# Extraterrestrial genetics research proposal (XG1)

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# Introduction

Genetics is a powerful tool for understanding the history and evolution of life on Earth. The Ancient Alien Hypothesis posits that extraterrestrial beings have significantly influenced human evolution. Aliens intervened in the development of Homo sapiens from Earth primates by introducing genetic material from various alien races at different stages. These interventions created distinct human races and involved ongoing genetic manipulations throughout history, with intensified activities in the 1950s, particularly within English-speaking populations.

Population genetics has made huge progress recently. Many human genomes from various populations have been sequenced and genotyped, allowing science to trace population migrations, mixing, evolution, and expansion. This mainstream science is based on the model that all human populations evolved from primates through natural evolution. However, our hypothesis suggests extraterrestrial genetic engineering events occurred throughout human history, creating new human races and manipulating genetics across centuries. Occasionally, members of populations were transported by extraterrestrials from one location on Earth to another.

The hybridization program began in the late 1940s and 1950s, potentially through agreements between extraterrestrials and governments, including the American government, which allowed aliens to run hybridization programs with military assistance. Initially, hybridization occurred off-planet, with subjects being returned to Earth. Children born from these programs were hybrids between earthly and extraterrestrial parents. This program continues today with some modifications.

**Scientific Analysis**

The genetic data on human races, primates and hominids will be examined. Natural evolution has distinct signatures that are studied not only in humans but in other species as well. Patterns of genomic rearrangements in natural evolution differ significantly from those in artificial genetic manipulation. We will look at the human genome from this perspective, searching for signs of artificial genetic manipulation based on genomic sequences and patterns.

Evolutionary geneticists have identified several missing links where sudden jumps from previous ancestors to more modern ancestors include significant genomic changes. In modern human history, there were sudden appearances and expansions of new races. We will look for potential insertions of new genes and signs of genetic manipulation in these sequences. We will test the hypothesis that these new races were artificially created through genetic engineering from existing human races by adding alien sequences. Additionally, we will investigate sudden gene transfers and migration patterns that were historically impossible, verifying these migrations as potential evidence of extraterrestrial intervention.

Certain tribes, such as the Dogon tribe in Africa, have legends of specific extraterrestrial origins. We will combine these historical accounts and legends with genetic information to identify genetic insertions of alien genes. Importantly, modern geneticists often ignore so-called junk DNA, which comprises about 95% of the genome. We will specifically pay attention to intergenic and intronic sequences located between the protein-coding genes.

With the advancement of genetic analysis techniques, it is now possible to investigate ancient and modern extraterrestrial genetic manipulations. Our research will employ advanced bioinformatics methods to analyze publicly available human genome data, living volunteers, and ancient skulls to uncover evidence of extraterrestrial genetic contributions. This approach will provide valuable insights into the extent and nature of these genetic interventions, advancing our understanding of human evolution and the role of extraterrestrial influences.

## Aim 1: Bioinformatics Analysis of Publicly Available Sequence Data

Bioinformatics offers a cost-effective and efficient starting point for our investigation into extraterrestrial genetic influences. By analyzing publicly available human genome data, we can leverage existing resources to uncover potential evidence of alien genetic contributions. This approach allows us to quickly identify patterns and anomalies that indicate historical and modern genetic manipulations by extraterrestrials, setting the foundation for further experimental studies involving living volunteers and ancient skulls.

## Subaim 1: Incomplete Parental Contribution Analysis

**Rationale:** The hypothesis that alien abductions involve a hybridization program suggests that aliens mix DNA from two Earth parents and two alien parents. In normal inheritance, a child inherits 50% of their DNA from each parent. However, with alien hybridization, the child may inherit anywhere from 25% to 50% of their DNA from each human parent, with the remaining DNA coming from alien parents. This leads to **supplemental inheritance** patterns. When I worked in a genotyping lab, we often observed exceptions to Mendelian inheritance, but these data were usually filtered out. We aim to dig out and analyze these cases from public genetic data. We are introducing the term **supplemental inheritance** to describe this unique pattern, as it is necessary to describe the novel hypothetical genetic phenomenon introduced by alien hybridization.

**Analysis:** We will explore public genetic data to examine genotype patterns in healthy parent-child pairs. By analyzing allelic inheritance, we aim to identify pairs where less than 50% of parent alleles were inherited by the child. This incomplete inheritance has not been previously described and represents a potential new discovery. Next, we will explore triads with genotypes of both parents and children. In those triads where incomplete parental contribution is observed, the genome areas not inherited from either parent will likely be alien sequence insertions. These would be the first candidate extraterrestrial sequences discovered. We also anticipate that some unrelated triads would share similar alien sequences, providing additional evidence of extraterrestrial hybridization.

