

The Starchild Skull



The Starchild Skull is similar to a human skull - with all eight of the major human components evident—a frontal bone, two sphenoids, two temporals, two parietals, and an occipital. However, each component is profoundly redesigned, with the bone itself astonishingly reconstituted into something uniformly 1/2 as thick as normal, weighing 1/2 as much as normal. Choose 30 points of reference on it and compare them to the average of the same 30 points on 100 normal skulls. The result falls 10 Standard Deviations from the statistical norm—well off the chart.

THE
Starchild Project

WWW.STARCHILDPROJECT.COM



Collected from the writings of Lloyd Pye

www.starchildproject.com and www.lloydpye.com

Dedication to Lloyd Pye

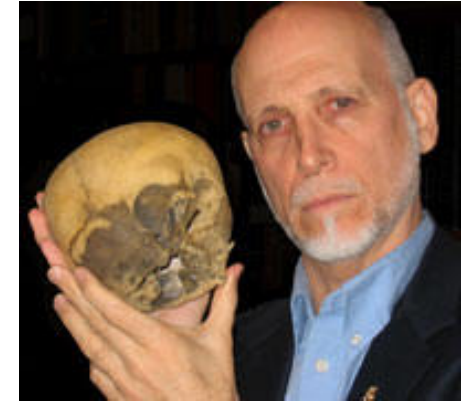
This booklet/pamphlet is dedicated to my friend **Lloyd Pye**, who died from Lymphoma Cancer on Dec 9th 2013. He is sorely missed, both as a friend, and as a diligent and sincere researcher, author and authoritative and enthusiastic speaker.

I first met Lloyd in 2004, when he had made a trip to London to undertake new research into the “Starchild” Skull. I was honoured to meet and help him with some IT related matters. I couldn’t believe he didn’t already have some support in the areas I gave him a little bit of help with. It was clear to me that the **Starchild Skull** was a relic of vast importance. I was immediately friends with Lloyd – his sharp mind, warmth, humour and humility were a rare combination. Within an hour of that first meeting, these qualities, along with his expression of gratitude to me, cemented a decade-long friendship. Over this period, I had the pleasure of accomodating Lloyd on several occasions and he was always gracious and appreciative. He was a friend to everyone he met. We shared the desire to pass on important information we had learned - to anyone that would listen.

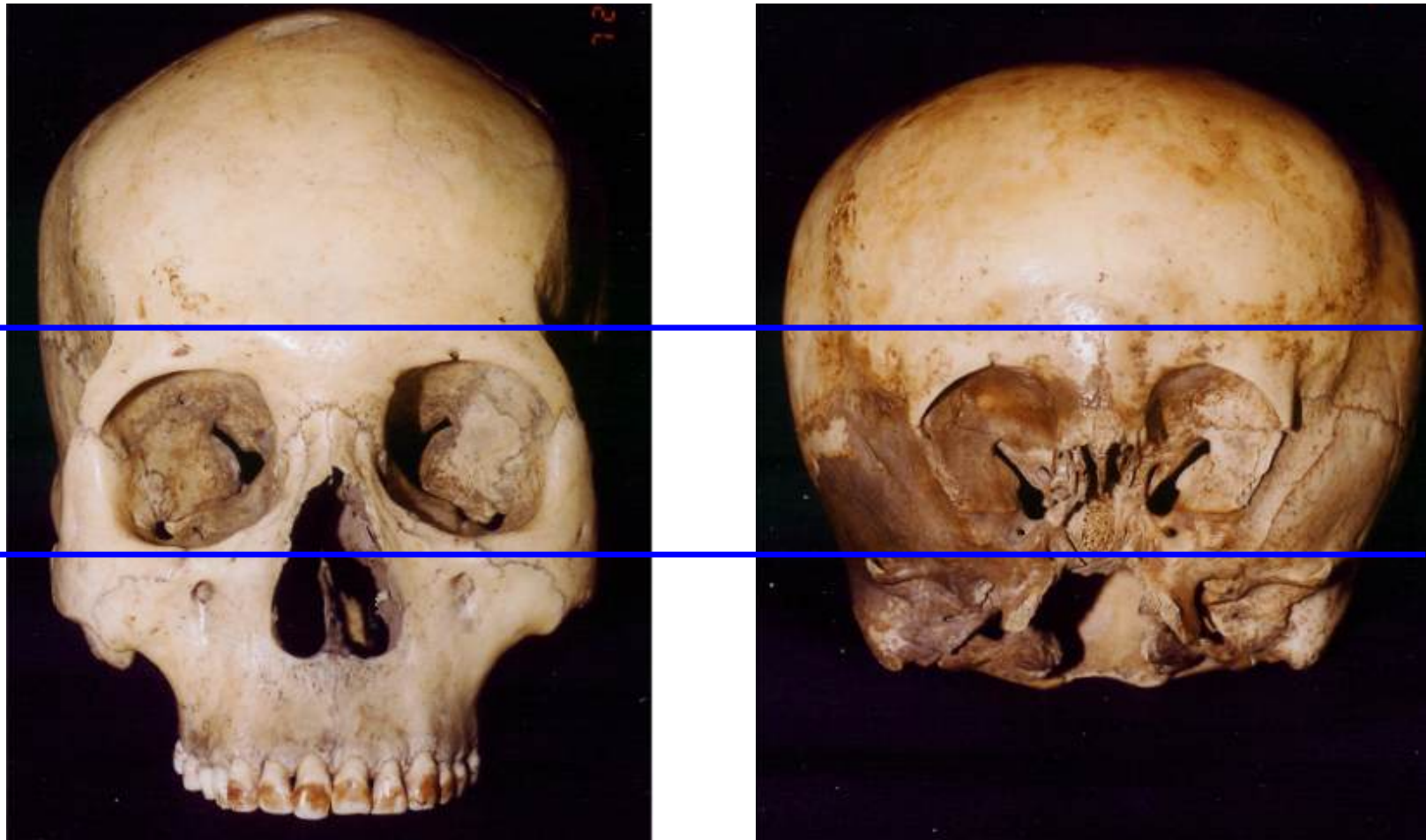
Lloyd even came along to at least 2 of my own presentations - he was also interested in what I had to say. I learned a great deal from Lloyd – not just about the Skull, but about The Electric Universe, Hominids and Hominoids, and important facts about human “evolution” (as it is called) that few other people discuss. I also learned from his experiences in dealing with scientists who would not look at the most important evidence that had ever been put under their noses – and those that *did* look at it, but wished to remain anonymous.

I shared his frustration when they refused to *look at the evidence* – or when they acted like they couldn’t even see it. I also shared his delight when we would see people open their mouths in wonder – and try to comprehend why they had never heard about the Starchild Skull before...

I hope that by reading this booklet you will, like I did, learn about world-changing evidence and consider it carefully. Who knows, maybe it will have the same profound effect on you as it did on us...and you will choose to try and share what you have learned with others...

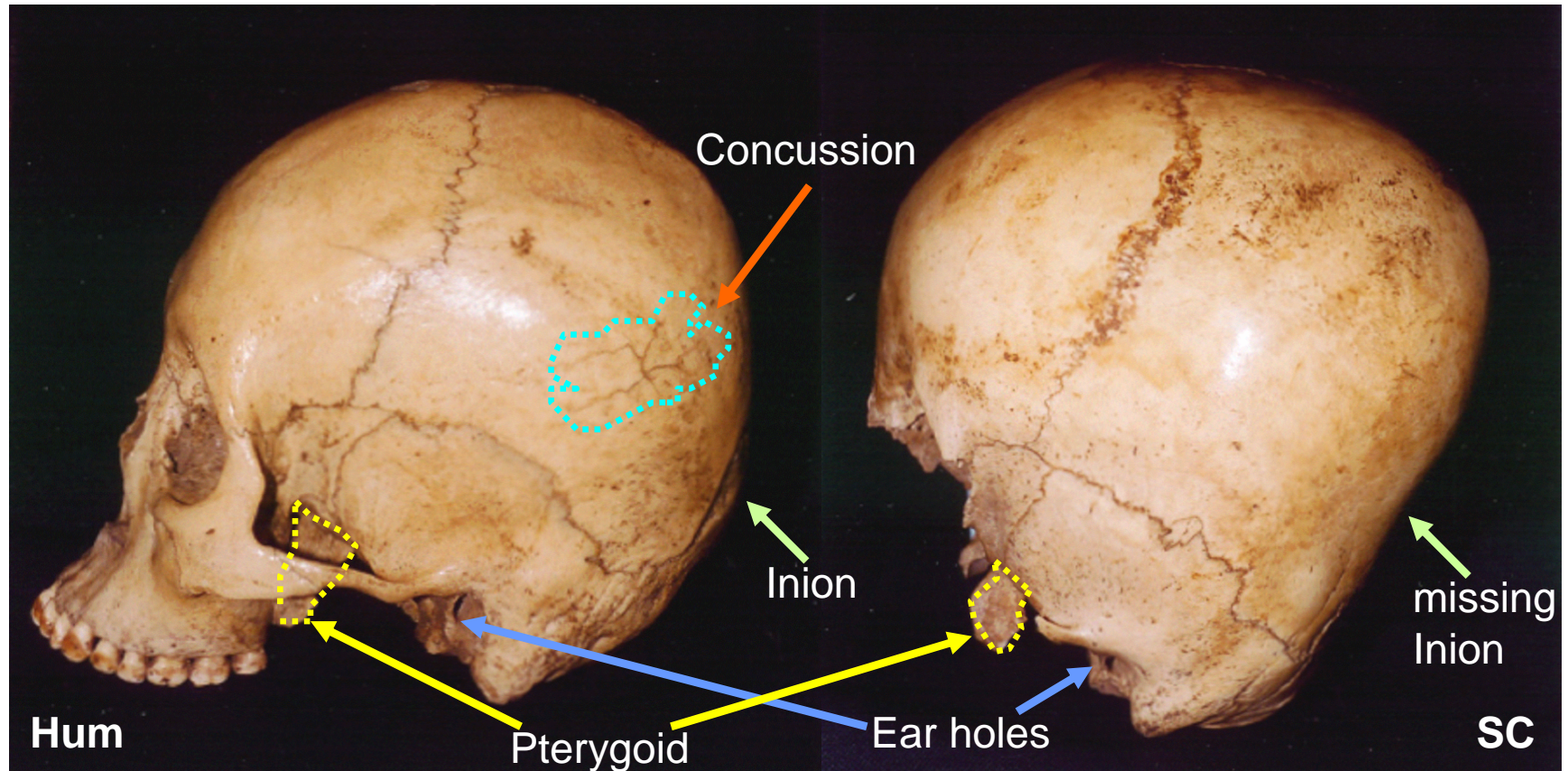
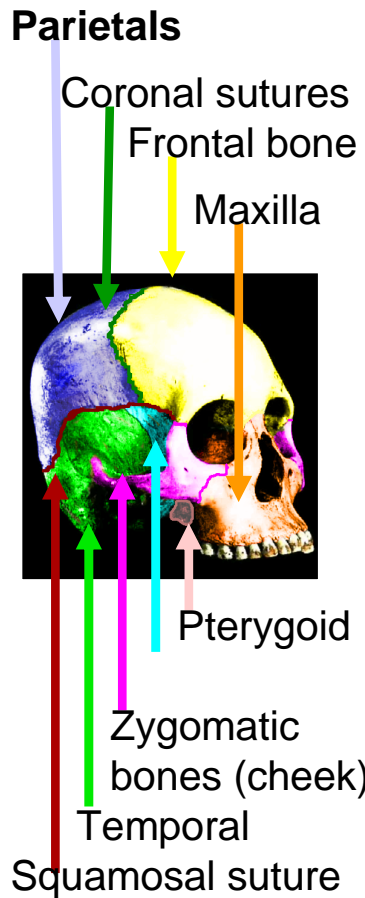


Front View



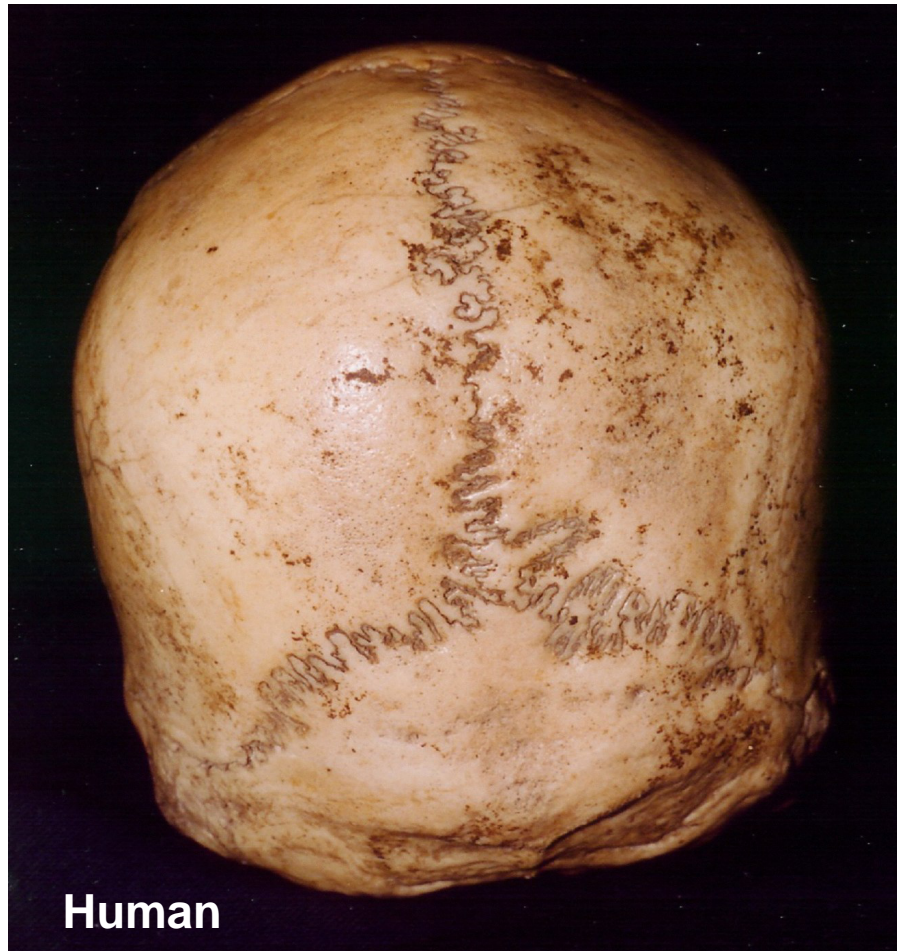
Human female (HF) found with Starchild Skull (SC). Both size of a small adult or 12-year-old. SC has no brow ridges, no dip from brow to nose. Nose widths equal. Human's eye sockets 2" deep; SC 1/2" deep. SC optic foramens (slits) lower by 1/2". SC eyeballs—if present—rest in middle of nose, require 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.

