Preliminary evidence of traces of alien genetic manipulation in humans

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Abstract. I analyzed DNA from 581 complete families in the 1000 Genomes Project to search for nonparental genetic contributions that could indicate recent alien genetic manipulation. My screening of variants in 77 Mb on Chromosome 3 identified 11 families (2%) containing large fragments of DNA sequence in children that matched neither human parent. The most significant case displayed a cluster of 348 nonparental genetic variants with precise simultaneous substitution of identical fragments on both chromosomes. There is no known biological mechanism or technical error that could produce such a change. Achieving such a genetic manipulation at the time of conception with current methods is possible but difficult using CRISPR technology, which emerged in 2013. Since the studied children were born before 1990, human genetic manipulation cannot be an explanation of the observed 16 Kb substitution in homologous chromosomes. This is strong evidence for extraterrestrial genetic manipulation. Further, two unrelated families showed major nonparental insertions at the same genomic hotspot on chromosome 3, suggesting this region serves as a preferred integration site. Quality control analysis confirmed these represent genuine biological signals through low background variation in normal (98%) of studied families, contrasted with sharp nonparental variant density peaks, achieving statistical significance of $p < 10^{-13}$. Families identified as having nonparental insertions displayed a clustered density of nonparental variants 50 times stronger than normal families. The non-random chromosomal clustering and technical precision required for these insertions provide solid evidence for extraterrestrial genetic modification with technology that went beyond human capabilities at the time of conception. Additionally, my pilot analysis of two families with self-reported self-suspecting alien abduction experiences using inexpensive, generic commercial 23andMe genotyping detected similar nonparental contributions, supporting this approach for self-suspecting alien abductee volunteers to identify traces of genetic manipulations as an affordable "do-it-yourself" method. Future research should test the biological significance of alien genetic modifications and see what functions were altered in people.

Introduction

The idea that ancient aliens used genetic engineering to contribute their genetics to humans is deeply embedded in our culture. Zachariah Sitchin documented stories of genetic manipulation of humans by aliens from the over 4000 years old Sumerian tablets (Sitchin 1976). Similar

themes appear in the ancient Indian Rigveda (c. 3500 years old), which includes stories about extraterrestrials and humans producing hybrid offspring (Doniger 1981). Moreover, it is suggested that alien genetic manipulations continued throughout history and were intensified in the 1950s, particularly within English-speaking populations. Claims of U.S. government agreements with aliens for hybridization programs are most widely associated with researchers such as William Cooper (Cooper 1991), David Jacobs (Jacobs 1998), and Linda Moulton Howe (Howe 1989).

A substantial part of the information about the recent Alien Hybridization program was obtained from self-reported abductees. An important contribution to this research was made by John Mack (Mack 1994), a Harvard psychiatrist who interviewed over 200 abductees. Jacobs interviewed 60 abductees first-hand (Wangerin 1993). Barbara Lamb documented alien abductions through hypnotic regressions (Lamb & Piérre 2015). I have conducted my own research into alien hybridization, hosted an experiencer support group, published my video interviews with abductees and described conclusions in my books (Rempel 2023; Rempel 2011).

The principle

For the practical identification of traces of alien genetic manipulation of humans, it is helpful to appreciate the difference between the historical and modern alien genetic manipulation events. In this study, I only examine recent genetic manipulation events.

According to the abductees, typically both parents are taken to the ship, the sperm and eggs are extracted, genetically manipulated and the mother is impregnated with the hybrid embryo. The child is born here and often develops autistic qualities and possesses psychic, artistic and scientific talents.

Since it is now easy and inexpensive to analyze the DNA of both parents and the child, I developed a method to detect alien DNA insertions in the child's DNA. In normal inheritance, a child inherits 50% of their DNA from each parent. However, with alien hybridization, the child would have additional alien DNA sequences absent in the parents. Now, using genetic analysis, these traces of genetic manipulation can be discovered even without prior knowledge of the alien genetic sequence.

Specifically, classical genetic inheritance is that for each chromosome pair, the child receives one chromosome from each parent. In classical inheritance, the child never gets chromosomal DNA from anywhere other than the parents. Since the introduction of CRISPR editing, genetic manipulation has become commonplace for non-human life: mice and other model organisms are routinely manipulated for research, farm animals and agricultural plants are genetically modified for commercial purposes. Genetic manipulation of human germlines (reproductive cells, producing either sperm or eggs) has been very limited, but technically is feasible.