This approach is easy and straightforward, and it directly challenges traditional genetic inheritance models by revealing anomalies that cannot be explained by natural evolution alone.

## Subaim 2: De Novo Assembly of Public Genome Data

**Rationale:** Thousands of human genomes have been completely sequenced, including some with detailed, long-read technologies. This comprehensive sequencing allows for accurate reconstruction of genetic insertions, which is crucial for discovering potential alien gene contributions. Normally, insertions are mismapped because researchers align new genomes to a standard reference genome, which overlooks unexpected sequences. Mainstream science focuses on finding a consensus genome, but we are looking for large insertions that might indicate extraterrestrial influences.

**Analysis:** We will take all known human genomes that have been sequenced and reassemble them de novo. This process will allow us to identify any insertions that were previously missed because they did not fit the standard reference genome. By starting from scratch, we aim to uncover candidate alien gene insertions that have gone unnoticed.

**Outcomes:** Identifying novel DNA insertions that were missed in previous analyses will provide evidence of potential alien genetic influence. This approach is critical for discovering new sequences that align with the hypothesis of extraterrestrial genetic contributions.

## Subaim 3: Comparison of Genomic Rearrangements

**Rationale:** Until now, our focus has been on individual genomes. In this subaim, we will test the hypothesis of ancient genetic manipulation by examining consensus sequences of races, subraces, and tribes. Unlike mainstream researchers who look for consensus genomes, we will specifically search for large insertions that might have been missed. Additionally, we will focus on groups known for their connection with abductions and extraterrestrial hybridizations, such as individuals with blood group O, the Basques, Ashkenazi, Dogon and other subraces and tribes.

A great overview of the genetic evolution of races is offered by David Reich in his 2018 book "Who We Are and How We Got Here." The book highlights surprising inconsistencies that arise from the disagreement between real data and the mainstream model of natural evolution. Extraterrestrial involvement will explain these inconsistencies, and inversely, from these inconsistencies, we will be able to identify which sequences were added by ancient extraterrestrial genetic engineers.

**Analysis:** We will reassemble consensus genomes for various races, subraces, and tribes to identify large insertions overlooked by standard alignment to the consensus assembly.

**Outcomes:** By identifying novel insertions in consensus genomes, we will identify patterns and sequences that were potentially added by ancient extraterrestrial genetic engineers.

## Subaim 4: Domesticated Animals

**Rationale:** We will look for genetic traces of ancient genetic manipulations in domesticated animals. Surprisingly, there are only about 10 species of domesticated animals out of hundreds of thousands of species. The hypothesis is that domesticated animals were created by aliens when they were creating human civilization. Zecharia Sitchin suggested that the Anunnaki, ancient extraterrestrials, genetically manipulated animals as part of their efforts to engineer life on Earth.

**Analysis:** The modifications resulting in domestication should carry traces of artificial manipulation, potentially including special codes and sequence patterns inserted by aliens. We will examine genetic patterns in genomes of domesticated animals such as chickens, cows, horses, lambs, goats, geese, cats, dogs, and donkeys. Additionally, we will investigate domesticated plants for similar patterns.

**Outcomes:** Identifying common genetic signatures across different domesticated species will provide evidence of artificial manipulation, supporting the hypothesis of alien involvement in the creation of domesticated species.

## Subaim 5: Cancer Genomic Data Analysis

**Rationale:** Normally, mainstream genetic studies focus on point variations present in the consensus reference genome assembly and often miss large insertions. The exception to this is cancer studies, which specifically look for large chromosomal rearrangements caused by cancer tumors. Conveniently, these public data contain sequences in normal, healthy, noncancerous tissues as well. Also, conveniently, there are tens of thousands of individuals available in public databases, providing a rich dataset for our purposes. By focusing on the normal tissues and ignoring the cancer data, we can utilize this extensive resource for our research.

**Analysis:** In the context of modern alien hybridization, many of the tens of thousands of patients studied could be children of abductees. In the USA, these could represent 1-3% of the population. So say from 100,000 cancer patients in public databases we expect to find about 300 children of alien abductees. We will look for such individuals by searching for outliers in the population that have large genomic insertions in normal healthy tissues.

**Outcomes:** Discovering novel insertions in normal tissues will provide additional candidate regions of potentially alien origin.

## Subaim 6: Celebrities with Extraordinary Traits

**Rationale**: Among the sequenced genomes of unusual and talented individuals are those of notable figures who possess extraordinary abilities and achievements. These individuals are prime candidates for studying potential alien genetic contributions. The hypothesis is that their unique talents and abilities could be due to alien genetic infusions. By examining these individuals, we aim to uncover genetic markers indicating alien influence.