Profile of Human (HF) and Starchild Skulls

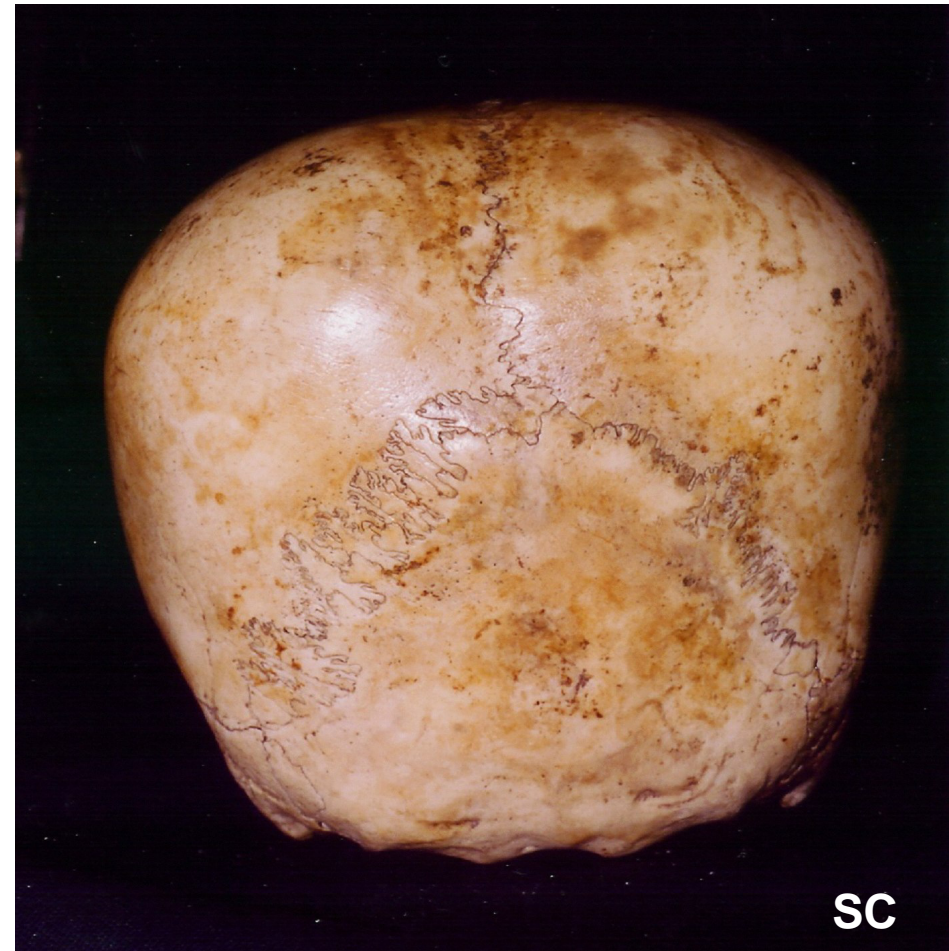


Same parts; frontal, sphenoid, temporal, parietal. Note HF concussion rear middle of parietal. HF cradle-boarded in infancy; occipital (rear of head) is flat as board it was strapped to. SC has normal convolutions across occipital; not cradle-boarded or bound in any way. HF has 1200 cc brain. SC has 1600 cc's angled steeply down onto a cerebellum base 1/4 to 1/3 normal size. Reduced cerebellum (lower brain) has greatly reduced internal struts (transverse ridges) to support a much greater volume of cerebrum (upper brain). SC inner ears roughly 50% larger than normal.

Rear View



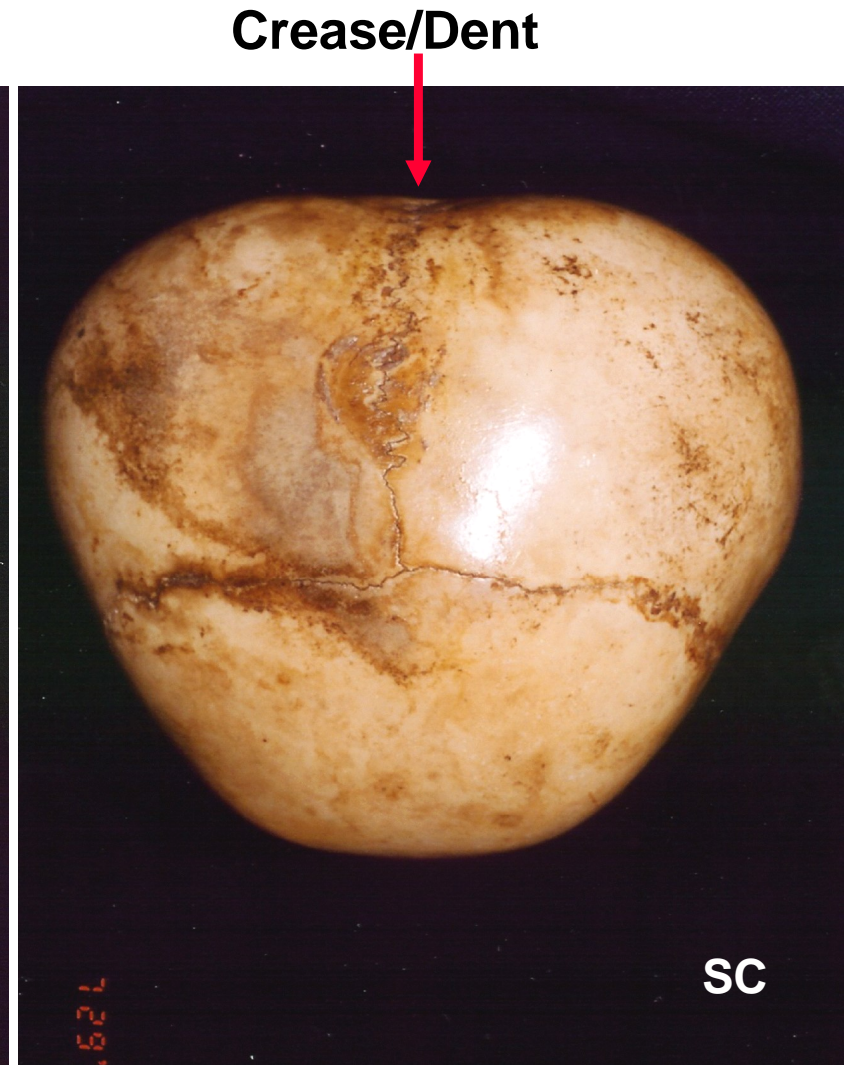
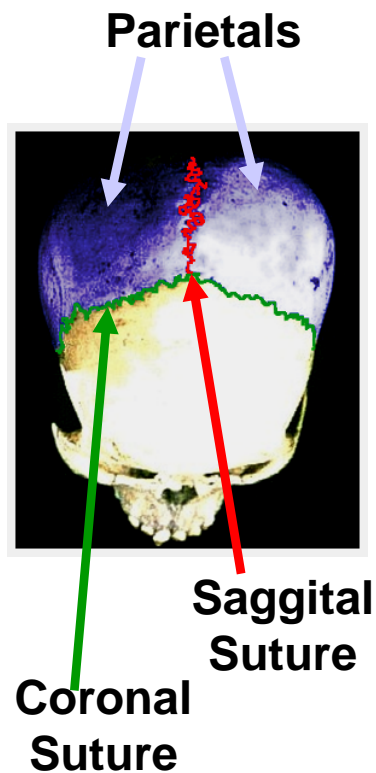
Human



SC

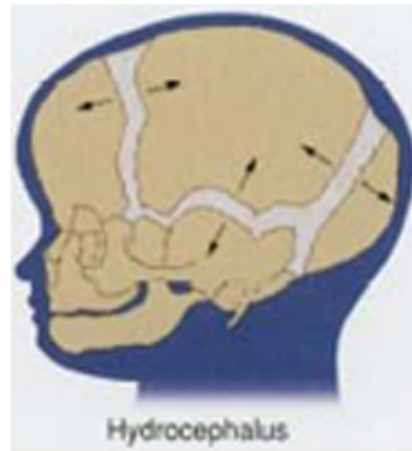
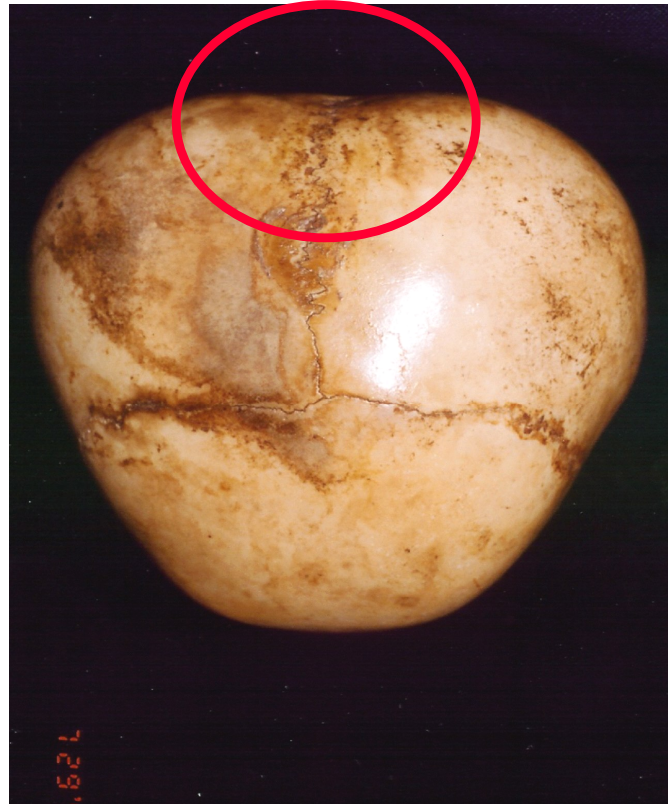
SC occipital stretched high and flattened, though not as flat as if cradle-boarded. It lacks an inion (bump at back of human skulls). HF inion (at bottom) has wide fossa (depressions) on sides. SC inion should be at circle of dark flecks in mid-occipital. Only slight fossa remains. HF neck muscles sweep 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 lambdoidal suture (against left parietal) is indication of an age at death beyond childhood.

Top View of Human and SC



Tilt angles in these shots not quite equal; SC tilted more forward than HF. Coronal sutures on view. All sutures of both skulls healthy; no premature fusing. Stains on SC due to soil it was buried in. Shine on both due to an application of shellac for preservation at some point after discovery. Again note difference in crowns. SC has a “crease” of highly uniform depth and breadth across entire rear of upper crown, ruling out upward pressure from hydrocephaly (water on brain).

Is The Starchild Hydrocephalic? ⁸

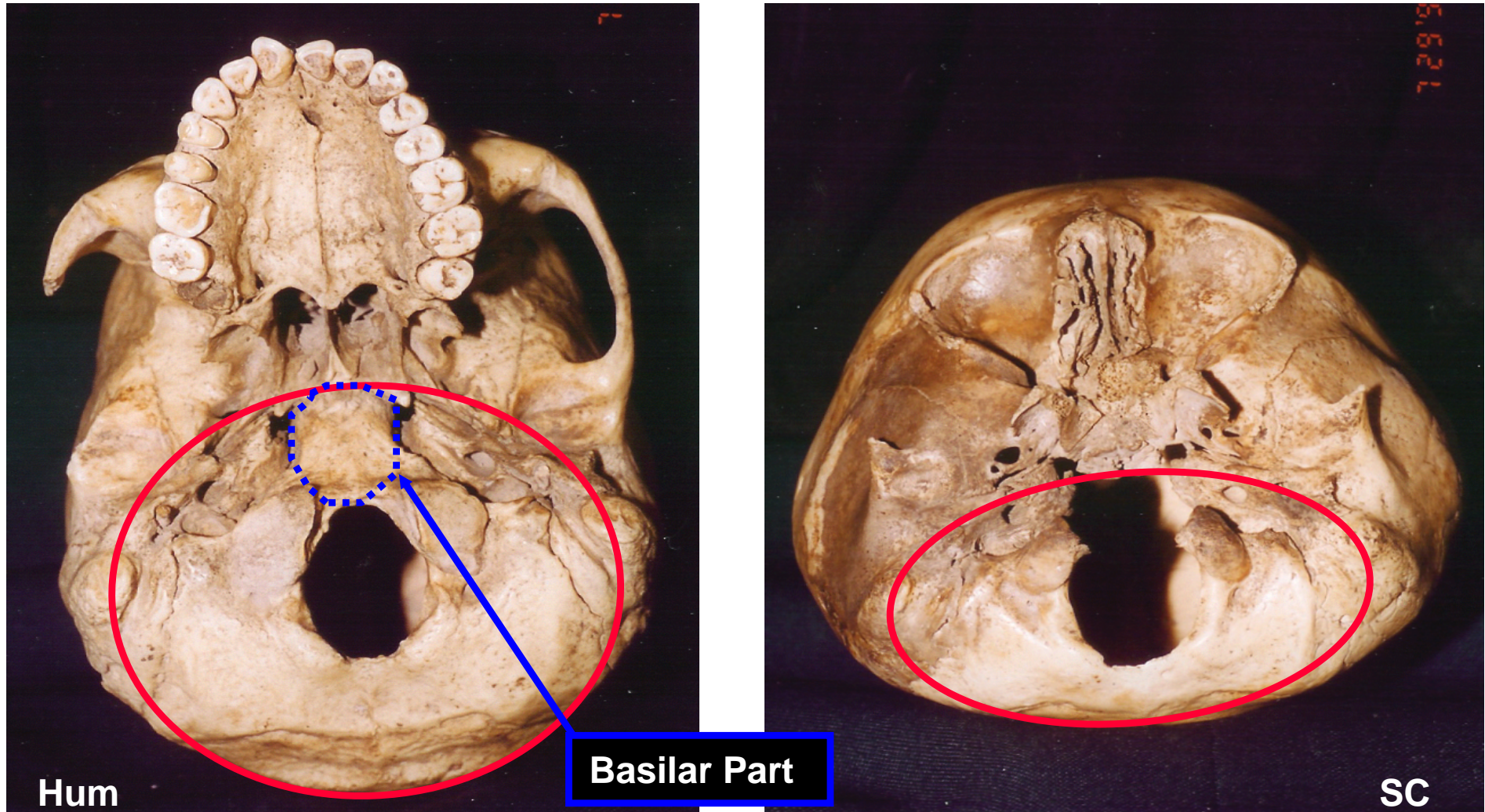


HYDROCEPHALY



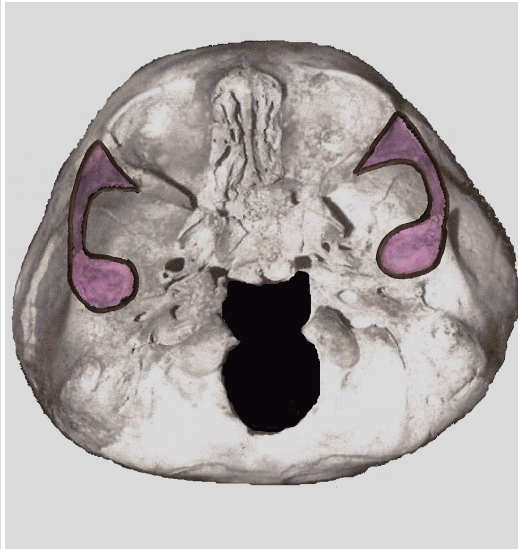
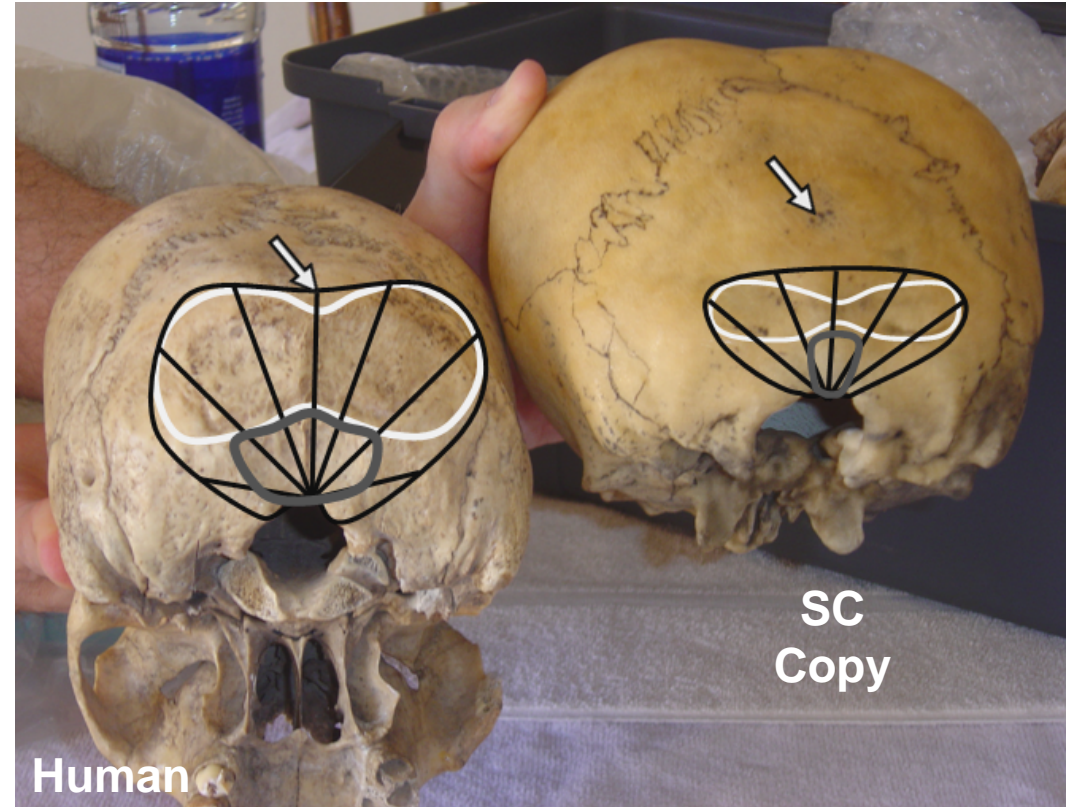
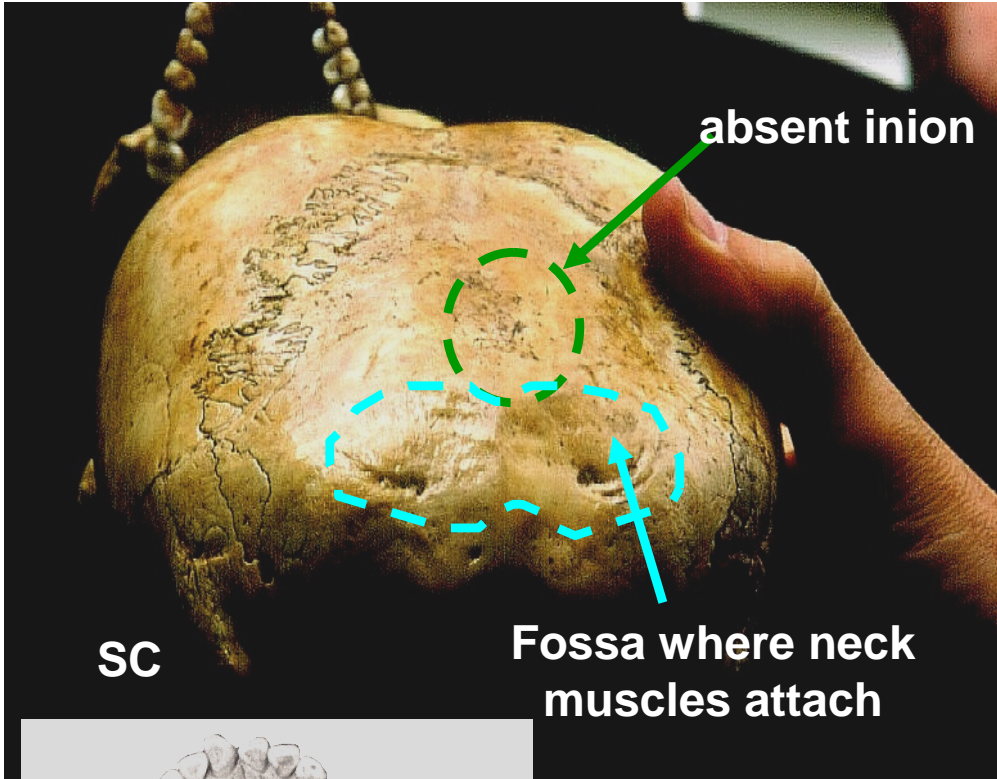
STARCHILD SKULL

