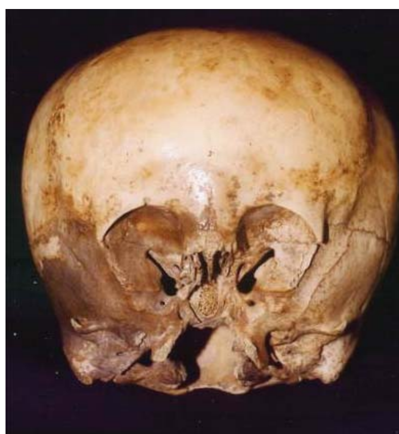
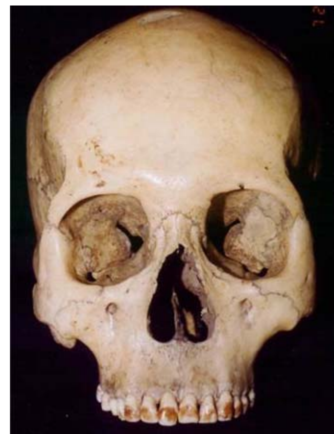
Starchild Skull DNA Analysis Report—2011

SUMMARY:
Early in 2011, a geneticist attempting to recover Starchild Skull DNA identified several 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 160 ± 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), would it be enough to consider establishing a new Earthly species? It would certainly throw open the door to serious consideration.

REPORT:
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 of the Starchild Skull 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 Skull 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.

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.[1]

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.[2] 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.

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

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, 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.

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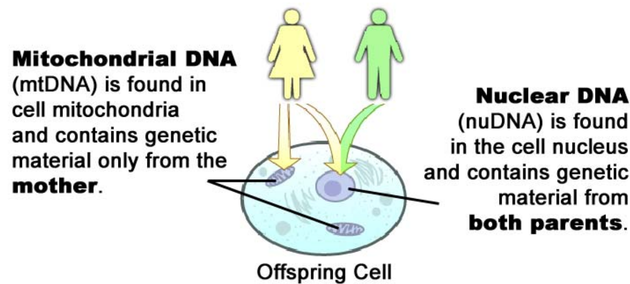
[1] Many results and references for research on the Starchild Skull are available at www.StarchildProject.com, with additional information available in Lloyd Pye's book *The Starchild Skull*, available through Amazon.com and Barnes & Noble, and the *Starchild Skull Essentials* eBook available through www.StarchildProject.com.
[2] Trace Genetics was acquired by DNA Print Genomics in 2005.

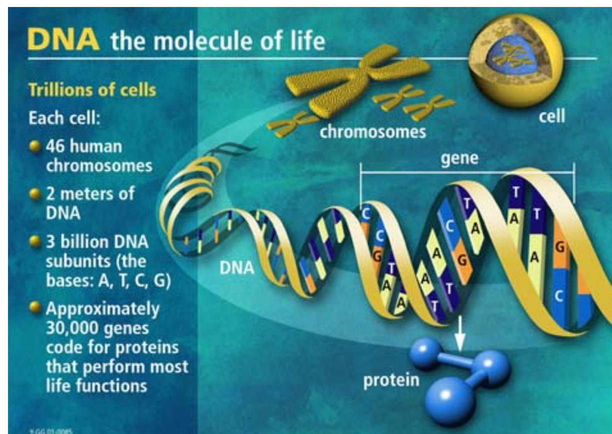
All humans have two types of DNA.



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

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

All DNA is created from only four building blocks called nucleo*sides*, 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 nucleo*tides*.



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.*

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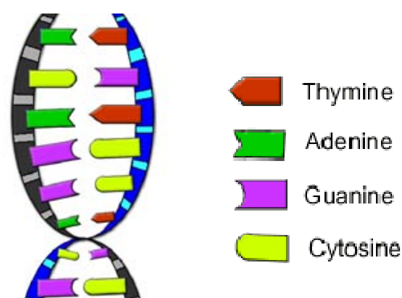
In 2003, Trace Genetics began their sequencing analyses of the DNA recovered from both skulls. The methodology they utilized was based on PCR (Polymerase Chain Reaction), a powerful amplification technique that enabled analysis of tiny amounts of DNA too small to be detected by other methods. The principal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