By now, only three children are publically known to have undergone clinical germline genome editing in 2018 (Anon 2018). From animal genome editing, we can clearly see that types of genome editing can range from minimal point substitution, to multiple point substitutions, to

large insertions, substitutions, deletions and rearrangements. While individual mutations and deletions can happen at random and frequently do happen, the emergence of large sequence nonparental insertions is not expected by mainstream geneticists since only parental DNA is thought to contribute to the child's genome. So, large nonparental insertions typically could be a sign of genetic manipulation. The initial genetic manipulation techniques of mammals were published in 1980 (Gordon et al. 1980), and modern CRISPR-based techniques appeared in 2013 (Cong et al. 2013). Therefore, genetic manipulation traces that can be found in people born before 1980 are strong candidates for alien origin.

Genetic approach

In genetics, two types of DNA analysis are used: genotyping and sequencing. True whole-genome sequencing involves reading each chromosome from end to end (T2T - telomere to telomere). Due to technical challenges and since very few scientists can interpret telomeric and centromeric sequences, typical whole genome sequencing doesn't include centromeres and telomeres. Long-read whole genome sequencing includes repetitive elements and is a true whole genome sequence, except telomeres and centromeres. So-called long-read whole-genome sequencing is perfect for identifying and mapping large insertions. Short-read whole-genome sequencing only covers the nonrepetitive 45% of the genome and reads large insertions with less confidence and precision, but it is about 20-fold cheaper than long-read sequencing. Specifically, short-read sequencing is about $400 per sample, and long-read sequencing is about $2000 per sample. Both estimates include DNA extraction and bioinformatics. Yet, traditional genetics heavily relies on genotyping, which is cheaper. The current 23andMe chip v5 provides 650K point mutation markers (direct, not imputed, SNPs) per genome for $120 (as of May 2025). That cost includes DNA extraction and bioinformatics. The ability of standard genotyping to identify large insertions is very limited. Essentially, if a large piece of alien DNA is inserted that has no homology to the human DNA, it will be completely missed by genotyping. If a piece of alien DNA is inserted that is very similar to human DNA and duplicates it, then each marker in the duplicated piece will have duplicated variants, and the duplicated fragment will show an abnormal set of readings on the human map. That can be an indication of an alien insertion, but it will be inconclusive. Most informative would be genotyping results if the aliens would replace a long fragment of parental DNA with DNA from other humans or aliens that are similar to humans, not only in original sequence but also in variants. Then, even 23andMe analysis would recognise the sequence fragment substitution. It will be statistically informative if many SNPs[1] located sequentially in a row have nonparental variants[2].

Importantly, since we don't know the sequence of alien genomes, we can only tell if the insertion is nonparental. For that, we need the data from both parents and at least one child. Such

[1] SNPs - (pronounced snips) - single-nucleotide polymorphisms, also called mutations
[2] variants are called "alleles" in genetics

families are called full families. We will only consider the results when the child is a genetic descendant of both parents. Families where the child is unrelated to one or two parents will not be informative enough to map traces of genetic manipulation.

This study was intended as a pilot study for a future larger study of families of self-reported alien abductees and control families. To make it affordable, I was planning to utilize the 23andMe genotyping service. It was better than others due to reputation, popularity, high coverage, convenience and price per sample. However, since lately, in 2024-2025, 23andMe has become financially unstable, competitors are more suitable to provide a more stable universal option. AncestryDNA and MyHeritageDNA have a good reputation and provide similar 700K SNPs coverage for $99. Moreover, Nebula Genomics offers short-read 30x coverage whole genome sequencing from saliva for $500. This option would be substantially more informative to detect nonparental insertions than genotyping, especially for the insertions that have sequences substantially diverging from human.

In this study I exclusively relied on genotyping of SNPs for several reasons: (1) SNP genotyping is more affordable and will pave the way for families of self-reproted alien abductees to genotype themselves and discover their origins, (2) In the public databases, there is many more open source genotype than sequencing data for familes. So this provides better numbers for statistical analysis. (3) Statistically, it is harder to prove that unusual sequence insertions have not come from genomic duplications. At the same time, local substitutions of a string of parent variants with nonparental variants are very statistically significant and convincing.

Methods

Family genotypes from the 1000 Genomes Project

I downloaded 602 family trios from the 1000 Genomes Project NYGC 30x coverage dataset (https://www.internationalgenome.org/data-portal/data-collection/30x-grch38). This open-source repository contains high-quality whole-genome sequencing data that has been extensively characterized by the international genomics community. The dataset represents father-mother-child trios sequenced to 30x coverage using an Illumina NovaSeq 6000 sequencer. This sequencing depth provides genome-wide variant detection with high accuracy. VCF files and pedigree information were downloaded from the IGSR data portal (https://www.internationalgenome.org/data-portal/data-collection/30x-grch38). These families represent diverse global populations. I performed quality control analysis to verify true Mendelian inheritance patterns. After this verification step, I excluded 21 families that had incomplete data, producing the final dataset with 581 trios. Although the data was produced by sequencing, I used only genotypes (variation information) from the data since it was more informative.