Neck Sizes of Human and SC

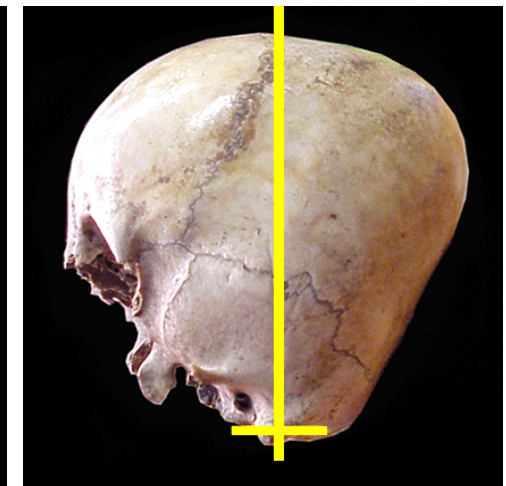


Basilar Part in front of foramen magnum (neck hole) is normally fused by age 25. Absence in SC indicates less than 25 at death, though it could have snapped off at some point. Note great reduction of SC's lower face connection points (condyles, mastoids, mandibular fossa, zygomatic bases). If SC is adult, lower face less than 1/2 normal. Note bone plates where neck muscles attach—HF surface area is at least twice SC's. Note HF cheekbone (zygomatic arch)—allows two average male fingers to easily fit under; two soda straws would fit under SC's if it were present. Note HF maxilla (teeth and roof of mouth). Part of SC maxilla will be seen later.

Neck Muscle Attachments & Zygomatic Arches



Balance Points of Craniums



Area of Chewing Muscles



Chewing muscles leave imprints on the sides of skulls that reveal where they were attached in life. Notice SC's chewing muscles are roughly half normal size on both sides of skull. The mandibular fossa—the dents in the skull where the mandible (lower jaw) fits—indicate a very narrow lower face, also in the range of half normal size. If such extensive reduction of muscle mass were to have been the result of a natural deformity, how would its genes know to also halve the size of the jaw?

CAT Scan, Braincasts (Done in 2013)¹²

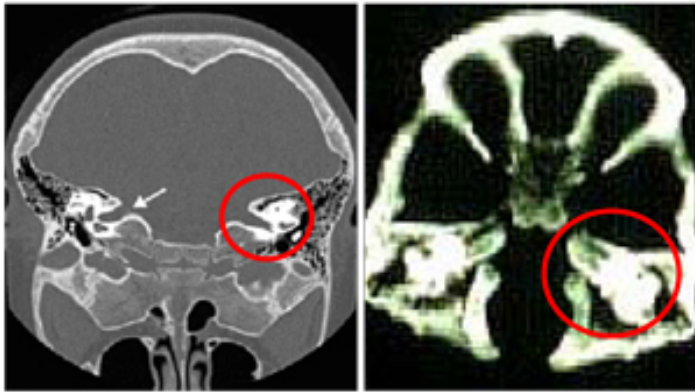
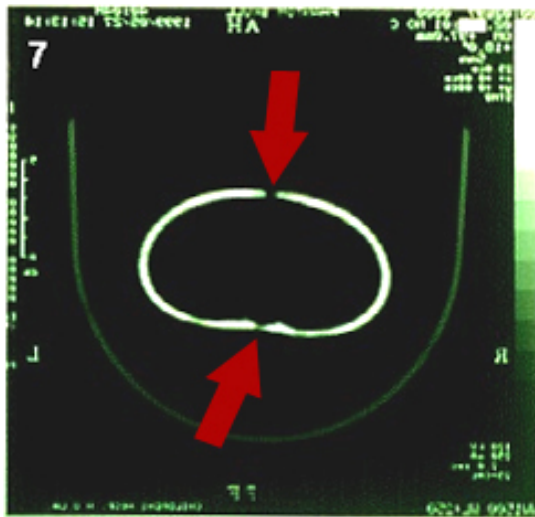
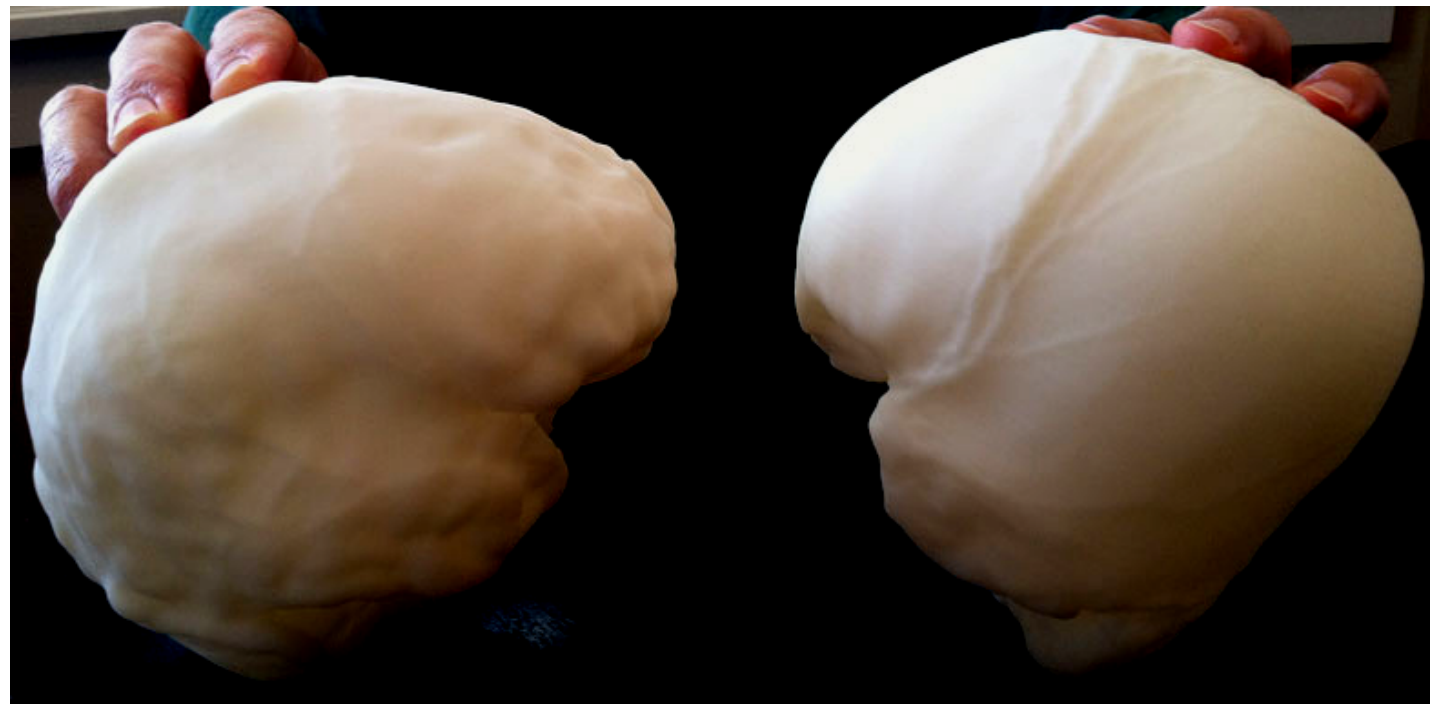


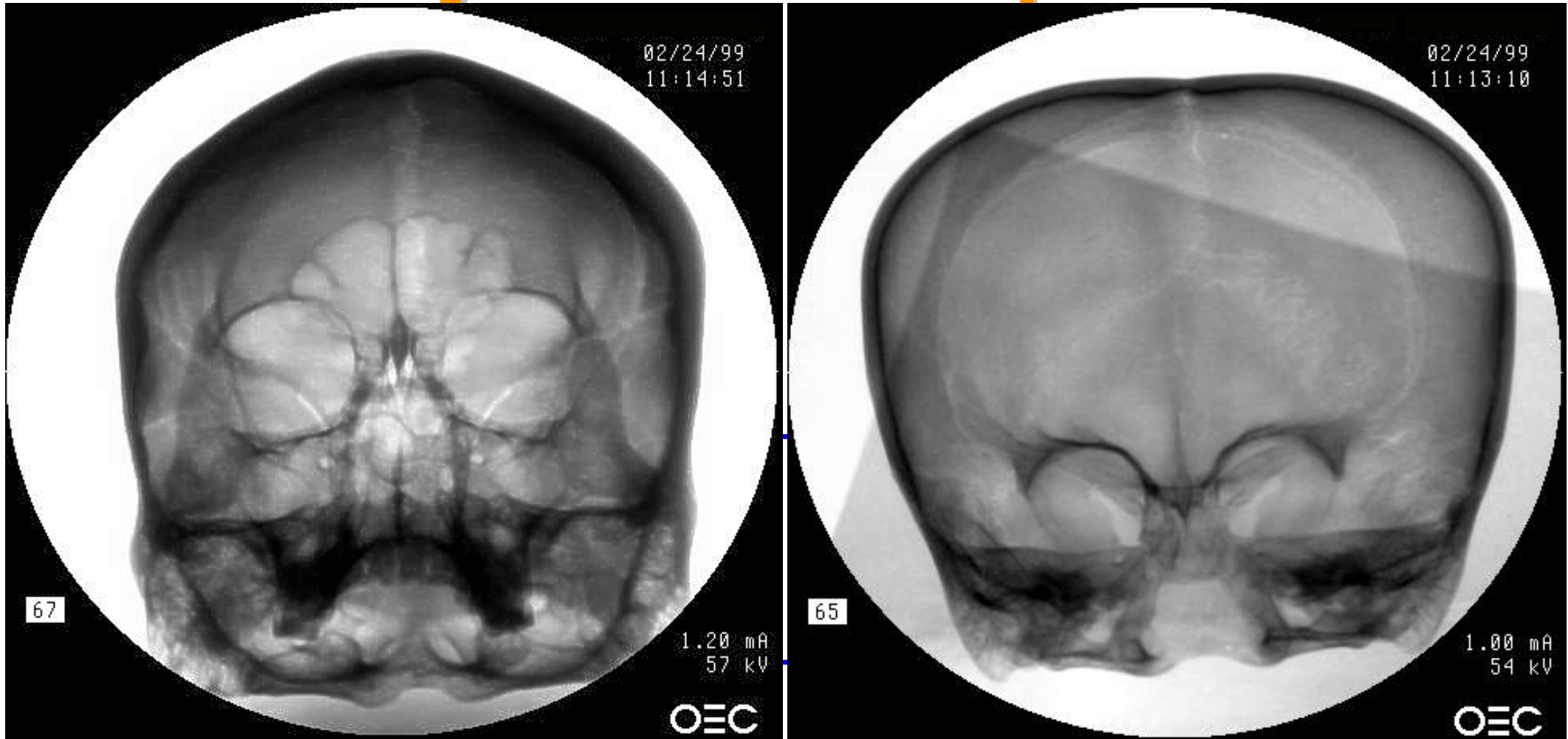
Fig. 6. CAT scan shows much larger inner ears in the misshapen skull (right) as compared to the human skull (left)



Starchild Skull CT Scan Image showing open, healthy suture lines

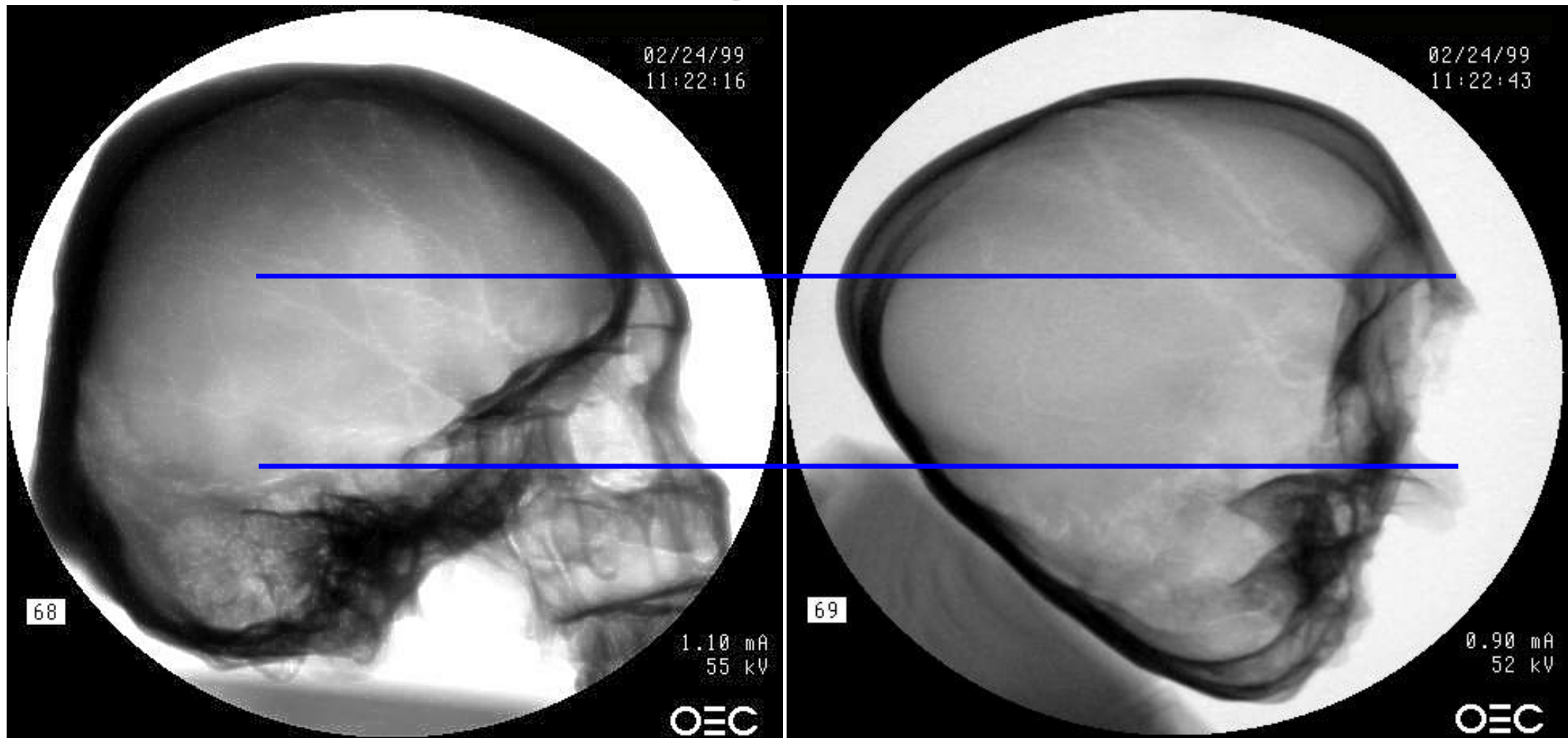


X-Ray Sinus Comparison



HF frontal sinuses behind eye sockets, look like cauliflower. No trace of frontal sinuses in SC, not even vestiges or nubs. Highly unusual. Note “afterimage” of brain-within-brain in SC. Too symmetrical to be water atop brain. No idea what it means. Also note in SC eye sockets the round shape, lower placement, and odd upsweep at upper outside corners. No idea what this means, either, but different enough from HF to be worth noting. Actually, differences here are numerous.

