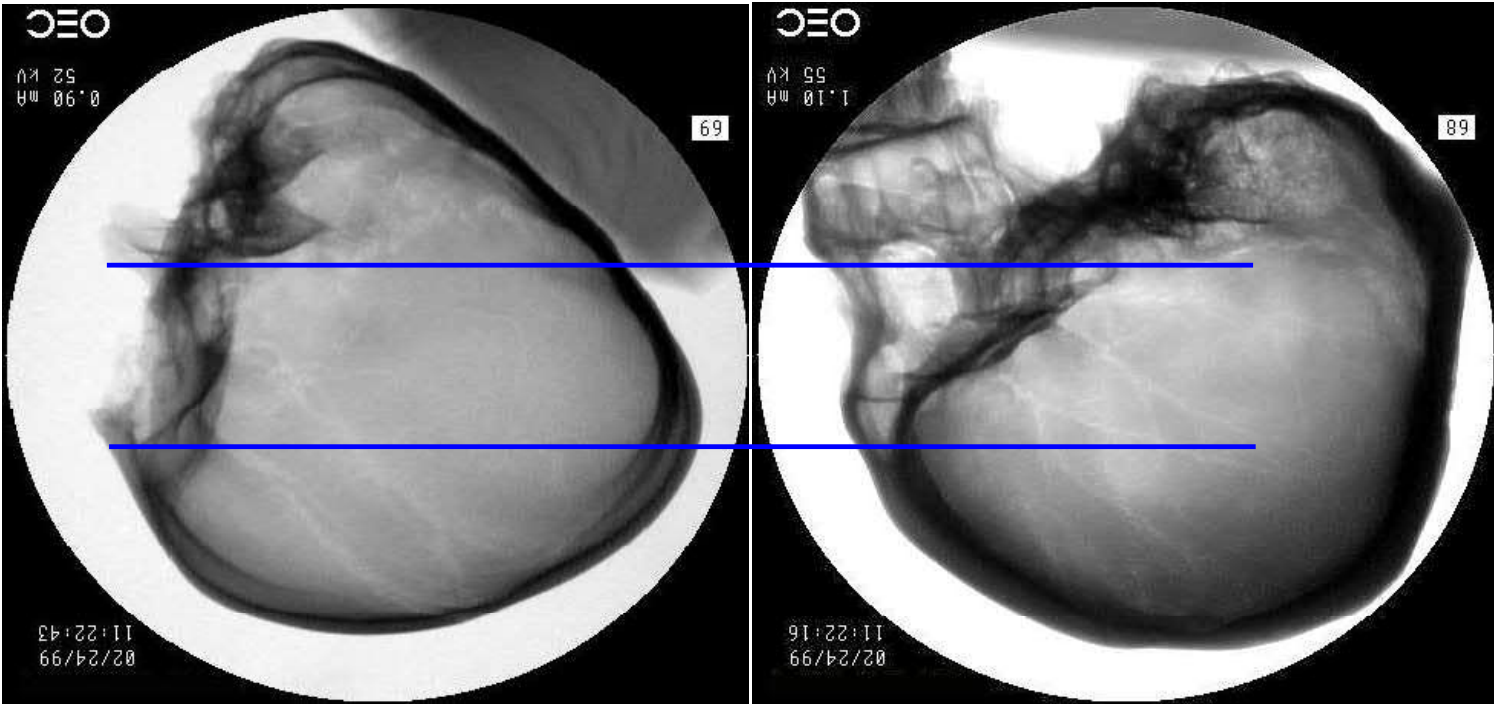
The 454 technique was also based on using primers, but these primers were standardized for every imaginable analysis, not specific to the DNA to be analyzed. It was exactly what was needed to recover and sequence the Starchild's elusive nuclear DNA.

Unfortunately, the first full genome analyses using the 454 methodology were extremely expensive (millions of dollars each), and so could be afforded only by those involved in well-known, high-profile cases such as sequencing the Neanderthal genome.

By 2009, 454 sequencers were in use worldwide and were competing with next-generation genome sequencers from other companies, so the cost of sequencing entire genomes was decreasing steadily. The Starchild's DNA was now a candidate for such comprehensive genetic



Gel sheet representing six failed attempts to detect Starchild Skull nuDNA by PCR



Despite parallel eye sockets, images not balanced. SC forehead tipped higher than normal position during X-ray process. HF classic example of cradle boarding. Flat as the board it was strapped to from top of crown to top ofinion (bump at back of head), where neck muscles must attach. SC has no inion and little room for neck muscles to attach. Veins in HF run from temple to crown of skull. Same with SC, meaning no water on brain's outer surface. Brains pressed into bone enough to leave imprints. Great expansion of brain in SC's parietal area—bulge is clear.