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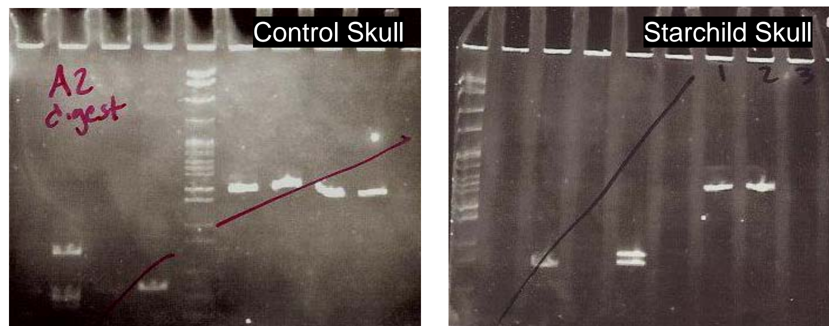
To test the DNA of the Starchild Skull and the control skull, Dr. Eshleman and Dr. Malhi used the PCR technique with primers designed on the basis of known human sequences.

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.[3] The Starchild's mtDNA was also recovered on the first attempt, but it belonged to haplogroup C.

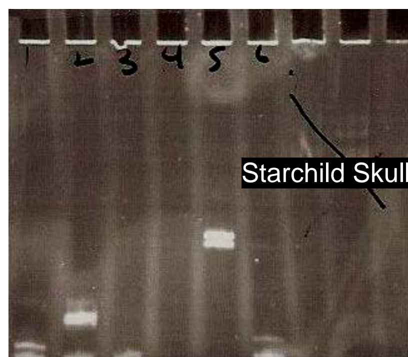
This result indicated that the female and the Starchild could not be maternally related because their mtDNA did not belong to the same haplogroup. (Remember, everyone inherits only their mother's mtDNA, their grandmother's, etc.)



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

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.

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.



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

[3] 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.

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*[4] genetic heritage?

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.

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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

[4] 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.

genetic 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.

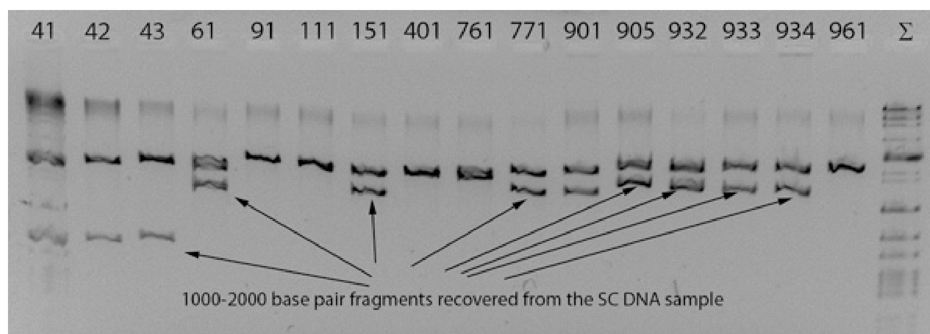
Although access to advanced DNA recovery technology was rapidly expanding, the price for recovering and sequencing ancient DNA remained well beyond the Starchild Project's meager financial resources. Then, in early 2010, that tide of frustration suddenly turned.

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*.

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.

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.

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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.

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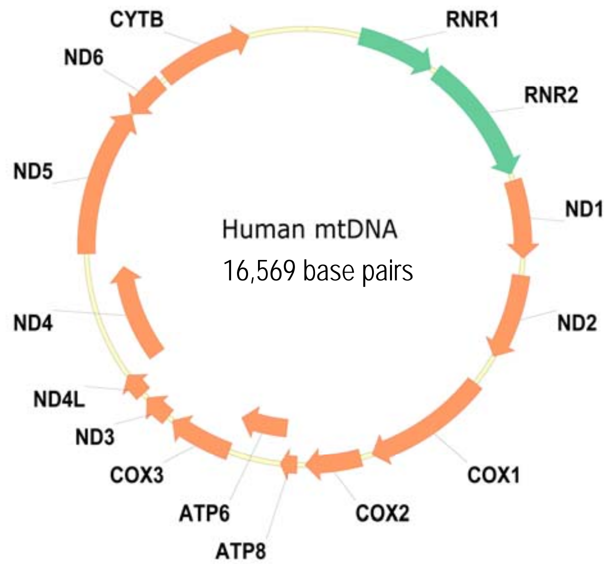
Mitochondrial DNA is quite distinct from nuclear DNA. While both mtDNA and nuDNA exist as double-strand molecules forming the famous "double helix," nuDNA is segregated into 46 chromosomes (in humans). Due to the massive amount of DNA in chromosomes (each consisting of millions of base pairs), DNA is 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. In the entire course of human existence, our mtDNA has accumulated only 120 ± variations across the entire population. Compare that to nuDNA, whose 3 + billion base pairs have as much as 15 million variations between individuals.