X-Ray Profile



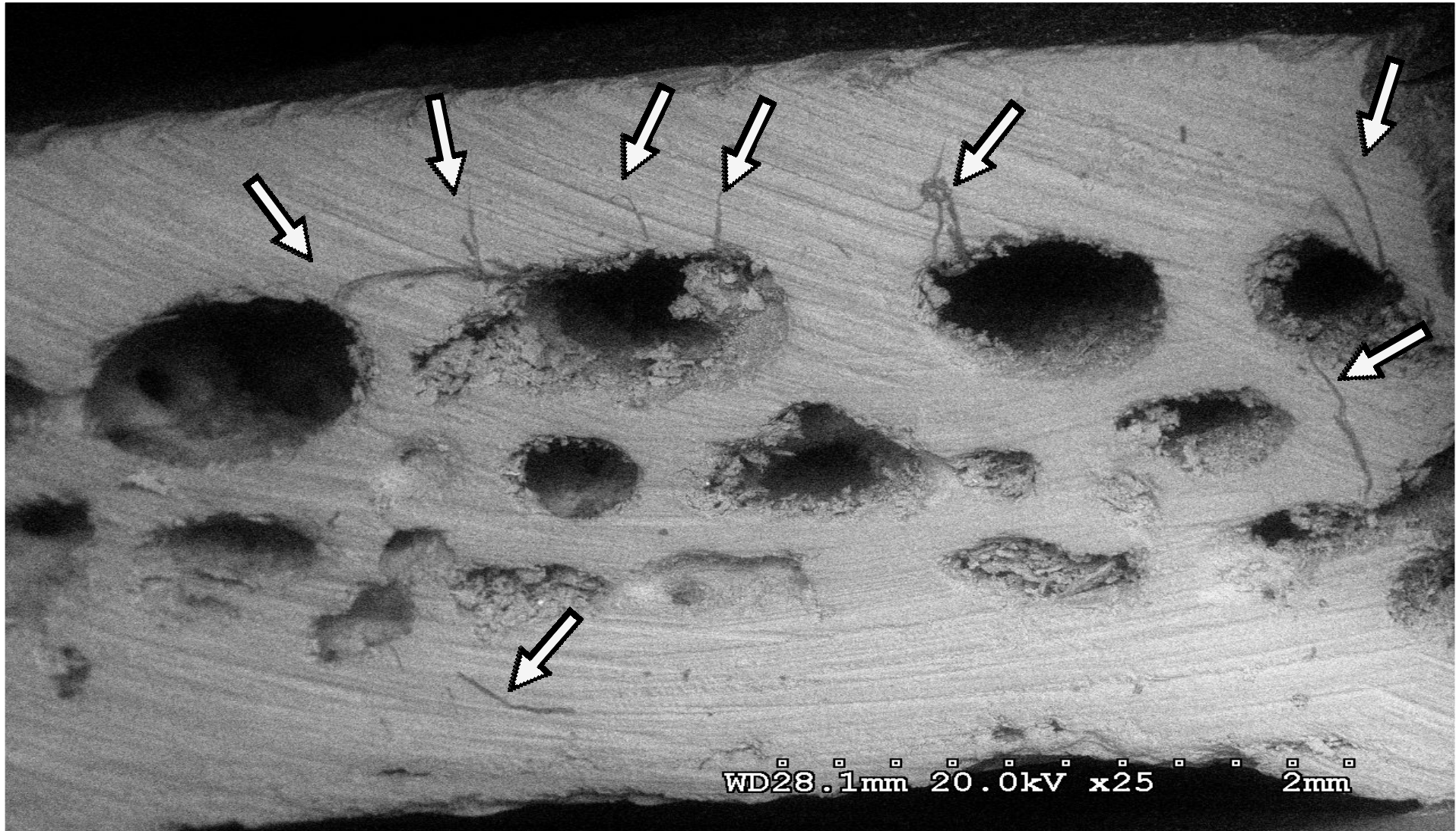
Despite parallel eye sockets, images not balanced. SC forehead tipped higher than normal position during X-ray process. HF classic example of cradle boarding. Flat as the board it was strapped to from top of crown to top of inion (bump at back of head), where neck muscles must attach. SC has no inion 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.

Rt. Maxilla—2 Deciduous Molars



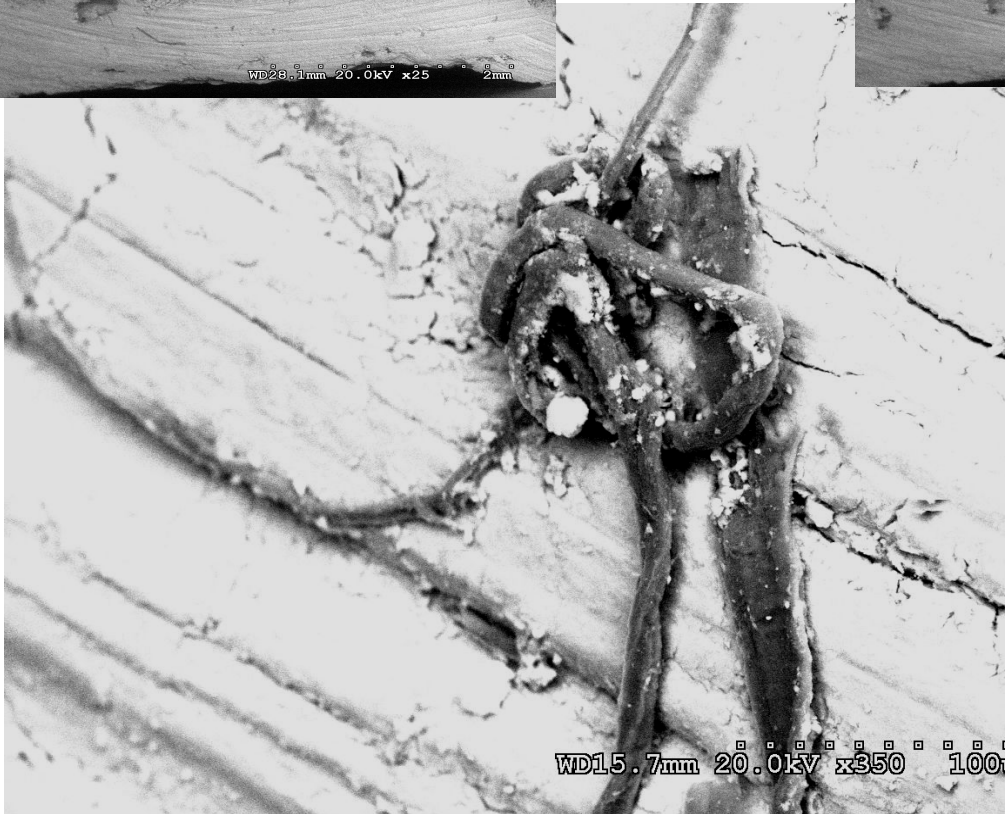
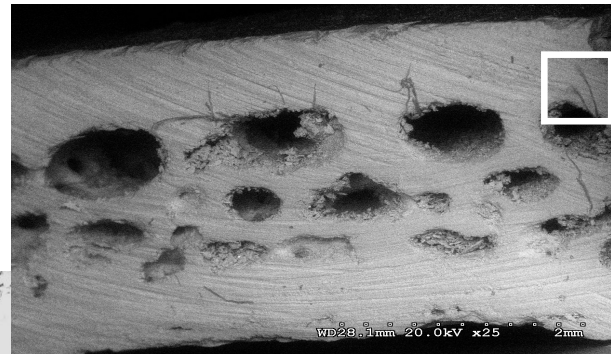
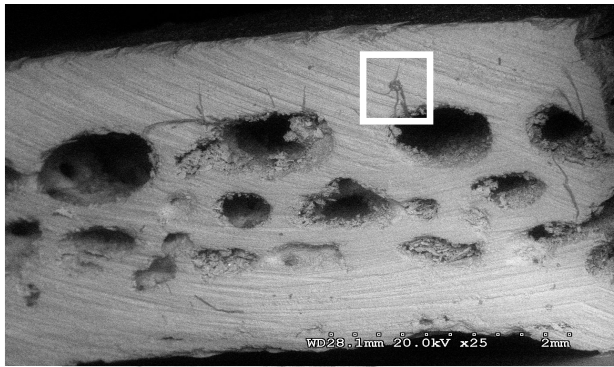
Maxilla piece recovered with SC skull. In left image, smooth curve from top middle to left center is nasal passage; thus, SC had nose opening (if not a nose) similar to humans. Unlike the missing frontal sinuses, maxillary sinuses are present. Above two teeth that are visible, and also visible at the tops of the three extraction holes, other teeth are impacted into bone, suggesting child's teeth. Arrangement of teeth also suggests first dentition. Larger tooth is now gone, sacrificed to first DNA test, but small one remains in situ and is seen in extreme close-up in next slide.

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.

Fibres: “Knot” and “Threads”



Knot: At first glance, characteristic of capillaries (too small for veins). Closer analysis does not bear this out. Until tests are completed, we will not know if it is organic or inorganic. We have no idea how it could have been tied into a knot under the pressure of bone cutting, much less how it survived the process. Everyone who has seen it is baffled. Serious explanations are welcomed.

Threads: Found near the knot, yet completely different in size, shape, and apparent texture. More like threads or hairs than capillaries tied into a knot. Here, too, we have no idea what to say until tests reveal biochemical makeup.

Fibres – 3 - Rough/Smooth Cut



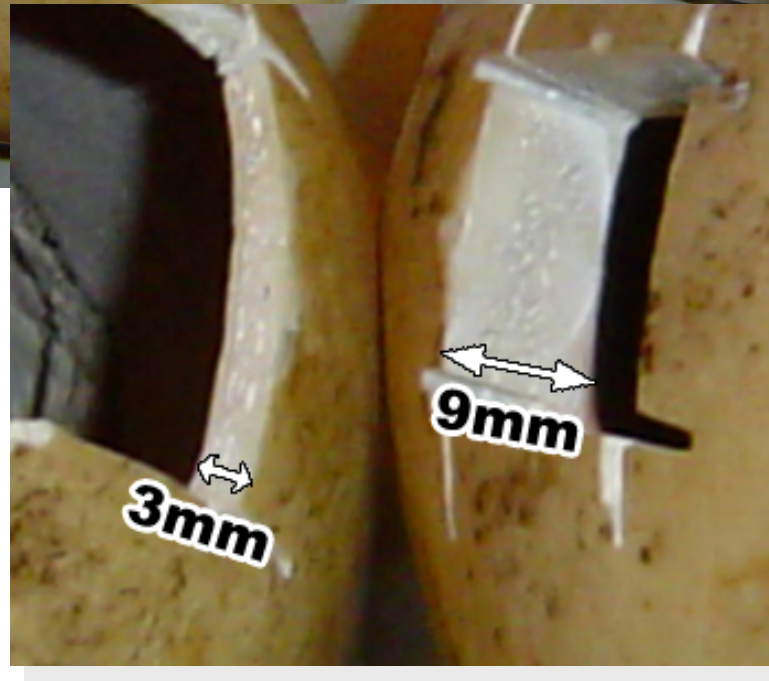
We call this a “claw,” for lack of a better term. Notice fiber-like things hanging on it, upward and downward.

Fibres – 4 - Above “Claw”

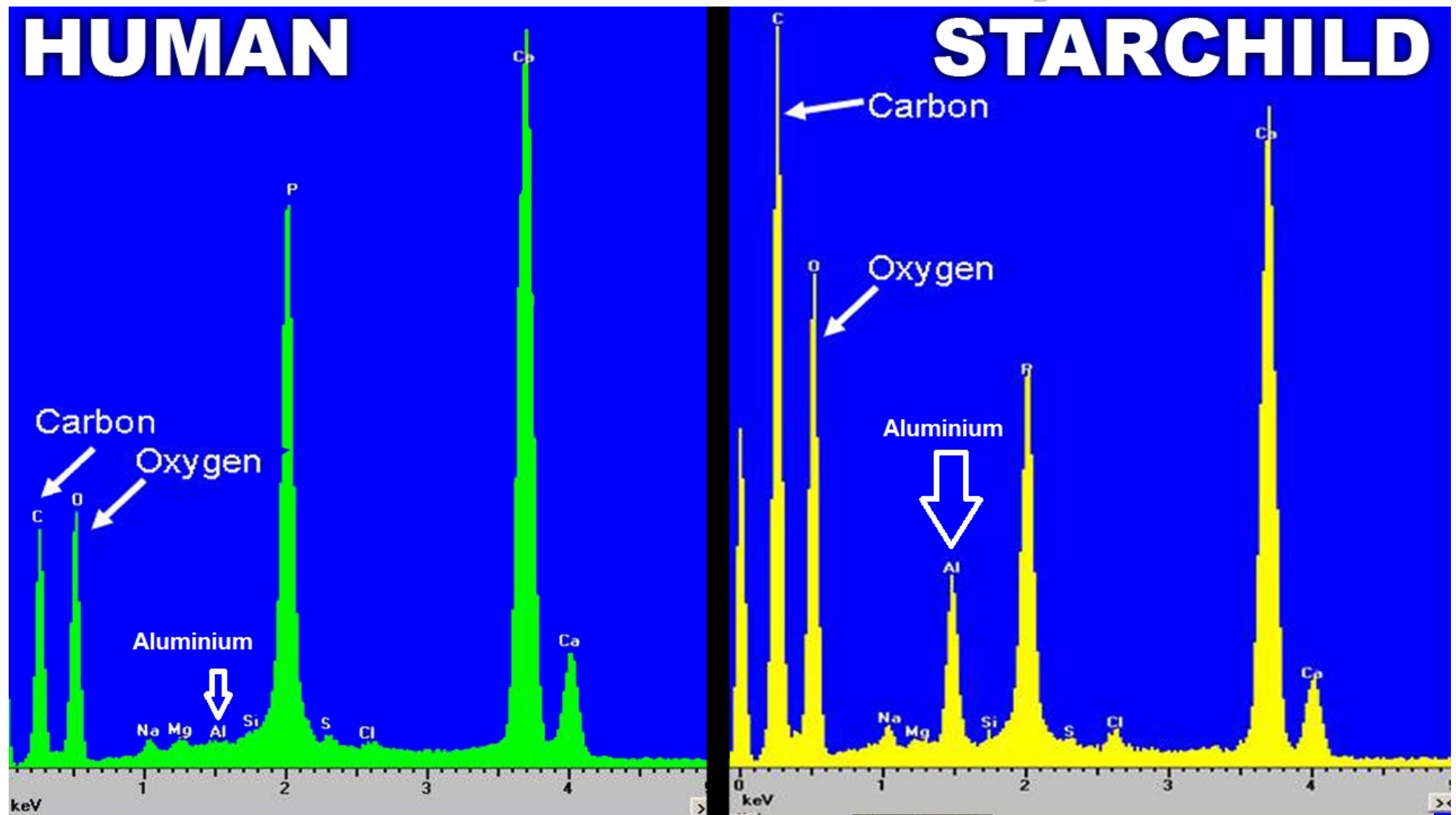


“Button” is now near center. We think button is remnant of another kind of fiber, or the snapped-back base of one like the one on view. We can’t tell. Notice a piece extending opposite button, on other side of fiber.