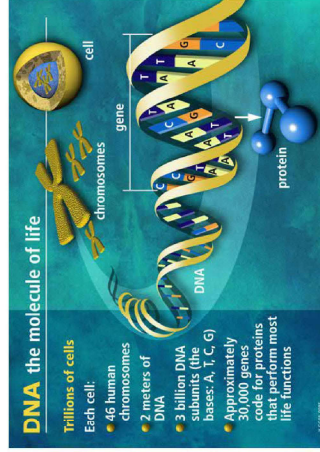
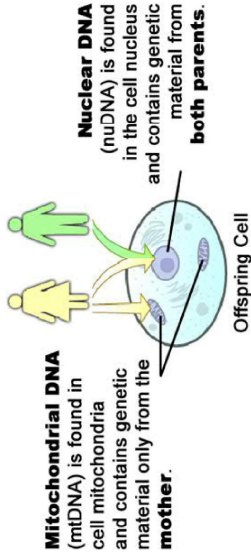
years old. Dr. Malhi and Dr. Eshleman had previously worked on the high profile 5,000 to 9,000 + year old Kennewick Man skeleton found in Washington State in 1996.

Drs. Malhi and Eshleman took samples of the Starchild bone, along with control samples from a human skull reportedly found lying beside the Starchild's buried skeleton. [Carbon 14 dating](#) of the two skulls confirmed they died at or near the same time, 900 years ago, and later analysis of staining on both skulls, and the inorganic chemistry of their bone, supported the C-14 result that both were exposed to similar conditions after death. That made the human an ideal control to compare contamination and degradation of its DNA against the Starchild's.

What You Need To Know About DNA:

All humans have two types of DNA.

Mitochondrial DNA (mtDNA) comprises the genomes of all mitochondria, which are subcellular (within a cell) elements located in the cytoplasm of eukaryotic cells (those with a nucleus). Mitochondria are responsible for energy production in cells. They are inherited through female eggs; thus, mtDNA is inherited only from mothers, grandmothers, great-grandmothers, etc., for countless generations to a species' point of genetic origin.



Nuclear DNA (nuDNA) is the combination of genetic material from both parents, and comprises the human genome. NuDNA gives humans their unique individual attributes.

All DNA is created from only four building blocks called nucleosides, which are bound together the way train cars are coupled, with the help of a binder made of phosphoric acid. These four nucleosides are adenosine, guanosine, thymidine and cytidine, abbreviated as A, G, T, and C. Nucleosides with the attached phosphate couplers are called nucleotides.