The primary genes within human mtDNA

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

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

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

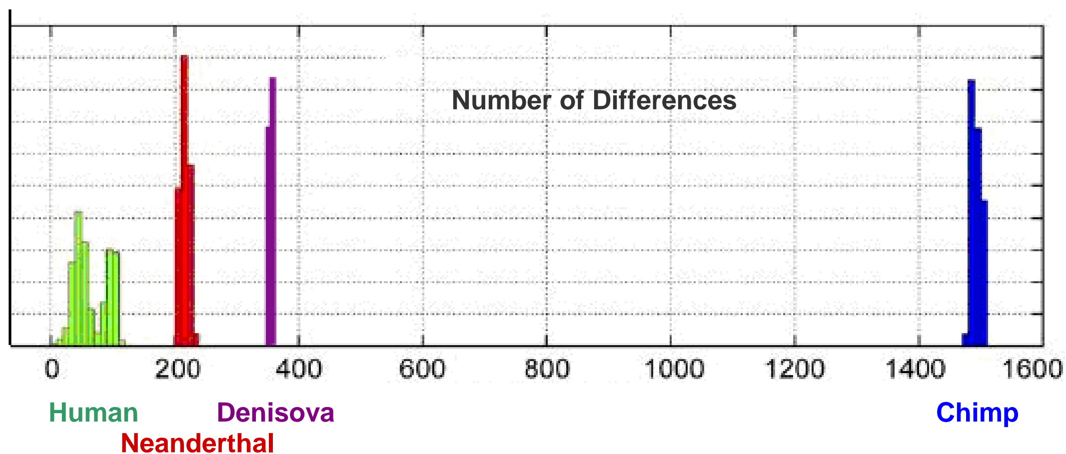
Mutational change in the human mtDNA nucleotide sequence is exceptionally rare (only 120 ± among all humans), and each mutation is well documented. The chart below is a screen capture of the output from a computer program that compares the entire mtDNA sequences of 33 different human haplogroups, one 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	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT A	1249	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT C	1245	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT H1	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT H2	1251	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT I	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT J2	1249	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT J1b	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT K	1253	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT L1a	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT L1b	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT L1c	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT L2	1249	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT L3b	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT L3d	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT M*1	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT M11	1252	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT M12	1252	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT M*2	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT N1b	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT R11	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT T1	1251	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT T5	1251	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT U2	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT U21	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT U22	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT U31	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT U32	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT U5	1251	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT U6	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT U7	1249	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT V	1251	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT W	1250	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
HPT X	1248	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
Neanderthal mtDNA	1245	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
DenisovaBone	1246	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA
DenisovaMolar	1246	TCAGCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCCACGTAAAGACGTTAGGTCAAGGTGTAGCCCA

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 ± base pairs. The Denisova differ from it by 385 ± 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 ± base pairs, as shown 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% 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 4500 4610 4620
Human mtDNA CRS	4584	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT A	4583	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT C	4579	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT H1	4584	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT H2	4585	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT I	4584	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT J2	4583	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT J1b	4584	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT K	4587	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT L1a	4582	GCCTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT L1b	4582	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT L1c	4581	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT L2	4583	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT L3b	4582	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT L3d	4582	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT M*1	4584	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT M11	4586	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT M12	4586	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT M*2	4582	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT
HPT N1b	4582	GCTTTTATTCCAGTTCTAACCAAAAAAATAAACCCT

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 NIH. The fewer substitutions a DNA segment has, the more conserved it is. Human mtDNA, with only 120 ± variations in 16,569 base pairs, is considered 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 of a few hundred 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 newly sequenced fragments from the Starchild Skull's DNA samples. A computer program similar to the BLAST program mentioned earlier matched several 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 .