Cuts in Skulls for DNA Testing

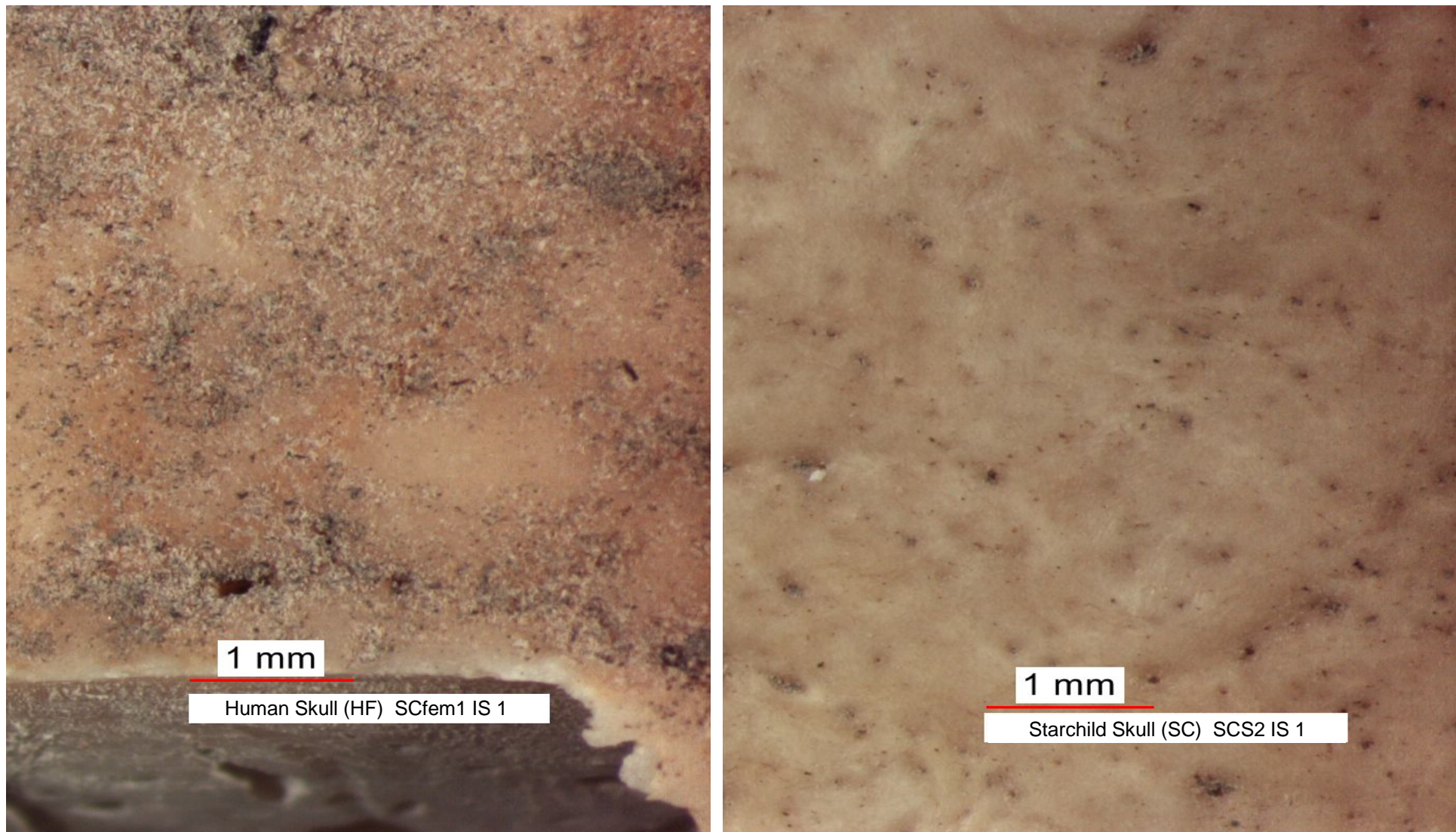


Bone Chemistry



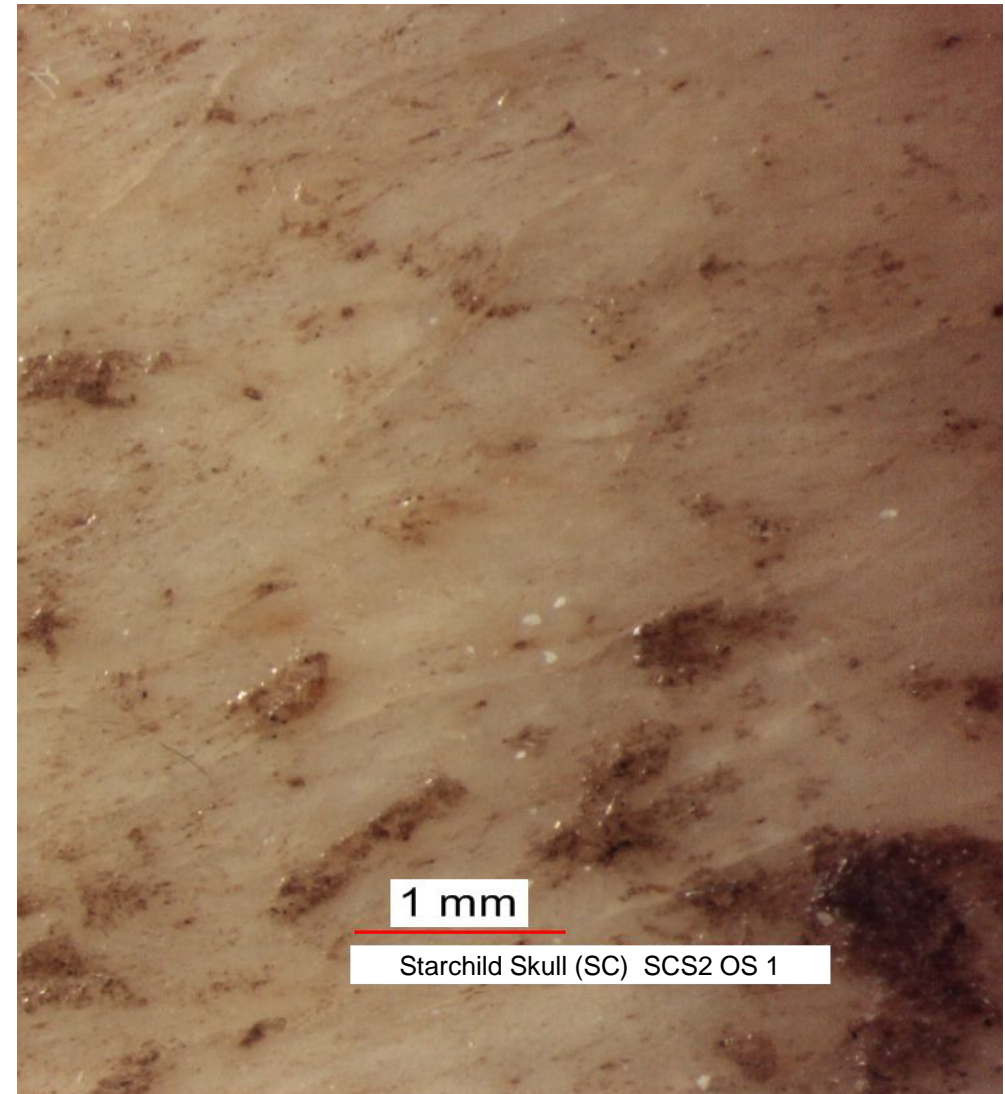
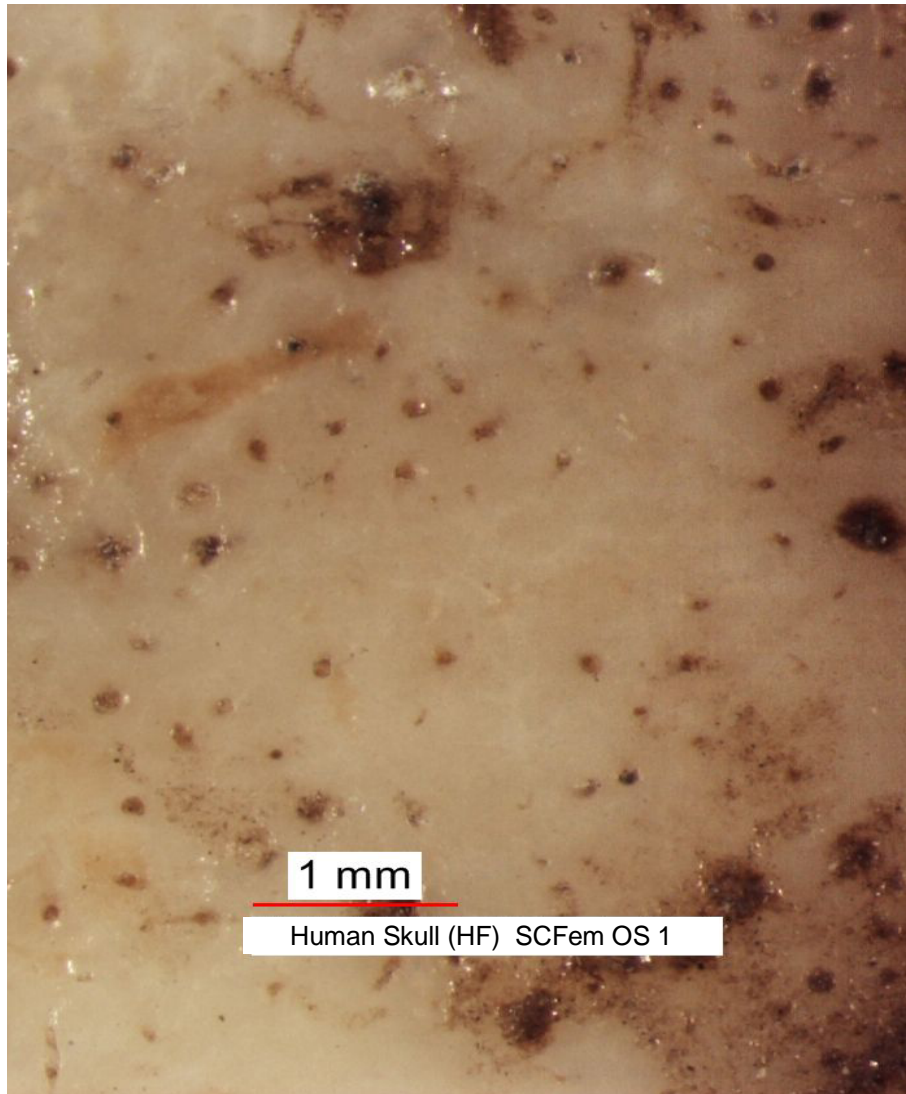
This elevated aluminum spike came in the first S.E.M. analysis of the SC bone. Aluminum is poisonous to humans in these quantities, so we assume it arrived by contamination. However, we can't think of a viable way for a skull buried in a mine tunnel to be contaminated by aluminum without water as a dissolving medium.

Human/SC Inner Surfaces



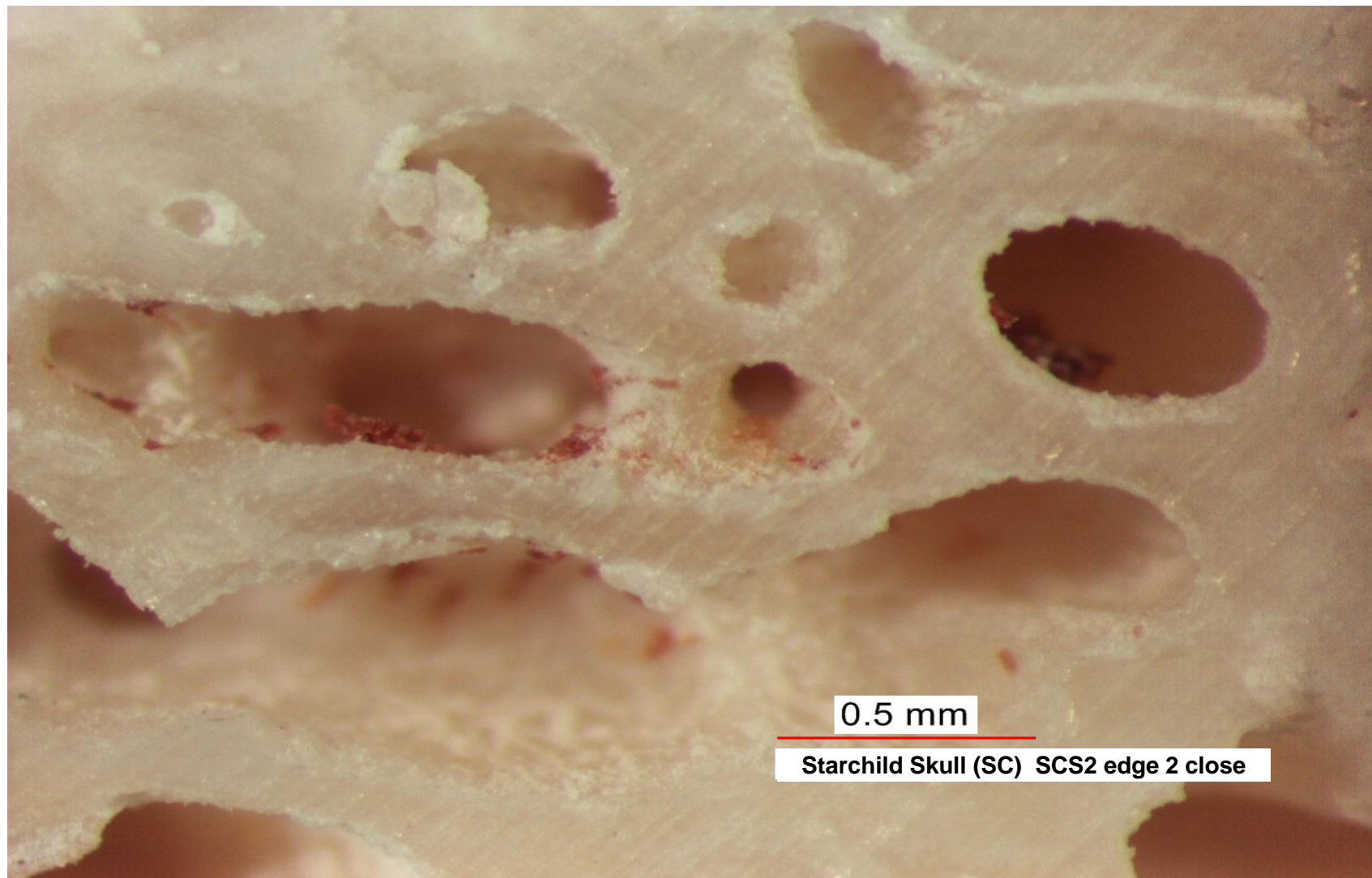
Comparison of inner surfaces shows stark difference. Recall that Human remained on surface of mine tunnel, while SC was buried for 900 years. Even buried, at least some degree of encrustation might be expected. Its absence is puzzling.