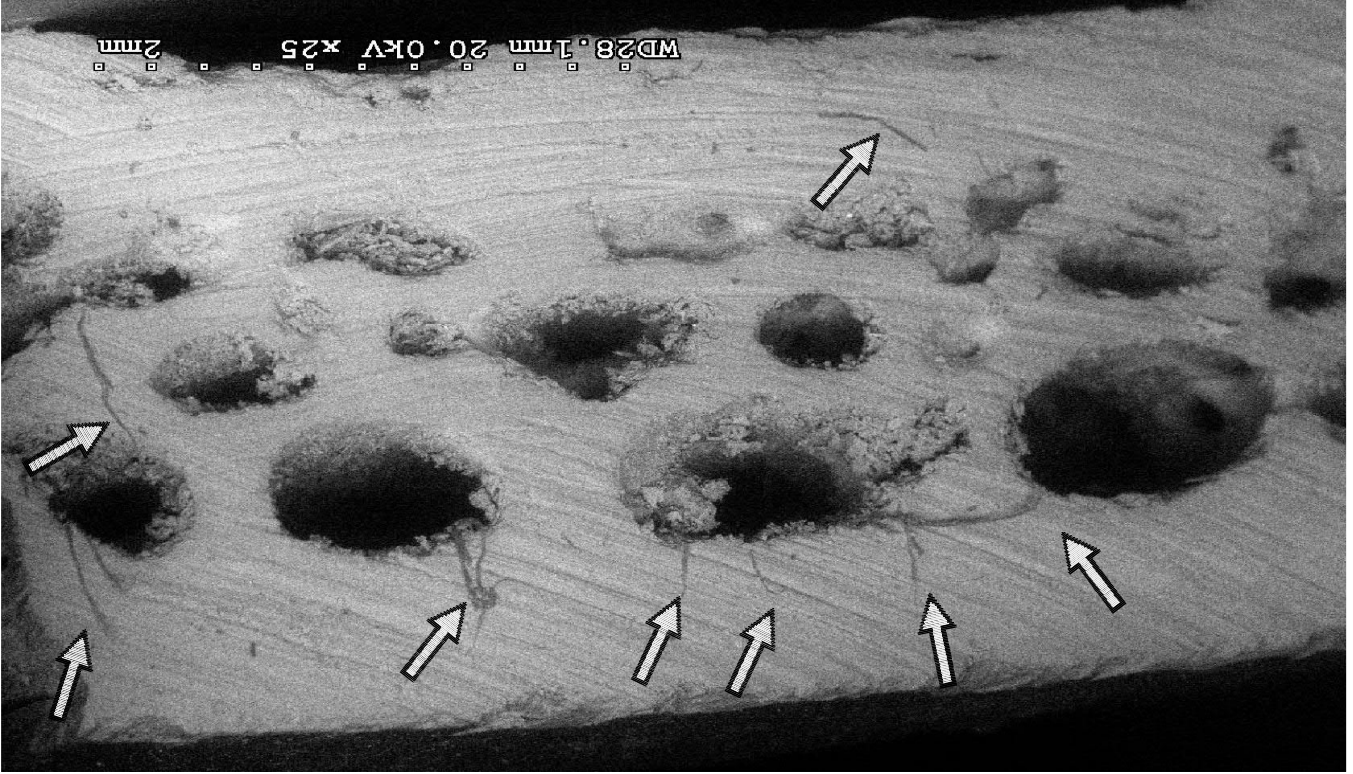
The four resulting nucleotides link together in DNA to form chains that are different in their order and length for each gene. Whether short or long, when linked together these nucleotide chains comprise the 30,000 genes that are organized into the 46 chromosomes (23 from each parent) within the nucleus of almost every cell in the human body. Each chromosome is basically an enormously long, uninterrupted chain of the four nucleotides connected in a specific order that is unique to the chromosome's host and species.

Regardless of length, each chain of nucleotides is complexed with (connected to) another DNA chain that faithfully reproduces the connection order of nucleotides in the first chain, but in a mirrored manner. Each nucleotide in one chain is always connected to a specific nucleotide in the opposite chain to create what is known as a base pair. Base pairs always occur as T-A (or A-T) and G-C (or C-G). Those 46 chromosomes taken together contain over 3 billion base pairs, which in total comprises the human genome.

What You Need To Know About DNA Testing:

In 2003, Trace Genetics began their sequencing [analyses of the DNA recovered from both skulls](#). The methodology they utilized was based on PCR (Polymerase Chain Reaction), a powerful amplification technique that enabled analysis of tiny amounts of DNA too small to be detected by

SEM: View of SC Bone Fibers



S.E.M. view of fibers emerging from AS's cancellous holes. Such microscopic entities are never present in normal human bone. Not profuse, nor consistent in appearance, but evident in multiple views. Note cutting blade did not sever them, indicating extreme durability. Slides were shown to mycologists to learn if fibers were fungi or bacteria. Mycologists said they were unlike anything they knew, but with 30,000 possibilities, they suggested a MALDI-TOF test to definitively rule out fungal or bacterial contamination. This view of these fibers, and others to follow, provide the first glimpses of a phenomenon that could prove to be entirely new.

We believe it would be irresponsible for us to close any avenue of exploration until hard evidence exists to justify doing so. We carry an obligation to continue to theorize that the Starchild Skull may be the result of alien interference, and to continue trying to prove ourselves wrong at every turn. That is how the truest scientific method is utilized.

They contend that it has other abnormalities such as the thickness, density, and strength of the bone that support their beliefs.

This is true, but it is far from complete as a list of the characteristics that have led to the theory that the Starchild Skull may be something other than entirely human. It should be noted that the author of this "Wackypedia" article fails to use a neutral unbiased tone, calling our theories "beliefs" and their theories "plausible scientific hypotheses," a clear violation of Wikipedia's guidelines (2010c).