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

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

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

To make the Starchild's mtDNA match the human CRS, the program added gaps marked as dashes either to the Skull's mtDNA or to the CRS to obtain the highest matching score between them. Adding spaces to such misalignments in both samples provides a total cumulative difference, which in this case is a10-gap differential (167 – 157 = 10).

It is important to distinguish that adding gaps is not the same as outright changes in the nucleotides, as was seen earlier with the single C found in a row of Ts. Such changes are only one of three ways that differences are recorded when samples are being compared.

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

In the latter two cases, insertions and deletions, the program makes no distinction between which is the cause of the gap. All it does is insert the gaps into either sequence to keep the matching count as high as possible. Those gaps are called **in**sertion-**del**etions, or *indel(s).*

Indels are clear points of variation between samples, but not all of them can be considered ironclad. All DNA testing requires multiple "runs" to be certain of every result. When the same sample is sequenced again and again, any of the three possibilities above might be corrected. Several runs will establish which variations can be catalogued as confirmed.

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

```
>GRGEF1201A07KP, 167..1 of 218 and chrM, 1269..1426 of 16571   (154/171 ident

167   TCTTCAGACCAAA-CCTGATAGGAAGGCTAACAAAGTAAGCGACAACGTACCCAACGTAAAGTACGGTTAG
1269  TCTTCAG--CAAACCCTGAT--GAAGGCT-ACAAAGTAAGCG-CAA-GTACCC-ACGTAAAG-AC-GTTAG

      GTACGAAGGTGTAGCCCATGAGGTGGCAAGAAAT-GGCTACATTTTCCTACCCCAGAAAACTACGATAG-
      GT-C-AAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTACATTTT-CTACCCCAGAAAACTACGATAGC

      CCTTATGAAACTTAA-GGTCGAAGGTGGAT 1       < STARCHILD SKULL
      CCTTATGAAACTTAAGGGTCGAAGGTGGAT 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.

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 ± 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 that one, and three of those are depicted and analyzed in the *Starchild Skull Essentials* eBook available at www.StarchildProject.com.

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 ± 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 ± nucleotides in the Starchild's mtDNA are sequenced, they will contain far more than the 120 ± 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 ± of Neanderthals. It will carry far more than the 385 ± of Denisova. Could it possibly, or conceivably, reach the 1500 ± of chimps? Only further investigation will tell, but this is already a monumental discovery.

CONCLUSION AND CALL TO ACTION

After 12 years of struggle, the Starchild Skull is truly poised to make history. When we have secured the funding needed to carry out the recovery and sequencing of its entire genome, it will provide uncontestable proof that at least once, 900 years ago, a being somewhat like us but definitely not human lived and died and was buried on our planet.

Unfortunately, achieving that historic moment requires far more than the Starchild Project team can deliver without substantial help. A wealthy investor—not merely a donor, an *investor*—must be found to provide the funding necessary to do what must be done.

In this extraordinarily special case, the investment needed is $7 million USD. Why that amount? Every step of the DNA recovery and sequencing process will have to be verified with multiple repetitions until no possible doubt remains about any specific result. Also, in order that those completed results can be confirmed by independent researchers, the entire process must be recorded on film for academic scrutiny and historic posterity.

The Starchild Project intends to incorporate some of that footage into creating two theater-quality documentary films during the 1.5 to 3 years required for the DNA's recovery and analysis. These films will cover the Starchild Skull's entire story, from its discovery to completion of the DNA analyses. They will be valuable both historically, as the record of this milestone event in human history, and financially, as market research indicates they will be enthusiastically welcomed in virtually every country on Earth.

It should be obvious to anyone that much more than $7 million can be made from two high quality films about such a pivotal shift in human awareness. If anyone reading this report personally knows anyone who might be interested in taking a front-and-center position as this historic event unfolds, please ask them to email: contact@StarchildProject.com.

A business proposal is available to any serious potential investor. The film project already has its producers, director, entertainment attorney, accountant, production team, and the enthusiastic cooperation of a state film council. Everything is in place except for the investment, the final hurdle that now requires only one astute decision to clear it.

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Final 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.

Potential investors who want to know more, or to verify our geneticist's work, can meet with him and tour his lab if they sign a Non-Disclosure Agreement. This will be on a case-by-case basis.