**Analysis**: We will search for publicly available sequence and genotyping data for modern and historical celebrities with extraordinary abilities. These include:

- James Watson: Extraordinary scientific intellect and contributions to genetics.
- Craig Venter: Exceptional talents in combining science with business in fast-paced projects.
- Richard III: Unique physical characteristics.
- Ozzy Osbourne: Resilience to heavy substance use.
- Stephen Colbert: Quick wit and intellectual humor.

We will search for data on other extraordinary celebrities. Additionally, we will offer free full genome sequence analysis and analysis of extraterrestrial traits to exceptionally talented individuals.

**Outcomes**: Identifying unique genetic markers in the genomes of extraordinarily talented individuals will provide candidate regions and patterns of potential extraterrestrial genetic influence. This will enhance our understanding of the potential influence of extraterrestrial genes on human abilities and talents.

## Subaim 7: Analyzing Genetic Markers of Self-Identified Starseeds Using 23andMe

**Rationale:** 23andMe is a popular personal genomics company that offers genetic testing services directly to consumers. Users submit a saliva sample by mail, and 23andMe analyzes their DNA to provide information about ancestry, genetic traits, and potential health risks. With a vast database of genetic information from millions of users, 23andMe provides an invaluable resource for genetic research.

For a fee of $25,000, 23andMe allows researchers to ask custom questions to their user base. We will leverage this feature to ask users if they identify as starseeds, individuals who believe they originate from extraterrestrial civilizations and possess unique genetic and psychic traits. Users who receive the question will have the option to respond if they identify as starseeds. We will then collect the responses and corresponding genetic data from those who self-identify as starseeds. By analyzing this genetic data, we aim to identify specific genetic markers or patterns that distinguish starseeds from the general population. This approach allows us to see if the genetic markers of starseeds align with certain known subraces and blood types, such as the

Basques and individuals with blood type O, providing evidence of potential extraterrestrial genetic influence.

**Analysis:** We will download all genotype data of users who self-identify as starseeds and perform a comprehensive bioinformatics analysis to map the regions of their genomes. We will compare these genetic markers to those of the general 23andMe user population to identify significant differences.

**Outcomes and Interpretation:** Identifying specific genetic markers and alien genomic regions prevalent among starseeds may suggest non-human genetic contributions.

## Aim 2: Experimental sequence analysis of volunteers

**Rationale:**
We will recruit and genotype volunteers self-identifying as alien abductees, starseeds and alien hybrids.

Advertising will be done in social media, UFO conferences, yoga retreats, spirit dance festivals, the Burning Man festival and similar events. Volunteers will be electronically interviewed using AI. This approach ensures that data collection about participants' abduction experiences and backgrounds is consistent and thorough. The use of AI in interviews also helps in standardizing the process and gathering detailed information efficiently. We will prioritize the volunteers based on their interviews.

DNA samples will be collected from participants by mail using buccal swabs or saliva kits, which are non-invasive and easy to administer. These samples will be sent to 23andMe or a comparable service for initial genotyping. This genotyping process covers approximately 600,000 to 700,000 SNPs, providing a comprehensive overview of each participant's genetic makeup for approximately $100 per individual.

The initial analysis will focus on identifying genetic anomalies such as unusual haplotypes (combinations of unusual variants on chromosomes), excess rare variants, and unusual patterns of homozygosity and heterozygosity (unusual similarity or dissimilarity in variants between parents).

For participants with identified genetic anomalies, we will conduct long-read whole genome sequencing. This follow-up sequencing, costing $2,000 per genome, will allow the localization of large sequence insertions and small-sized but presumably large-in-number modifications in repetitive parts of the genome.

This intends to identify unique, presumably alien genetic markers, patterns and sequences that differentiate abductees from the general population. Additionally, we will investigate whether abductees belong to specific populations or subgroups, such as descendants of the Basques, individuals with blood type O, or Ashkenazi Jews, which are known to be more frequent among abductees. Especially interesting will be locating common large sequence insertions in unrelated abductees.

For those abductees who will provide samples for families, we will look for genetic anomalies such as "incomplete parental contribution," where an individual inherits less than 50% of their DNA from each parent. When such cases are identified, we will sequence the complete genomes of these individuals and identify large alien sequence insertions.

## Aim 3: Genetic Analysis of Unusual Ancient and Modern Skulls

**Rationale:** We will analyze the DNA of unusual ancient and modern skulls. Our focus will be on skulls with atypical shapes and large brain capacities, hypothesized to belong to ancient aliens or hybrids. These skulls may contain non-human genetic sequences, providing evidence of extraterrestrial influence.

Max Rempel's interest in sequencing alien skulls was sparkled by the late Lloyd Pye, an anthropologist who studied an alien skull nicknamed Star Child. Max advised Lloyd Pye on experimental and computational methods of sequence analysis of DNA from old bone material. In this project, we are proposing to expand the work started by Lloyd. We will search for these unusual skulls in various countries, engaging with local museums, archaeological sites, and other institutions. We will collaborate with international anthropologists to gather samples of skulls with proper permissions. Additionally, we will engage Ancient Aliens and similar researchers.