Summation by Lloyd Pye: I hope anyone who reads this has no trouble seeing or understanding how unfairly the Starchild Project's efforts have been treated at the hands of Wikipedia and its biased editors and administrators. As much as I would like to argue that they are victims of the errors that they inaccurately reference, I think their continual "undoing" of our corrections and those of our supporters indicates that this is a concerted effort on their part. They obviously don't want the truth about what we're doing to be reported on Wikipedia for reasons we can only speculate, but which I theorize about in my article [Why Science Is Wrong](#).

The bottom line is this: we have references that meet their requirements (with the possible exception of the new DNA results, which have not been formally reported), we have highly credentialed and respected doctors and specialists who have authored reports about the skull, and there is no valid reason for their continued refusal to allow the evidence from these reports to be included in the article. I encourage anyone with Wikipedia skills to help us correct this article*, and all of you to spread the word about this injustice.

**Before any of you attempt corrections, please make sure that you are versed in the rules that they have for tone and style, because if people start making changes without proper phrasing, referencing etc. Wikipedia will lock the article and then no one can do anything with it for as much as several months. I also recommend that you use a dummy account, what Wikipedia calls "sock puppeting" to avoid having your primary account suspended should "they" take offense at your edits and block you.*

Search for "Wikipedia Censorship" to find additional examples of where Wikipedia is covering up evidence and truth. Try to avoid using the site and encourage others not to use it if they can avoid it.



Fibres – 3 - Rough/Smooth Cut

We call this a “claw,” for lack of a better term. Notice fiber-like things hanging on it, upward and downward.



See www.starchildproject.com for more information

This is only partly accurate. Several dentists have stated they believe the Starchild Skull to be a child in this age range (Robinson, 2004; Dr. David Sweet as cited in Pye, L. 2007, p. 148). However, other specialists unwilling to be named (Pye, L. 2007) felt that extensive wear on the crowns of the teeth (p. 126) and the extensive size of the roots indicate the skull belonged to an adult (p. 156).

DNA testing

DNA testing in 1999 at BOLD, a forensic DNA lab in Vancouver, British Columbia found standard X and Y chromosomes in two samples taken from the skull, "conclusive evidence that the child was not only human (and male), but both of his parents must have been human as well, for each must have contributed one of the human sex chromosomes".[1]

This quote comes from the 2006 re-dating of the 1999 Novella article, which was based on the invalid DNA test results from the BOLD lab in Canada. In 1999 the BOLD lab was a forensic teaching lab where students performed the majority of the work being done in it. The lab was not equipped in the many special ways necessary for handling samples more than 50 years old (the Starchild Skull is 900 years old).

After the lab's student technicians contaminated its first two attempts (Pye, L. pp. 153-162), they claimed to recover nuclear DNA from a "Y" chromosome (**not** the "X"). However, this was only 200 picograms of material, 1/5th of the minimum amount of genetic material normally required for a valid result. This small and dubious recovery was shown to be another contamination in 2003 by Trace Genetics, a DNA lab capable of recovering ancient DNA (over 50 years old), and whose founders (Dr. Jason Eshleman and Dr. Ripan Mahli) had previously worked on the high-profile Kennewick Man skeleton (Eshleman & Mahli, 2003). Dr. Mahli and Dr. Eshleman (2003) state: "[t]he inability to analyze nuclear DNA indicates that such DNA is either not present or present in sufficiently low copy number to prevent PCR analysis using methods available at the present time."

That statement means it was impossible to recover nuclear DNA from the Starchild Skull using the technology available in 2003, which made it equally impossible to do so four years earlier in 1999, thereby invalidating the BOLD result as yet another contamination.

Further DNA testing at Trace Genetics, which specializes in extracting DNA from ancient samples, in 2003 recovered mitochondrial DNA from both skulls. The child belongs to haplogroup C, while the adult female belongs to haplogroup A. Both haplotypes are characteristic Native American haplogroups, but the different haplogroup for each skull indicates that the adult female was not the child's mother.

This is correct and here is the missing reference: (Eshleman & Mahli, 2003).