Human/SC Outer Surfaces



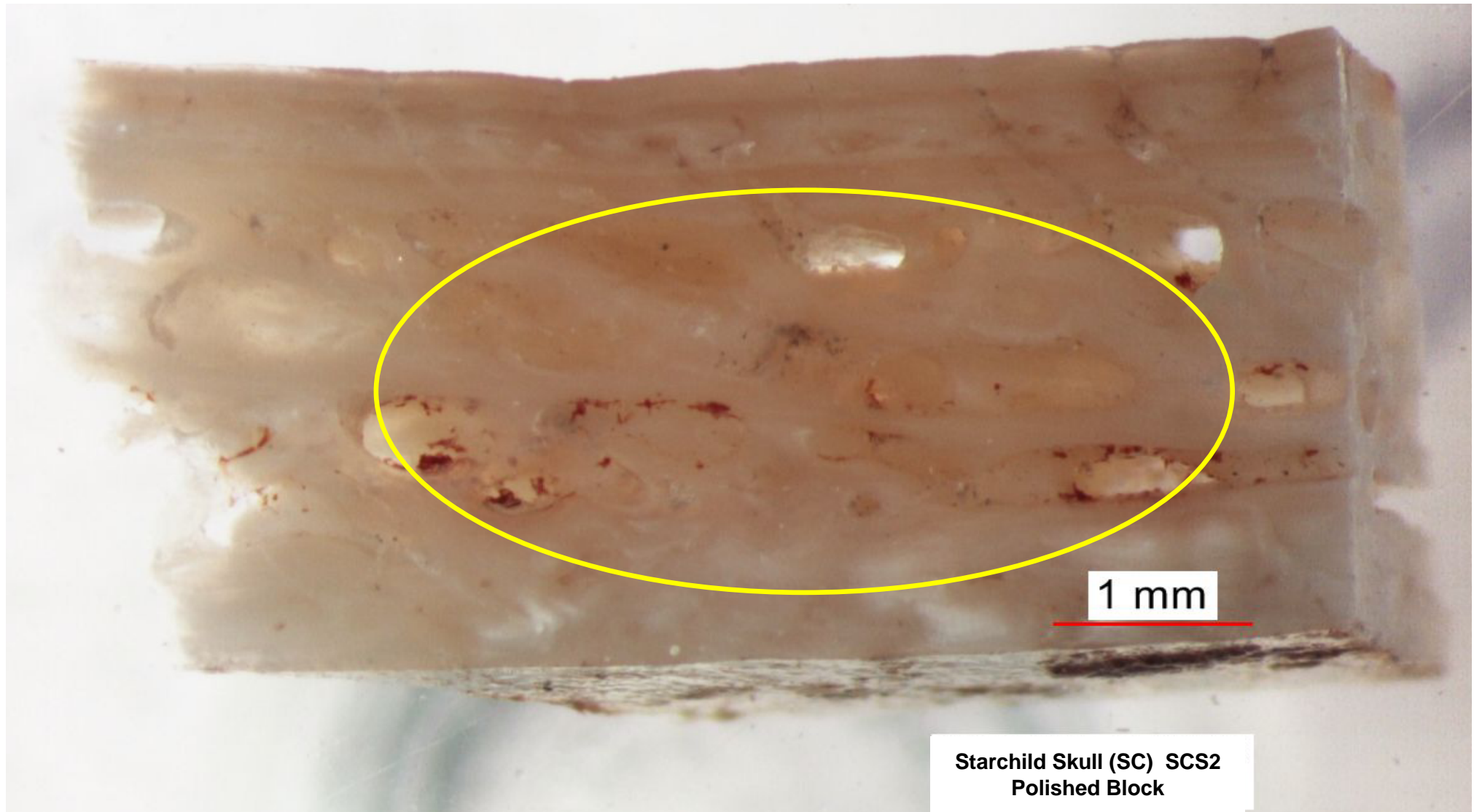
Outer surfaces of Human on left and SC on right make clear they are apples and oranges in this comparison.

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.

PROVENANCE (HISTORY)

The person who first recovered the Starchild Skull passed away in the 1990s, making the story of its discovery in situ hearsay.



She never pinpointed the exact location where she found the skulls, and claimed that the other bones were washed away in a flash flood, making finding the burial place, or recovery of any other bones, unlikely. However, the staining on the skulls matches the story that Ray and Melanie were told, as does the silicate encrustation on the skulls. But whether the story is true

or not, the fact remains that the Starchild Skull is real, and unlike anything previously found on Earth.



Ray and Melanie Young, skull owners

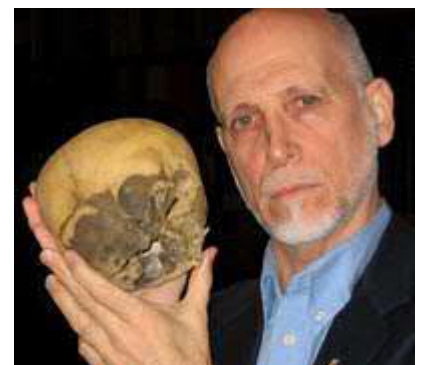
The known history of the Starchild Skull begins in the 1930s, when an American teenage girl was on vacation with her family near Mexico's Copper Canyon region. She went exploring alone and found a long-abandoned mine tunnel. Inside it she found a full human skeleton lying on its back. Beside it was a grave-like mound of dirt with an arm bone sticking out of the dirt and the hand bones wrapped around the upper arm bone of the skeleton lying on the surface. Using her hands she dug the buried skeleton out of its shallow grave.

The girl attempted to recover both skeletons but lost most of the bones in a flash flood. Ultimately, all she brought back to her home in El Paso was the two skulls, both somewhat battered in the flood, and a detached piece of maxilla that belonged to the "misshapen" skeleton she found in the grave. For the remainder of her life she kept both skulls in a cardboard box as souvenirs of her trip, assuming the odd

looking skull was the result of some kind of human deformity.

The woman died in the early 1990s, and in 1998 the two skulls were given to Ray and Melanie Young of El Paso, Texas. Melanie, a neonatal nurse and physical therapist who understood that the "misshapen" skull was in no way the result of a typical human deformity. She was determined to have it expertly evaluated to find out what it really was. To do that, she and her husband Ray enlisted the help of Lloyd Pye, an author and researcher in the field of alternative knowledge, who became the skull's caretaker and research coordinator.

Lloyd Pye became Director of the Starchild Project in February of 1999, and in the course of the past twelve years has overseen the scientific testing of the skull in three countries (the US, Canada, and England). While doing that he has regularly informed the media and the public about those results, and he continues to oversee ongoing research that will lead to an ultimate definitive conclusion about the unusual skull.



COMPREHENSIVE LIST OF STARCHILD SKULL ANOMALIES:

1. 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.
2. 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.
3. The skull itself weighs half as much as human skulls of comparable size.
4. 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.
5. 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.
6. 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.
7. 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.
8. 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.
9. 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.
10. 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.
11. The optic foramens 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.
12. The Starchild's optic foramens 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.
13. The inner surfaces of the Starchild's eye sockets appear to any visual inspection to be perfectly smooth. No convolutions can be seen on their surfaces. Yet the sensitive nerve endings of a forefinger can feel distinct convolutions 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.
14. 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.
15. 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.
16. The Starchild's zygomatic arches (cheekbones) are broken off, but both ends of the breaks present unusual

characteristics. At their bases where they connect to the skull, they fuse at a much tighter angle than humans exhibit.

17. Where the Starchild's zygomatic arches attach to the eye sockets, rather than folding into the socket itself, as do human zygomatic arches, they break off clean and with a distinct edge. This is a major difference from humans.

18. The chewing muscles that extend up through and under the Starchild's zygomatic arches fan out to cover an area roughly half the area that normal human chewing muscles cover. This, too, is a significant difference.

19. The Starchild's foramen magnum (the hole where its spine entered its cranium) is located about 1.5 inches farther forward than where it would be placed in a normal human. This is far beyond the range of normal variation.

20. The Starchild Skull's ear holes are positioned significantly lower and farther forward than normal human ear holes. This is due in part to being pushed out of position by the extreme flattening of the rear of the head.

21. X-rays have revealed that the Starchild's inner ears are approximately twice the size of normal human inner ears. We have no idea why this would be the case. Perhaps it required a better balance mechanism that we need.

22. The Starchild's neck muscles attach in a way that indicates it was a very small neck relative to typical humans, no more than half of normal size. And it is positioned directly under the center of balance of the skull, which is very different from the way a normal human skull rests on its neck.

23. Human neck muscles normally attach at an elevated point in the rear center of the occipital bone. That elevated point is called

the "external occipital protuberance," or "inion" for short. All humans, and indeed all primates on Earth, have an inion. The Starchild Skull does not have one.

24. The external occipital protuberance has a corollary inside the skull, called, not surprisingly, the "internal occipital protuberance." Inside the Starchild Skull is a version of this that is greatly reduced from normal.

25. Though the rear of the Starchild Skull is widely expanded and greatly flattened, this is not the result of deliberate binding or cradleboarding. It has all of its natural convolutions, which means it grew the way it looks because its genes directed it to grow that way. This seems to be the case with every one of its many variations from normal.

26. At the top of the rear of the Starchild's head is a noticeable "crease" at the rear of its saggital suture, where it meets the lambdoidal suture. The only possible explanation for such a configuration in a human would be a fusion of the suture. A CAT-scan shows this was not the case with the Starchild.

27. The Starchild Skull's physical size is of a small adult in the range of 5 feet tall, or an average 12-year-old. Surprisingly, its brain capacity is much larger than a skull that size should contain. A 12-year-old has about 1200 cubic centimeters of brain. An average adult has 1400 c.c. of brain. The Starchild has a whopping 1600 c.c.! We don't know where it all goes.

28. The Starchild's expanded parietal bones and the steep angle of the rear of its head strongly indicates that its overly large brain should have pressed its way out of the foramen magnum hole. Yet that didn't happen, so it seems the Starchild has a brain made of material stronger than normal human brain.

Note: Explanations and terminology in this report are aimed at non-experts. Those with expert knowledge in genetics will naturally find its concepts and descriptions simplified. The identity of certain research team members requires temporary anonymity. Their names will be revealed when they are ready to formally release reports for peer scrutiny.

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.”

It (the Starchild Skull) is primarily notable due to claims by paranormal researchers that it is evidence of extraterrestrial contact.

Merriam-Webster defines paranormal as “not scientifically explainable” (2010). Thus, the word “paranormal” does not apply to the Starchild Skull because two dozen Ph.D.s in various branches of science have provided written analysis of their opinions about it. In addition, several other Ph.D.s have given opinions they will not sign for fear of retaliation by vindictive peers who “police” the rigid status-quo belief system of mainstream science. Using those signed and unsigned data and opinions, Lloyd Pye has crafted two books filled with scientifically supported arguments. The printed book [The Starchild Skull \(2007\)](#), and the eBook [Starchild Skull Essentials \(2010\)](#).

As of this writing, ongoing research has provided proof that the Starchild Skull possesses physical characteristics (Robinson et al. 2004), biochemical attributes (Pye, K. 2005), fibers and residue inside the bone (Pye, L. 2007), and DNA that have never before been found on Earth (The Starchild Project, 2010). We propose that this array of facts counts as valid evidence supporting the theory that the skull is at least partially of extraterrestrial origin.

Mitochondrial DNA recovered from the skull establishes it as human.^[1]

Although Trace Genetics did recover human mitochondrial DNA from the Starchild Skull in 2003, this statement is inaccurate because it is possible to have the mitochondrial DNA (passed down through mothers) of one species and the nuclear DNA (passed down through both parents) of another species (Perdy, 2003). Therefore, human mitochondrial DNA alone does not establish the human species (Meadows, 2010). Examples of this phenomenon include the zebra/donkey hybrid “Zedonk” (BBC, 2010), the lion/tiger hybrid “Liger” (CBS, 2010), and the horse/donkey hybrid “Mule” (Perdy, 2003).

In 2003, Trace Genetics determined that nuclear DNA was impossible to recover using techniques developed up to that point in time. Therefore, it was impossible for them to establish if the Starchild Skull was entirely human or not. The citation here is the same outdated Novella article from 1999 (and its equally outdated 2006 reprint). Specifically, he references quotes from Lloyd Pye and Mark Bean regarding mitochondrial DNA, yet Mark Bean ceased working with the Starchild Project in 2000, and mitochondrial DNA was not recovered from the Starchild Skull until 2003, proving that this quote is inaccurate.

According to Pye, the skull was found around 1930 in a mine tunnel about 100 miles (160 km) southwest of Chihuahua, Mexico, buried alongside a normal human skeleton that was exposed and lying supine on the surface of the tunnel.^[4]

This references an article from 1999, when the report of how the skull was found had no scientific evidence to support it. Since then, analysis of the staining on the skulls (Pye, L. 2007, p. 21) and inorganic chemistry (Pye, K. 2005) have combined with the synchronistic Carbon-14 dates (Pye, L. 2007, pp. 206-7 and p. 218) to indicate that the provenance story is very likely true.

Analysis

The skull is abnormal in several respects.

This is a considerable understatement. Dr. Kaburda concluded that the skull presents 10 standard deviations from the norm (as cited in [Robinson, 2004](#)), is comprised of bone uniformly half as thick and weighing half as much as normal human bone ([Robinson 2004](#)), but is significantly more durable (Pye, L. 2007, pp. 171-172). [Note: A comprehensive list of physical and biochemical abnormalities in the Starchild Skull is available [HERE](#).]

A dentist determined, based on examination of the upper right maxilla found with the skull, that it was a child's skull, 4.5 to 5 years in age.^[5]

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 & Malhi, 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 & Malhi, 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]

All of these deformities and many others have been investigated as possible explanations for the Starchild Skull, and none of them match the attributes of the skull ([The Starchild Project, 2010b](#)).

Cradleboarding and all other artificial deformation techniques leave evidence on the surface of the skull bone, and no such evidence is present on the surface of the Starchild Skull. Thus, Dr. Robinson (2004) concluded that “the extreme flattening of the skull was caused by its natural growth pattern and is not artificial.”

Hydrocephaly (also called “congenital hydrocephalus”) is a condition where excess cerebrospinal fluid in the cranium causes internal pressure that pushes outward against the skull, expanding any unfused sutures to give the skull an “inflated” shape (MedicineNet, 2010). According to Dr. Bachynsky and Dr. Robinson (cited in [Robinson, 2004](#)) the sutures in the Starchild Skull were unfused and healthy at the time of death, with **no** expansion present at the suture lines. Thus, the Starchild’s unusual shape could not have been caused by internal pressure or the sutures would be expanded. Dr. Bachynsky specifically ruled out hydrocephaly in his examination of the skull ([Robinson, 2004](#)).

Brachycephaly simply means a skull that is abnormally wide, and is a possible symptom of multiple illnesses, deformities, and disorders. Therefore, it isn’t any kind of explanation for morphology; it is only an observation of a physical trait (Kelly, 2010).

Crouzon Syndrome is a condition where symptoms include the complete premature fusion (obliteration) of two or more cranial sutures (Matusiak & Szybejko-Machaj, 2010). In 2003 Dr. Bachynsky, a radiological expert, concluded unequivocally that there was no abnormal or premature fusion of any of the Starchild Skull’s sutures (as cited in [Robinson, 2004](#)). Therefore, Crouzon Syndrome is impossible as an explanation.

Progeria (also called Hutchinson-Gilford Progeria Syndrome) is a fatal condition that causes the appearance of premature aging in children (Progeria Research Foundation, 2010). In Progeria, bones can become thinner and weaker, and premature fusion of sutures can cause abnormal skull shape, which in turn gives the lower face and eyes an unusual appearance (Medline Plus, 2010). One of the primary symptoms of Progeria is open fontanelles on the top of the head, the “soft spot” on a baby’s head (UM Medical, 2010). This condition is not present in the Starchild Skull ([Robinson, 2003](#)).

The Starchild Skull’s bone **is** thinner than normal, but instead of being more brittle, as is caused by Progeria, it is observed to be much stronger than normal human bone (Pye, L. 2007, p. 176). Progeria does not remove the inion, change the location of the optic foramens, change the shape of the hardest sections of bone while leaving the weak sutures untouched, or increase the collagen content of bone (UM Medical, 2010), all features of the Starchild Skull (Pye 2010b). The only symptom that Progeria has in common with the Starchild Skull is “micrognathia,” an abnormally small jaw (UM Medical, 2010), leaving all of the other unusual features of the Starchild unexplained, and making Progeria a thoroughly incorrect diagnosis.

Proponents of a paranormal explanation for the skull's origin reject plausible scientific hypotheses involving non-paranormal causes.

This is flatly untrue. We consistently and continuously search for any provable explanation for the Starchild Skull, and we do so with complete disregard of whether the cause is “normal” or “paranormal.” Many mainstream scientists dismiss the work of the Starchild Project as “unscientific” because we allow for the possibility that the skull may be a human-alien hybrid. To those people we say, “Check your history books.”

Most of what is known as “science” today started as a theory that was then proven, or has not yet been disproven and so is treated as fact by those whose interests are served by the assumption. These unproved but near universally accepted theories include cosmology’s Big Bang, biology’s evolution-by-mutation, and much of the work of Pythagoras, Einstein, and Stephen Hawking.

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. ^[citation needed]

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.



STARCHILD SKULL DNA ANALYSIS REPORT—2011

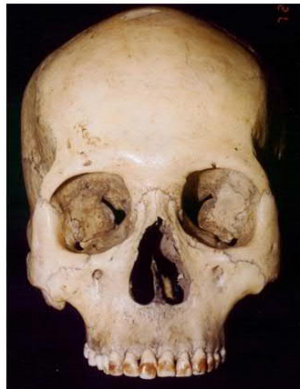
Early in 2011, a geneticist attempting to recover Starchild Skull DNA identified four fragments that matched with human mitochondrial DNA (mtDNA). Comparing those fragments with matching fragments from human mtDNA produced an astonishing result. In every comparison, the Starchild presented many more nucleotide differences than are normally found among humans. In one comparison detailed in this report, the compared segments of human mtDNA came from one of its most highly conserved regions. Across 167 nucleotides in this segment, only 1 single variation is found among the 33 human haplogroups. In contrast, the same length of Starchild mtDNA has 17 differences! Of those 17, a significant number should be confirmed by multiple repetitions of the test. If several are confirmed (which is highly likely), it will be enough evidence to establish a new earthly species. [In 2010 just such a new prehuman species, Denisova, was confirmed by having a significant number of differences in its mtDNA. This will be explained later in this report.]