Once skulls are identified and the permissions obtained, we will conduct three types of analyses:

1. **Shape Analysis:** Thoroughly examine the morphology of the skulls to document any unusual shapes or structures that might indicate alien or hybrid origins.
2. **Carbon Dating:** Determine the age of the skulls through carbon dating, which requires approximately 0.5 grams of bone. Since all hominids were extingwished by our species by the time 30 thousand years ago, modern unusual skulls would be of particular interest since they unlikely will be earth hominids.
3. **DNA Sequence Analysis:** Extract and sequence DNA from the skulls, also requiring about 0.5 grams of bone. The skulls will be carefully drilled to collect bone dust for these tests. This analysis will focus on identifying non-human sequences or a mix of human and non-human sequences.

Our DNA sequence analysis will look for non-human genetic markers and common large sequence insertions. By comparing these sequences with those from different skulls and with sequences from children of alien abductees, we aim to identify patterns indicating extraterrestrial genetic contributions. Finding non-human DNA sequences in these skulls would support the hypothesis of alien genetic influence.

### Combining the Results from All Aims

The integration of results from all three aims will provide a comprehensive understanding of potential extraterrestrial genetic influences on human evolution. By leveraging bioinformatics analysis of publicly available human genome data (Aim 1), experimental sequence analysis of self-identified abductees, starseeds, and hybrids (Aim 2), and genetic analysis of unusual ancient and modern skulls (Aim 3), we aim to identify unique genetic markers and patterns indicative of non-human sequence contributions.

For example, discovering genetic markers in public genome data (Aim 1) and finding the same markers in the genotypes of modern abductees (Aim 2) would be compelling. If these markers are also detected in ancient skulls (Aim 3), it would provide strong, cross-validated evidence of alien genetic influence.

Another potential synergy could involve identifying unique haplotypes (groups of variants colocalized on a chromosome) associated with extraordinary traits among modern abductees and starseeds. If these haplotypes are also found in ancient skulls, it would suggest a continuous genetic line influenced by extraterrestrials.

Additionally, if certain populations, such as descendants of the Basques or individuals with blood type O, share these genetic markers, it would indicate targeted genetic interventions by extraterrestrials across different time periods and human populations.

These integrated findings would support the hypothesis of extraterrestrial genetic manipulations and sequence infusions.

### Protecting the Rights of Hybrids and Raising Public Awareness

These studies aim to identify individuals with hybrid genetic markers, potentially indicating a mix of human and extraterrestrial DNA. It is crucial to recognize that these individuals may face unique challenges and discrimination similar to racial discrimination. Therefore, it is imperative to protect their rights and ensure they are treated with respect and equality.

As part of this initiative, we will launch a public awareness campaign to educate the public about the existence and rights of hybrids. This campaign will highlight the importance of inclusivity and protection against discrimination, promoting a broader understanding and acceptance of individuals with hybrid genetic backgrounds. By raising awareness, we aim to foster a more inclusive society that respects and values the diversity of all its members.

## Aim 4: Stardust Analysis

Rationale: The high orbit around Earth is theorized to contain spores not only from Earth but also from other celestial bodies such as Venus, Mars, and various moons in the solar system. Given the accuracy in DNA sequencing technology, which is both highly sensitive and precise, we can sequence samples of stardust and identify extraterrestrial sequences. We hypothesize that spores from other planets can survive radiation because they are small, DNA is packed in protein capsules and frozen. These spores are not typically found on Earth because they are outcompeted by local life forms. The goal is to verify the presence of extraterrestrial spores by collecting and analyzing stardust samples.

We will collaborate with space industry leaders such as Elon Musk's SpaceX and Jeff Bezos's Blue Origin. This collaboration will involve swiping surfaces of spacecraft that are deployed only in high orbit and kept hidden during the rocket's landing to prevent contamination. To establish a baseline of Earth-origin sequences; control swipes will be performed on designated surfaces before the spacecraft's launch, from Earth surface-level air filters and from airplane surfaces. Additional swipes will be conducted on the same surfaces after the spacecraft has returned from high orbit. If security prevents us from doing swipes ourselves, we will train rocket service personnel to collect swipes. The collected samples will undergo DNA sequencing to detect and analyze the genetic material. We will compare the sequences obtained before and after the flight to identify unique extraterrestrial sequences. The focus will be on finding identical sequences in independent space samples that are not present in the pre-flight samples. Even a few copies of identical extraterrestrial sequences obtained in independent experiments, as compared to the Earth-origin sequences found before the flight, would be considered a significant discovery and a mission accomplished. This would provide evidence of extraterrestrial life in our solar system.