Trace Genetics was not able to recover useful lengths of nuclear DNA or Y-chromosomal DNA for further testing.[7]

This is true up to a point. It fails to mention the critical fact that Trace Genetics was easily able to recover both mitochondrial and nuclear DNA on the first attempt from the adult human female skull reportedly found with the Starchild Skull (Eshleman & Mahli, 2003). That skull had the same general time of death as the Starchild Skull (Pye, L. 2007, p. 212), and was exposed to similar conditions post mortem (Pye, L. 2007, p. 21). Therefore, the Trace Genetics team expected the Starchild's nuclear DNA to be similarly easy to recover, and indeed the Mitochondrial DNA did recover easily. However, in 6 full attempts no nuclear DNA could be recovered from the Starchild Skull (Pye, L. 2007, pp. 177-183).

Explanations

Potential explanations for the skull's unusual features include the use of cradle boarding on a hydrocephalic child,[8] brachycephaly, Crouzon syndrome,[9] congenital hydrocephalus, or potentially progeria.[citation needed]

THE STARCHILD VS WIKIPEDIA (SHORTENED VERSION)

Intro by Lloyd Pye: We at the Starchild Project have repeatedly tried to correct the outdated and incorrect information about the Starchild Skull presented in the article on Wikipedia (which I refer to by the more appropriate name "Wackypedia"). Virtually no one realizes that Wikipedia's stated mission isn't actually to provide the truth about selected subjects, it is to determine the consensus opinion of what they think most people believe to be the truth (Wikipedia, 2010a). In fact, Wikipedia rejects any form of original research (Wikipedia, 2010b). The astounding fact is that current Wikipedia "quality standards" would prevent Darwin, Einstein, Edison, and many other geniuses from contributing their original research. This is why we call them Wackypedia, and it's why that name is so apt for the entire organization.

It is massively unfortunate that so many people worldwide consider Wikipedia a reliable source of information. By basing its "truth" on popular vote rather than actual facts, it distorts beyond recognition the entire purpose of science and science advocacy, of which it considers itself a bastion. This is not to say there is no truth or reliability in anything found in the mass of Wikipedia writings, but you can be certain that anything they feel is "alternative," or a challenge to what they perceive as their "status quo," will definitely be distorted beyond recognition.

Sadly, one or two Wikipedia administrators have made it their personal responsibility to prevent any meaningful edits to the Starchild Skull article, promptly reversing any changes back to the biased and error-filled text they prefer. Doubly sad is that this counterproductive practice is within the rights of any Wikipedia editor or administrator, accomplished with a single mouse click, and virtually nothing can be done to stop it. On many occasions we have made the effort to resubmit corrections to the article every time they were "undone," however this back and forth happened so many times and in such rapid succession that the article was locked, preventing any of us from making changes. When editing was finally permitted again, the article had been reverted to its original and incorrect state, and we were forced to accept that it would require significantly more public pressure to effect any real change to the flawed article.

Corrections:

Starchild Skull

from Wikipedia, the free encyclopedia, retrieved Sept. 12, 2010

The Starchild Skull is an abnormal human skull. ...

This statement is wrong because no one has ever proven that the Skull is entirely human. In his 2004 report, Dr. Ted Robinson referred to the Starchild Skull more appropriately as "a highly unusual human-like skull," which is far more accurate than Wikipedia calling it "an abnormal human skull."