Introduction To The Starchild Skull:

The Starchild Skull is a 900-year-old human-like bone skull with [distinctly non-human characteristics](#). It was unearthed in a mine tunnel near Mexico's Copper Canyon around 1930. The Starchild Project is an informal research group that has coordinated numerous scientific investigations since its founding in February of 1999.



Starchild Skull



Normal Human Skull

By 2003, the Starchild Project had [completed enough research](#) to strongly suspect the Starchild was something never seen before by science. At minimum, it presented a level of deformity and function previously thought impossible, and perhaps something much more significant: a new type of human-like being living on Earth 900 years ago.

Formal research was carried out by credentialed experts in the USA, Canada, and UK. It included [cranial analysis](#), dental analysis, X-ray analysis, CT scan analysis,

radiocarbon dating (C-14), [microscopic analysis of multiple bone preparations](#), [scanning electron microscopy \(SEM\)](#), [bone composition analysis](#), statistical analysis, inorganic chemistry analysis, DNA analysis, and other investigations into possible natural explanations such as [genetic defects](#), [birth defects](#), and [skull deformation resulting from cultural practices](#). (Complete details of these studies can be found in the book "[The Starchild Skull](#)" by Lloyd Pye)

The collective conclusions were that the combination of skull features were unique and could not be explained by any known deformity or combination of deformities, mutation, cultural practices, genetic disorders, or illness. If a human were born today with physical abnormalities like the Starchild, it could not survive. Yet something about the essential nature of this being permitted it to do what would be impossible for a normal human.



Dr. Ripan Malhi (left) and Dr. Jason Eshleman (right)

Realizing the ultimate answer could come only from genetic testing, in 2003 the Starchild Project commissioned a DNA analysis of the Starchild Skull's bone by Trace Genetics of Davis, California. (Trace Genetics was acquired by [DNA](#)

[Print Genomics](#) in 2005.) Its owners and principal geneticists were Dr. Ripan Malhi and Dr. Jason Eshleman, specialists in the recovery of ancient DNA, meaning DNA from samples more than 50

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.

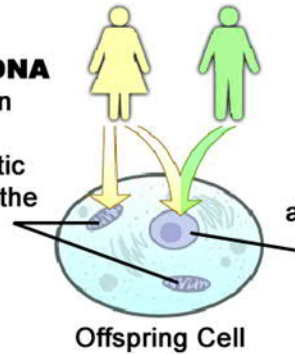
Drs. Malhi and Eshleman took samples of the Starchild bone, along with control samples from a human skull reportedly found lying beside the Starchild's buried skeleton. [Carbon 14 dating](#) of the two skulls confirmed they died at or near the same time, 900 years ago, and later analysis of staining 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

Mitochondrial DNA (mtDNA) is found in cell mitochondria and contains genetic material only from the **mother**.

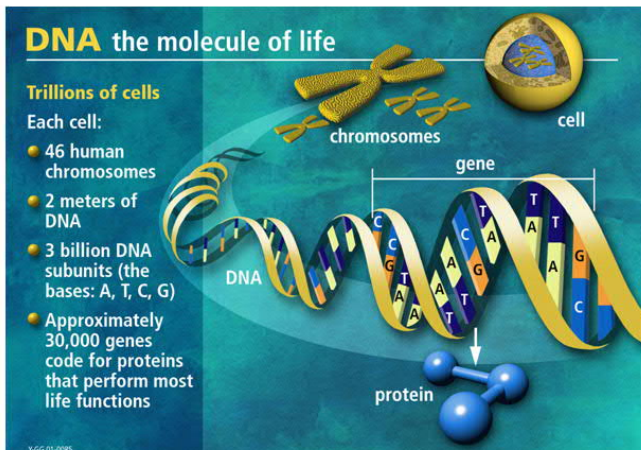


Nuclear DNA (nuDNA) is found in the cell nucleus and contains genetic material from **both parents**.

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

other methods. The principal drawback of using the PCR technique was its dependence on employing correctly designed *primers* for its amplification.

To design primers correctly, the target DNA sequence had to be known from the start, or at least the relatedness of known DNA to unknown DNA had to be understood, such as that between chimp DNA and human DNA (97% related). This made using PCR for unknown DNA sequences (those not catalogued) extremely problematic, if not impossible.

Primers are designed strings of nucleotides similar to those in DNA, but much shorter, often only 25 to 30 nucleotides long. Unlike DNA, which is double-stranded,

primers are single-stranded. When added to a sample of DNA being tested, a primer is designed to find its complimentary strand and bind to it at a specific *locus* (point of contact).

To create primers that accurately reproduce the *sequence* of nucleotides (their order of connection) at a specific locus requires knowing the exact sequence at the target locus. Imagine a human-specific primer is the string of nucleotides shown in grey (below left). When such a primer is added to a DNA sample, it will seek to connect with its other half (shown in blue) in the mirrored fashion mentioned above.

When a primer locates its counterpart (a complementary sequence, or complement), the PCR process is able to proceed and a positive result will register by whatever measurement an investigator chooses to utilize. Thus, with primers designed to conform to human DNA, a positive registration of a PCR result indicates that human DNA is present in the sample. Conversely, if the primers cannot find their complements, no human DNA is present.

2003 DNA Testing:

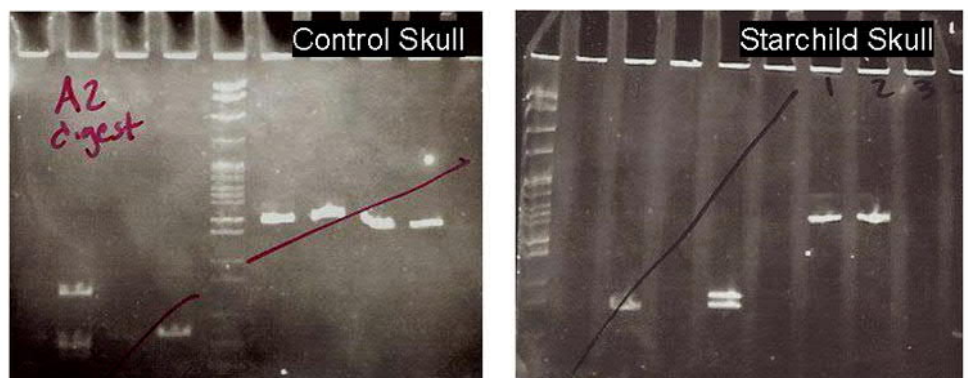
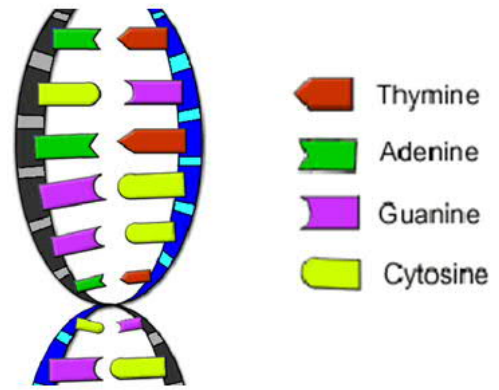
To test the DNA of the Starchild Skull and the control skull, Dr. Eshleman and Dr. Malhi used the PCR technique with primers designed on the basis of known human sequences.

On the first attempt with the control skull, both mtDNA and nuDNA were detected, revealing it was a female whose mtDNA belonged to haplogroup A. The Starchild's mtDNA was also recovered on the first attempt, but it belonged to haplogroup C. Haplogroups are how geneticists classify macro groups of people with similar yet slightly different mtDNA. The exact number of haplogroups differs depending on which reference is consulted, but 33 groups are commonly used for genetic comparisons.

This result indicated that the female and the Starchild could not be maternally related because their mtDNA did not belong to the same haplogroup. (Remember, everyone inherits only their mother's mtDNA, their grandmother's, etc.)

Recovering mtDNA so

easily from both samples meant they were well preserved during 900 years in a dry mine tunnel. The fact that the Starchild's mtDNA apparently belonged to a normal human haplogroup indicated that its maternal line was entirely human.



Analysis of PCR products from mitochondrial DNA recovered from Human Female (left) and Starchild Skull (right) by gel electrophoresis.

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

analysis, even though its burial for 900 years meant that as much as 90% of the DNA recovered from its bone would come from contaminating bacteria.

Nonetheless, as demonstrated by the Neanderthal genome project, even very extensive contamination can be identified and eliminated from data sets by modern bioinformatics. Specialized computer tools enable various degrees of filtering, one of which removes all bacterial sequences to isolate only information pertaining to the Starchild Skull's nuDNA. That means its entire genome derived from the genetic package provided to it by both parents—its human mother and its potentially non-human father.

Although access to advanced DNA recovery technology was rapidly expanding, the price for recovering and sequencing ancient DNA remained well beyond the Starchild Project's meager financial resources. Then, in early 2010, that tide of frustration suddenly turned.

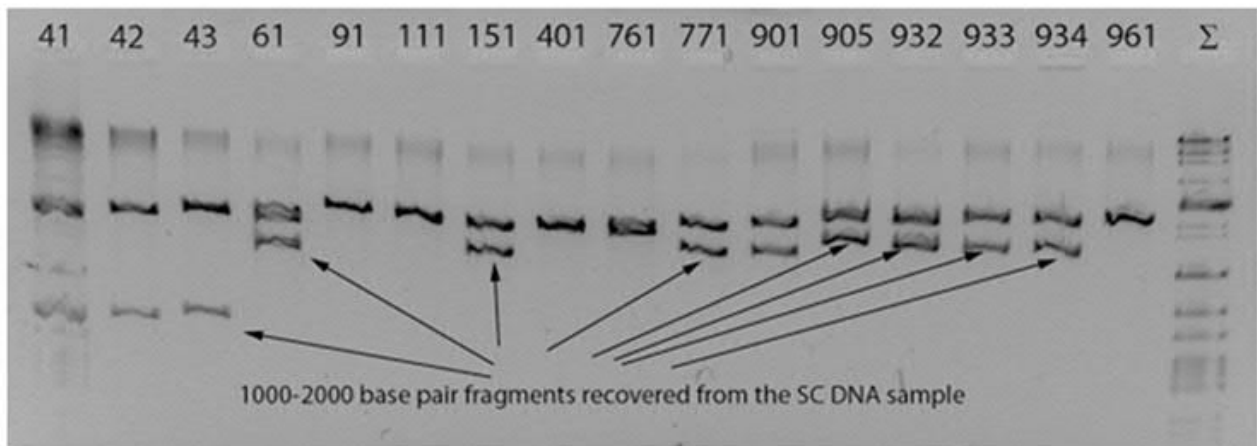
2010 DNA Testing & Results:

A geneticist from an established and well-accredited research facility in the U.S.A. offered to attempt to analyze the Starchild Skull's nuclear DNA using sophisticated genetic analysis techniques such as genome amplifications and classic shotgun sequencing, which were not available to Dr. Malhi and Dr. Eshleman due to the narrow specialization and commercial nature of the Trace Genetics business model.

As with any DNA analysis that involves enzymatic amplification, the techniques used by the new geneticist still relied on primers, but he used different approaches that were not narrowly connected to the origin of the DNA samples, and were not species-specific.

It was very labor-intensive work, and thus not cost effective for a full genome recovery. However, the geneticist's goal was to find a few fragments of the Starchild's "missing" nuclear DNA, which would clearly demonstrate that the entire genome was recoverable and therefore an investment in 454 sequencing would be warranted.

In February 2010, the geneticist was provided with a bone sample from the Starchild Skull. In March, he had recovered dozens of fragments of DNA from the sample, much of which resulted from the inevitable bacterial contamination. Nonetheless, others were clearly fragments of the Starchild Skull's nuclear DNA, so after 11 years of effort—*success!*



Gel sheet showing recovery of some of the Starchild Skull's (SC) nuDNA

All of the recovered fragments were completely characterized using the classic Sanger sequencing technique, and analyzed by capillary electrophoresis (also known as automated sequencing). These are standard DNA sequencing techniques. After obtaining sequencing data, the geneticist compared the new sequences to millions of sequences recovered by other researchers from all over the world, looking for a match.

Those worldwide results have been deposited into a massive database maintained by the National Institutes of Health (NIH) in Washington, D.C. That database was created by NIH scientists from genomes and partial genomes of thousands of plant and animal species—from sponges to humans—that have been recovered with the help of NIH funding.

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

Home Recent Results Saved Strategies Help My NCBI [Registered]

NCBI/BLAST/blastn suite/ Formatting Results - 7E030XS8013

Edit and Resubmit Save Search Strategies Formatting options Download

Nucleotide Sequence (265 letters)

Query ID: lc|45729
Description: None
Molecule type: nucleic acid
Query Length: 265

Database Name: 3 databases
Description: See details
Program: BLASTN 2.2.24+ Citation

Descriptions

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

Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
NT_004610.13	Homo sapiens chromosome 1 genomic contig, GRCh37 refer	488	488	99%	6e-136	100%	
NW_001835522.1	Homo sapiens chromosome 1 genomic contig, alternate assembl	488	488	99%	6e-136	100%	

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

Home Recent Results Saved Strategies Help My NCBI [Registered]

NCBI/BLAST/blastn suite/ Formatting Results - 7DZVRDW801N

Edit and Resubmit Save Search Strategies Formatting options Download

Nucleotide Sequence (342 letters)

Query ID: lc|14393
Description: None
Molecule type: nucleic acid
Query Length: 342

Database Name: 3 databases
Description: See details
Program: BLASTN 2.2.24+ Citation

No significant similarity found.

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 nuDNA is different from anything previously found on Earth!*

The largest composite fragment that could not be matched in the database was several thousand nucleotides long! However, until some biological sense can be extracted from these non-matching nuDNA fragments, it's too early to draw any definitive conclusions.

So, how can “biological sense” be extracted from them? One way would be if such DNA fragments are found to represent the coding part of a gene. That would mean it could be translated into a protein, and attempts could be made to predict the function of the protein.

Such a coding fragment is yet to be found among the recovered samples of the Starchild DNA because, as it happens, only about 3% of the total human genome is coding sections. Therefore, it is extremely unlikely that random sampling will miraculously discover a coding section, and all of the Starchild fragments have been obtained randomly.

The Starchild Project's team considered this development a vital step forward in the quest to establish the truth about the Skull's genetic heritage. However, skeptics and would-be debunkers soon pointed out that the submission parameters of a BLAST search *could be* manipulated by an unscrupulous researcher adjusting them to gain a favored result.

When those trying to discredit the Starchild Project suggest its results have been faked or fudged, they fail to acknowledge that all Project members have put their professional and personal reputations at stake. Project members have by far the most to lose from invalid results—much less faked results—so each of them works hard to ensure that appropriate steps are taken to secure accurate, repeatable results at every point in the process.

To serve that policy, the nuclear DNA results so far obtained have undergone sequential verification, but it must be stressed that they are now, and will remain, only fragmentary, and they will ultimately require subsequent repetitions for absolute confirmation. This will be completed by our geneticist and his colleagues as time and funding permit.

2003 vs 2011 Mitochondrial DNA Testing:

Early in 2011, the geneticist sequenced some fragments from the Starchild Skull DNA sample that, when examined by a program similar to BLAST, revealed they were segments of mitochondrial DNA rather than nuclear DNA. This was an intriguing development.

Up to that point, he had accepted the Trace Genetics result of 2003 (that the Starchild's mtDNA was entirely human) as accurate. However, the primer series utilized in 2003 recovered only relatively small and quite specific segments of human mtDNA. The situation at that time left room for error and therefore should be clearly understood.

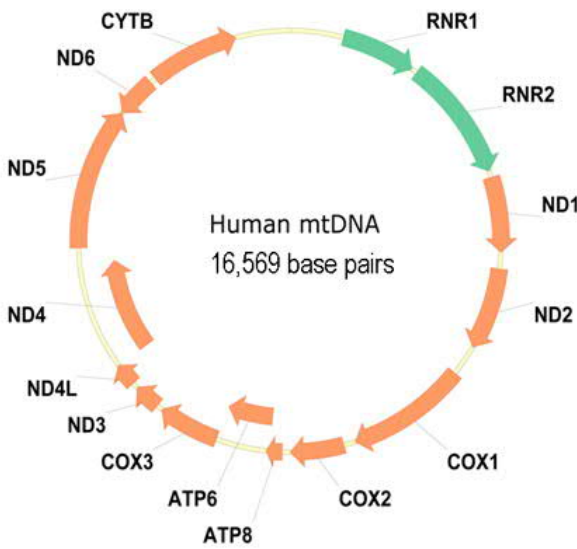
When the primers employed in 2003 found corresponding fragments on the Starchild's mtDNA, the primers rendered a positive signal from the PCR indicating “this particular part of the mtDNA is human, or highly human-like.” However, that did not mean other untouched sections of the mtDNA would not vary considerably from the human mtDNA. And this, apparently, is what happened—the 2003 sampling proved to be too small.