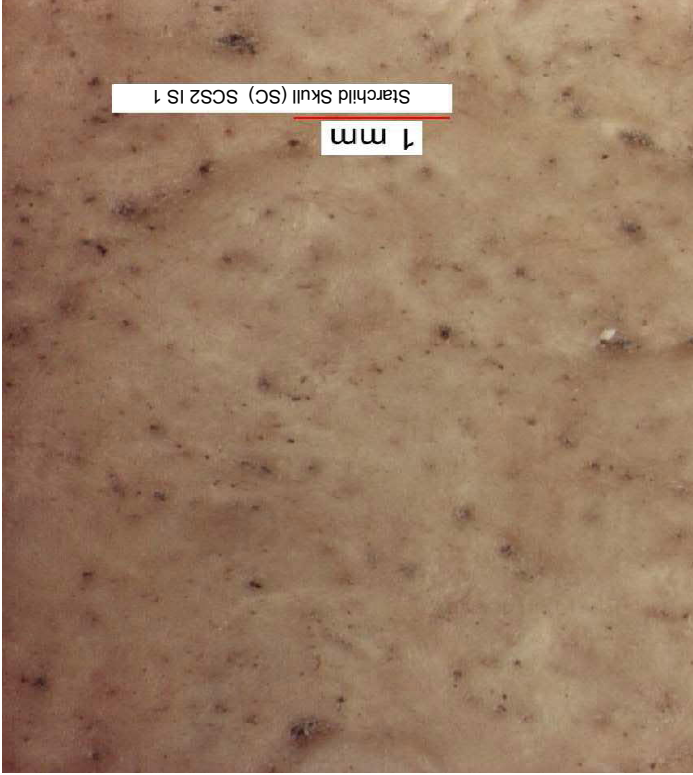
The Wikipedia reference for this statement is a poorly researched, badly out-of-date article written for the New England Skeptical Society in 1999, reporting the results of a nuclear DNA test done on the Starchild Skull's bone at the BOLD forensic teaching laboratory in Vancouver, B.C., which concluded that the Starchild was a human male (Novella, 1999). [Note: A detailed discussion of this article is available [HERE](#).] However, in 2003 the BOLD results were invalidated by Trace Genetics, a well-regarded ancient DNA lab in California that concluded the nuclear DNA could not possibly have been recovered using even the most sophisticated technology available to BOLD, and therefore their result must have been a contamination (Eshleman & Malhi, 2003). The 2003 test also indicated the Starchild Skull's paternal DNA was unlike normal human DNA (Eshleman & Malhi, 2003). As these are the only two DNA tests referenced by the Wikipedia article, and since human nuclear DNA was not recovered by either test, it is impossible for the article to state whether the skull is or is not human. In 2010 new DNA tests were conducted on Starchild bone using improved technology, and it was found that a significant portion of the nuclear DNA recovered does not correlate to any DNA yet found on Earth. Thus, there is simply no way to legitimately call the Starchild Skull a "human."



Cuts in Skulls for DNA Testing

COMPREHENSIVE LIST OF STARCHILD SKULL ANOMALIES:

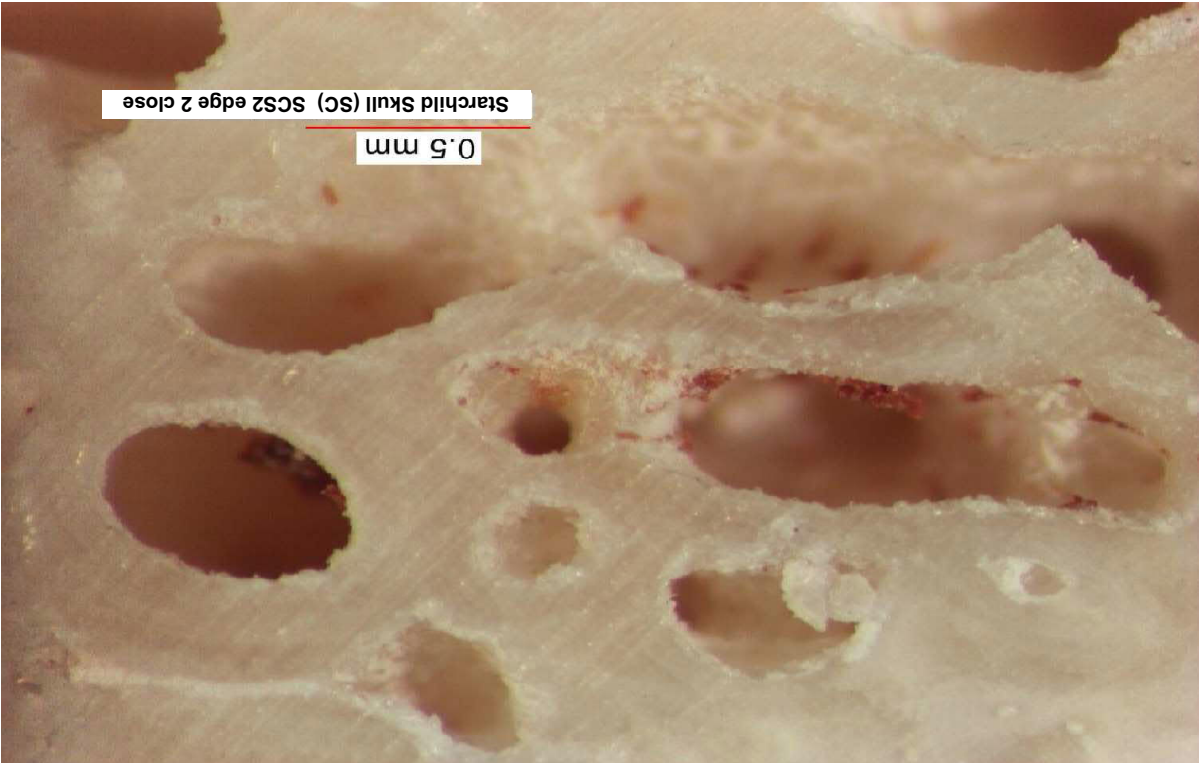
- The bone is like no other bone on Earth. Its biochemical signature is much richer in collagen than regular bone, making it more like tooth enamel.
- The bone is uniformly half as thick, or less, than normal human bone. It is not thin in a specific area or areas due to abnormality, it is thin all over.
- The skull itself weighs half as much as human skulls of comparable size.
- The surface of normal human bone is liberally sprinkled with what are called lacunae, which perform the vital function of replacing old bone cells with new ones. Astonishingly, the Starchild bone shows no lacunae.
- Inside the matrix of the Starchild bone is woven a variety of what we now call "fibers" but which might be something else entirely. All we know is that these fibers are highly durable and completely inexplicable. No other bone known on Earth has anything even approximating such fibers.
- Inside all bones are cancellous holes. They produce and carry marrow. After death, bacteria scour those holes sparkling clean of all marrow. The Starchild Skull exhibits a reddish residue in many of its cancellous holes. We have no idea what it is, but it, too, is unique among all Earth species.
- In the front of the Starchild Skull, the mid-face is completely different from a typical human. The entire mid-face is greatly reduced in size.
- It has no brow ridges, which all primates have. Its forehead is smoothly curved straight down to its upper eye sockets, unlike any higher primate.
- When a human forehead reaches its upper eye sockets, normally there is a sharp drop down to the pinched-together bones that create the upper nose. In the Starchild there is no drop. The nose extends straight and smooth from the forehead, staying wide and flat until the point where it is broken off. This is wildly different from not just humans, but from all other higher primates.
- The Starchild Skull's eye sockets are two of its most unusual features. Normal human eye sockets are 2 inches deep and shaped into rectangles. The Starchild's are 0.7 inches at maximum depth and curved into ovals.
- The optic foramina are the openings in the back of a human eye socket which let in the optic nerve and all the other nerves and blood vessels that "feed" each eyeball and allow it to function. Muscles surround each one to make them move in all directions while they remain deep in the sockets.
- The Starchild's optic foramina have shifted dramatically downward and inward so they rest against the nose at a position of 5 o'clock. Any human-sized eyeballs attached to them would bulge off the face like frog eyes, a dangerous situation for any child growing up with eyes easy to dislodge.
- The inner surfaces of the Starchild's eye sockets appear to any visual inspection to be perfectly smooth. No convulsions can be seen on their surfaces. Yet the sensitive nerve endings of a forefinger can feel distinct convulsions in each eye socket, and each one is exactly the same. Such incredibly precise symmetry is rarely seen in humans, and can only have come from a much different set of genetic instructions than humans get.
- The Starchild Skull had no frontal sinuses, not even miniscule vestiges. Humans can be born with sinuses reduced to the size of peas, but we have found no report of a human born without any vestige of frontal sinuses.
- All that remains of the Starchild's lower face is the right side maxilla. The roof of its mouth was flat, lacking any sign of the human arch, and its size is that of an infant rather than a size appropriate to its cranium size.
- The Starchild's zygomatic arches (cheekbones) are broken off, but both ends of the breaks present unusual



Comparison of inner surfaces shows stark difference. Recall that Human remained on surface of mine tunnel, while SC was buried for 900 years. Even buried, at least some degree of encrustation might be expected. Its absence is puzzling.

Human/SC Inner Surfaces

Closeup Reddish Residue



We have no idea what this is, but are compelled to find out. The possibilities are: (1) organic desiccated marrow; or (2) inorganic mineral residue. If mineral, what could it possibly be? If marrow, then DNA tests already carried out should have recovered nuclear DNA. If nuclear DNA was present but not recovered with the usual primers for ancient DNA, it becomes at least possible that the DNA of this sample is configured in an atypical human pattern.

Backlit Cross Section SC



Another piece of polished SC bone, unfortunately flipped upside down when being labelled. Nonetheless, a reddish residue is evident here too, clinging to upper and lower surface of cancellous holes. Again, bacteria should have scoured this clean; after 900 years nothing should be here— nothing.