2011 DNA Testing & Results:

Mitochondrial DNA is quite distinct from nuclear DNA. While both mtDNA and nuDNA exist as double-strand molecules forming the famous “double helix,” nuDNA is segregated into 46 chromosomes (in humans). Due to the massive amount of DNA in chromosomes (each consisting of millions of base pairs), DNA is tightly packed into multiple folds and is encased in a shell by large amounts of proteins called histones.

In contrast, mtDNA forms a tiny circle consisting of 16,569 base pairs. Despite its small size, its function is crucial to life. Unlike nuDNA, the vast majority of it works, so mutations seldom become permanent. In fact, in the entire course of human existence, mtDNA has accumulated only $120 \pm$ variations across the entire population. Compare that to nuDNA, whose 3 + billion base pairs have as much as 15 million variations.

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.



The primary genes within human mtDNA

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.

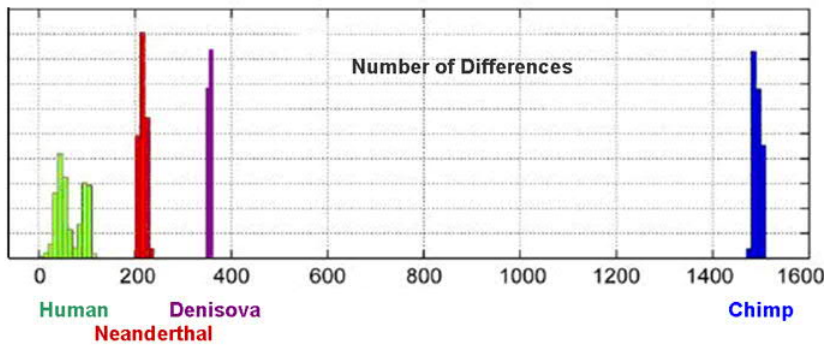
Since the beginning of eukaryotic cells (those with a nucleus) around 2 billion years ago, the mitochondria in them have carried out the most fundamental aspects of sustaining life. This has been true from yeasts to dinosaurs to humans. Their critical functioning is why very few differences are found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

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.

	1255	1260	1270	1280	1290	1300	1310	1320	1330	1340	
Human mtDNA CRS	1249	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT A	1249	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT C	1245	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT H1	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT H2	1251	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT I	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT J2	1249	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT J1b	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT K	1253	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT L1a	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT L1b	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT L1c	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT L2	1249	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT L3b	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT L3d	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT M*1	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT M11	1252	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT M12	1252	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT M*2	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT N1b	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT R11	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT T1	1251	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT T5	1251	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT U2	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT U21	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT U22	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT U31	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT U32	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT U35	1251	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT U6	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT U7	1249	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT V	1251	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT W	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
HPT X	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
Neanderthal mtDNA	1245	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
DenisovaBone	1246	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									
DenisovaMolar	1246	TCAGCCTATATACCGCCATCTTCAGCAAACCCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAGACGTTAGGTC									

Both Neanderthal and Denisova have mtDNA more varied than human mtDNA, but they still contain many long unvarying segments. Neanderthals differ from the human CRS by $200 \pm$ base pairs. The Denisova differ from it by $385 \pm$ base pairs, which is why they are designated as separate from humans and Neanderthals. As a comparison, chimp mtDNA differs from the human CRS by $1,500 \pm$ base pairs, as seen in the following graph.



MtDNA is so highly conserved because nature applies a very strong selective pressure against changes in its most critical regions.

When changes do occur in such places, it can lead to disruption of a crucial activity, which can lead to dysfunction and death. As a result, an unfavorable mutation is not passed along. However, mutations that do not change proteins, and those in regions that do not encode proteins, can and do slowly accumulate.

This explains why only 0.0072% (120th of 16,569 bp) of human mitochondrial DNA has any variation across its 33 haplogroups. Below is an example of variation in human mtDNA. The haplogroup L1a has a C (cytidine) nucleotide, while at the same location all the other haplogroups have a T (thymidine) nucleotide. (The program's output highlights all variations to aid researchers.)

	4590	4590	4600	4610	4620
Human mtDNA CRS	4584	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT A	4583	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT C	4579	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT H1	4584	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT H2	4585	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT I	4584	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT J2	4583	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT J1b	4584	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT K	4587	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT L1a	4582	GCCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT L1b	4582	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT L1c	4581	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT L2	4583	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT L3b	4582	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT L3d	4582	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT M*1	4584	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT M11	4586	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT M12	4586	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT M*2	4582	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			
HPT N1b	4582	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCCT			

researchers.)

Each variation like the one above is called a Single Nucleotide Polymorphism (SNP), and for human mtDNA such "snips" are catalogued in databases maintained by the National Institutes of Health. The fewer substitutions a DNA segment has, the more conserved it is. Human mtDNA, with only $120 \pm$ variations in 16,569 base pairs, is considered very highly conserved.

Notice that the first haplogroup in the chart below the Control Reference Sequence (CRS) is haplogroup A (HPT A). This is the haplogroup that was matched to the human female skull found with the Starchild Skull. The next down is haplogroup C (HPT C), matched to the Starchild with small fragments of its mtDNA in 2003.

When Trace Genetics detected the Starchild's mtDNA, they used human-specific primers that amplified segments only a few dozen nucleotides long. These segments were targeted for diagnostic analysis because they contained human haplogroup-specific changes that could determine whether mtDNA belonged (or not) to a specific haplogroup.

If the targeted segments also happened to be a part of a highly conservative sequence of human mtDNA that has a crucial biological function, the segments could be similar even among very different species (i.e., humans and chimps), leading to confusing conclusions.

In early 2011, our geneticist analyzed four newly sequenced fragments from the Starchild Skull's mtDNA samples. A computer program similar to the BLAST program mentioned earlier matched the four Starchild fragments to catalogued fragments of human mtDNA.

One fragment matched a segment in the chart shown earlier, seen expanded below. This is a highly conserved segment of human mtDNA, with only 1 nucleotide variation among 33 human haplogroups present (L1b). There is also one in Neanderthal and one in Denisova .

	1262	1270	1280	1290	1300	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420																			
Human mtDNA CRS	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT A	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT B	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT H2	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT I	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT J2	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT J1b	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT K	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT L1a	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT L1b	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT L1c	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT L2	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT L3b	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT L3c	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT M*1	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT M11	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT M12	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT M12*	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT N1b	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT R11	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT T1	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT T5	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT U2	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT U21	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT U22	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT U31	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT U32	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT U32*	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT US	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT U6	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT U7	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT V	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT W	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
HPT X	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
Neanderthal mtDNA	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG
Denisovan*10a	ATATACCC	CACTCTT	CAGCAA	CCCTG	TATGAAG	GTAC	CAAGT	TAAGGG	CAAGT	CCACG	GTAAAG	AGGTT	AGGTC	CAAGG	TGTA	AGCCCA	TGAG	GTGG	CAAGAA	TGGG	TAC	ATTTT	CTAC	CCCG	AGAAA	ACT	ACG	TATG	AAAT	CCCTT	TATG	AAAT	CTA	AGGG	TG	GAAG

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 Starch

haplogroups. In such a strongly conserved area, multiple differences in a matched sample would immediately alert geneticists that something major might be unfolding.

Below is a screen shot of the 167 Starchild mtDNA nucleotides compared to the 157 in the human CRS. The top line of each row (highlighted in pink) is the Starchild Skull sequence, which starts at 167 and works backward to 1. In the complementary Human CRS sequence (the second line of each row) the base pairs start at #1269 and end at #1426 (157 total) in the mirrored fashion mentioned earlier.

```

>GRGEF1201AO7KP, 167..1 of 218 and chrM, 1269..1426 of 16571 (154/171 ident
167 TCTTCAGACCAAA-CCTGATAGSAAGGCTAACAAAGTAAGCGACAAACGTACCCAACGTAAAGTACGGTTAG
1269 TCTTCAG--CAAACCCTGAT--SAAGGCT-ACAAAGTAAGCG-CAA-GTACCC-ACGTAAAG-AC-GTTAG

GTACCGAAGGTGTAGCCCATGAGGTGGCAAGAAAT-GGCTACATTTTCTACCCAGAAACTACGATAG-
GT-C-AAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTACATTTT-CTACCCAGAAACTACGATAGC

CCTTATGAAACTTAA-GGTCGAAGGTGGAT 1 < STARCHILD SKULL
CCTTATGAAACTTAAAGGTCGAAGGTGGAT 1426 < HUMAN CRS
  
```

Within the 167 comparisons above are 17 variations! *Seventeen!* That is 17 *indels* of difference between the Starchild mtDNA and the mtDNA of 33 human haplogroups!

After repeated sequencing, *some* of those 17 differences *could* be confirmed as reading errors by the program, but it is virtually impossible that *all* of them would be errors.

2012 - FoxP2 Gene Discovered

Our geneticist has now recovered a fragment of the Starchild's DNA that is so powerfully convincing, even standing alone, we are confident it provides a tipping point in our quest to recover the Starchild's entire genome. He has secured a fragment of a gene from the 5% of human nuclear DNA that codes for proteins, and it does most of the work of keeping our bodies functioning as they should. This gene is not only functional, it is a highly functional "master gene," one of the most vitally important genes in the body of any species on Earth.

Virtually any complex species has a variation of this gene, and it is without question one of the most highly conserved genes in the human body. It is the FOXP2 gene. That odd name comes from its technical title: Forkhead Box P2, or FOXP2. Here is one of a wide variety of illustrations that try to capture its vast importance in a single image.

In any creature, the overwhelming importance of their FOXP2 gene is that it controls a "downstream" cascade of genetic processes in hundreds of other genes, all coordinating the formation of various parts of a body as it gestates and grows to maturity. In mammals and other "higher" species, any single flaw in FOXP2, any isolated mutation or variation, can cause a severe negative impact in some of the most important aspects of development: the function of the brain, the sound or speech mechanisms, the lungs, heart, guts, and nerves, among others. Because it is so utterly vital, it is even more highly conserved than mtDNA.

Recall that in the 16,569 base pairs found in the mtDNA genome of normal humans, as many as 120 variations can be found in the first of us, southern Africans. That percentage of difference is quite small, only 0.7%. Compare that with the FOXP2 gene, which in normal humans is 2,594 base pairs long, and contains no variations. 0%! None! Nada! Every normal human has the exact same array of FOXP2 base pairs as every other normal human.

This is not to say mutations never occur in FOXP2. They can and do, and a number of them have been found. However, every mutation is debilitating in some way, and because FOXP2 is vitally important to so many bodily functions, most mutations in it will cause termination of life. When termination does not occur, the mutation's impact on its host is usually severe.

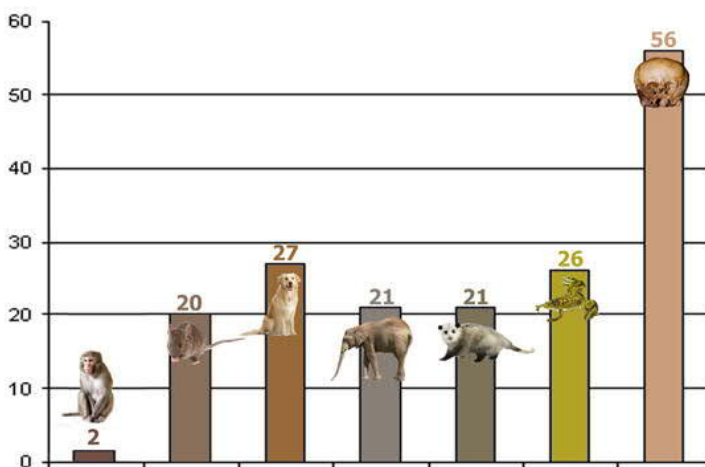
In one well-studied mutation in the section of the gene that influences speech development mechanisms in humans, those who inherit it will never be able to speak. This has led some to suggest FOXP2 is a language gene, or a speech gene, but that is not the case. Speech is much too complex an arrangement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

It is always possible that some kind of sequencing error has been made, so it needs to be repeated to confirm this initial analysis. In any case, after the mysterious “stop” codon, a new Gln stretch begins and continues to only three amino acids from the fragment’s end. This, too, is wildly different from the human sequence, but as with the other anomalies, further research is needed to determine what altered functions these differences cause.

Another comparison to make is to remove the Gln stretches from different species and examine what is left. For example, if we analyze the entire FOXP2 gene in humans and chimps, our closest genetic relative, with the Gln stretches removed from consideration, then only 2 amino acids (depicted by the three-letter codons) are different. The same 2 are found in gorillas and other higher primates. In mice, the difference is 3 amino acids.

If we remove the Gln stretches from the Starchild’s fragment of FOXP2, only 7 amino acids remain to be compared to the corresponding amino acids of the human FOXP2. These are the first four, at the beginning of the fragment, and the last three, the end of the fragment, and all 7 amino acids are different! Whatever we might say about this comparison, it is certainly not between two humans, or anything near two humans.

In addition to having a “stop” codon in its last quarter, the Starchild fragment is also missing the large intron (marked with a vertical green arrow) that normally intervenes in the human gene and in the gene of other species. This suggests that the Starchild fragment could be a pseudogene, dysfunctional ancestors of normal genes that have lost the ability to encode proteins, or are otherwise no longer capable of being expressed in a cell. This means they are nonfunctional, and are therefore another form of junk DNA.

Suggesting the Starchild’s FOXP2 fragment might be a pseudogene immediately collides with the fact that there is no currently known human FOXP2 pseudogene. Because it is a master gene, it must always function properly, and if it doesn’t function properly in even a small way, very negative things happen to the individual carrying the variation. Thus, since a human FOXP2 pseudogene is not known to exist, if it turned out that the Starchild Skull carried one, that would clearly establish it as not human.

What’s the bottom line? That can only be determined when the entire Starchild genome is recovered and compared—nucleotide by nucleotide, base pair by base pair, codon by codon, amino acid by amino acid—with humans, Neanderthals, Denisovans, chimps, and gorillas. Whatever it is, most of the preliminary evidence indicates it is quite distinct from humans.

Most important, perhaps, to keep in mind is that our FOXP2 results are preliminary, as are the results from the earlier nuclear DNA fragments, and the mitochondrial DNA fragments. All three preliminary results are highly indicative of what the final result will be, but they cannot be considered absolute proof. They can, however, be considered proof that absolute proof will come when the Starchild’s entire genome can finally be recovered.

What Does This Mean?

In any comparison of DNA samples between the human CRS and an “unknown” species (which technically categorizes the Starchild), even a *few* variations between them in a short stretch of highly conserved nucleotides strongly indicates that the entire mtDNA genome of that species would contain many more than the $120 \pm$ carried by the human haplotypes.

Such a difference, which is not hypothetical but actually exists within the Starchild Skull, is by itself sufficient reason to suspect a *new species* has been identified! Clearly such an extraordinary claim requires extraordinary evidence, but the preliminary results achieved so far with the Starchild DNA are immensely encouraging, to the point of near certainty.

To calculate the exact percentage of difference between the Starchild Skull and humans will require its entire genome to be sequenced using sophisticated technology such as the machines provided by 454 Life Sciences and/or similar companies such as Illumina. We intend to perform that sequencing as soon as we have the financial ability to do so.

In the interim, our research team is releasing this report to focus on the 167/157 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.

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...



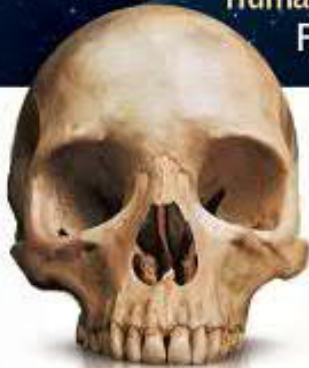
WHAT ON EARTH IS THE STARCHILD SKULL? IS IT EVEN FROM EARTH?

“In forty years of practice as a reconstructive plastic surgeon, I have never seen anything like it. I doubt if anyone else has, either.”

Dr. Ted Robinson, Vancouver, B.C.

SKULL COMPARISONS

Human / Starchild
FRONT



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