Genotyping

The self-reported or self-suspecting alien abductee families were invited by advertising at a webinar, resulting in the recruitment of two families. Only adult family members were included,

and they provided informed consent. Only full families with both living parents were included. The participants submitted their saliva to 23andMe, had their DNA genotyped, and submitted their data files to the study for analysis. Two families coded as F058 and F083 took part in this pilot study. Each family included 2 parents and two adult children. Alien abductions were suspected by at least one of two parents, but no explicit experiences of abductions were reported.

Bioinformatics analysis

Analysis Pipeline

I developed five sequential scripts to detect nonparental haplotype insertions in 1000 Genomes trio families. All scripts are Python-based and run on Linux or Windows under Anaconda. Scripts include error handling and automatic result saving with version control. Code is accessible at https://github.com/maxrempel/xg1/tree/main/xg1hybrids

Family Validation (TrioLoad49v01)

Validates trio completeness from the NYGC high-coverage dataset. Verifies true genetic father-mother-child relationships based on genotypes.

Nonparental Allele Detection (NPASearch45v14)

Performs sliding window analysis across chromosome 3. Uses 60-SNP windows with 20-SNP steps. Calculates nonparental allele counts and records windows with ≥5 nonparental alleles per 60 SNP window.

Window Ranking (WinRank46v04)

Ranks windows by nonparental allele count. Outputs top 50 significant windows, density metrics, non-parental allele counts, coordinates and family identifiers.

Overlap Analysis (WindowCollapse50v02)

Collapses overlapping outlier windows into single nonparental substitution regions. Classifies families as hybrid or normal based on maximum nonparental allele counts.

Family Comparison Plots (NPAPlotter51v11)

Plots genomic position versus nonparental allele count for selected families. Uses family-specific zoom windows centered on substitution area peaks.

Hotspot Analysis (HotspotPlotter53v01)

Visualizes chromosome 3:75.5Mb insertion hotspot focusing on families HG01505 and HG02293.

Results

In the set of genotypes of 581 families from the 1000 Genomes project, I searched for stretches of nonparental variants (nonparental haplotype substitutions). Because of time and compute constraints, I analyzed 2M (2.3%) out of 87M SNPs in the dataset. I found that 98% of 581 families showed normal traditional inheritance patterns as expected. In these normal families, with the exception of very few anomalies (~0.001% of SNPs), for each child and each SNP, one allele came from the father and one allele came from the mother. The rare anomalies could be explained by a very low mutation rate or a very low error rate, since the DNA samples were extensively sequenced.

However, in 2% of families, I found non-parental pieces of DNA that cannot be explained by standard inheritance Table 1. Since we looked only at human SNPs, the nonparental pieces of DNA looked as if a piece of normal DNA on one of the paired chromosomes was substituted with DNA from an unrelated individual.

These 2% of families with nonparental substitutions included 7 families with moderate numbers of NPA (nonparental alleles) and 4 families with high NPA counts containing hundreds of genetic variants absent in their parents. The most striking case, family HG01505, showed a stretch of 206 nonparental alleles with statistical significance $P<10^{-13}$. These preliminary results suggest that roughly 2% or 1 in 50 people may carry evidence of non-human genetic integration. This number is preliminary since this is the first pilot project, and only 2.3% of the genomic sequence was analyzed.

Table 1: Nonparental alleles (NPA) in 581 families

Classification	NPAs in a stretch per 60 SNPs	Number of Families	Percentage of Population	Statistical Significance (p-value)	Details
Normal Families	<10 NPAs	570	98.1%	$p > 0.0001$	Normal inheritance patterns
Possible Hybrids	10-19 NPAs	7	1.2%	$p < 0.0001$	A stretch of 10-19 NPAs per 60 SNPs
Definite Hybrids	≥20 NPAs	4	0.7%	$p < 10^{-13}$	HG02809: 24 NPAs HG02293: 27 NPAs HG02596: 31 NPAs HG01505: 206 NPAs clustered
Total	**All ranges**	**581**	**100%**	**-**	**Analysis of 77 Mb (2.5%) of the genome**

Key Finding: Approximately 2% of families (11 out of 581) show evidence of unusual genetic insertions that deviate from standard Mendelian inheritance patterns.

Note: NPA = Nonparental Alleles. Analysis conducted on chromosome 3 spanning 77 megabases, representing approximately 2.3% of the total human genome.

In Fig.1, I plotted the peaks from the top 4 hybrid children (the families containing the highest numbers of NPAs, nonparental alleles). I also plotted the same areas in normal children as a reference. You can see that the background is normally very low (~0.001% of NPAs), and the peaks of high NPA density are very sharp.

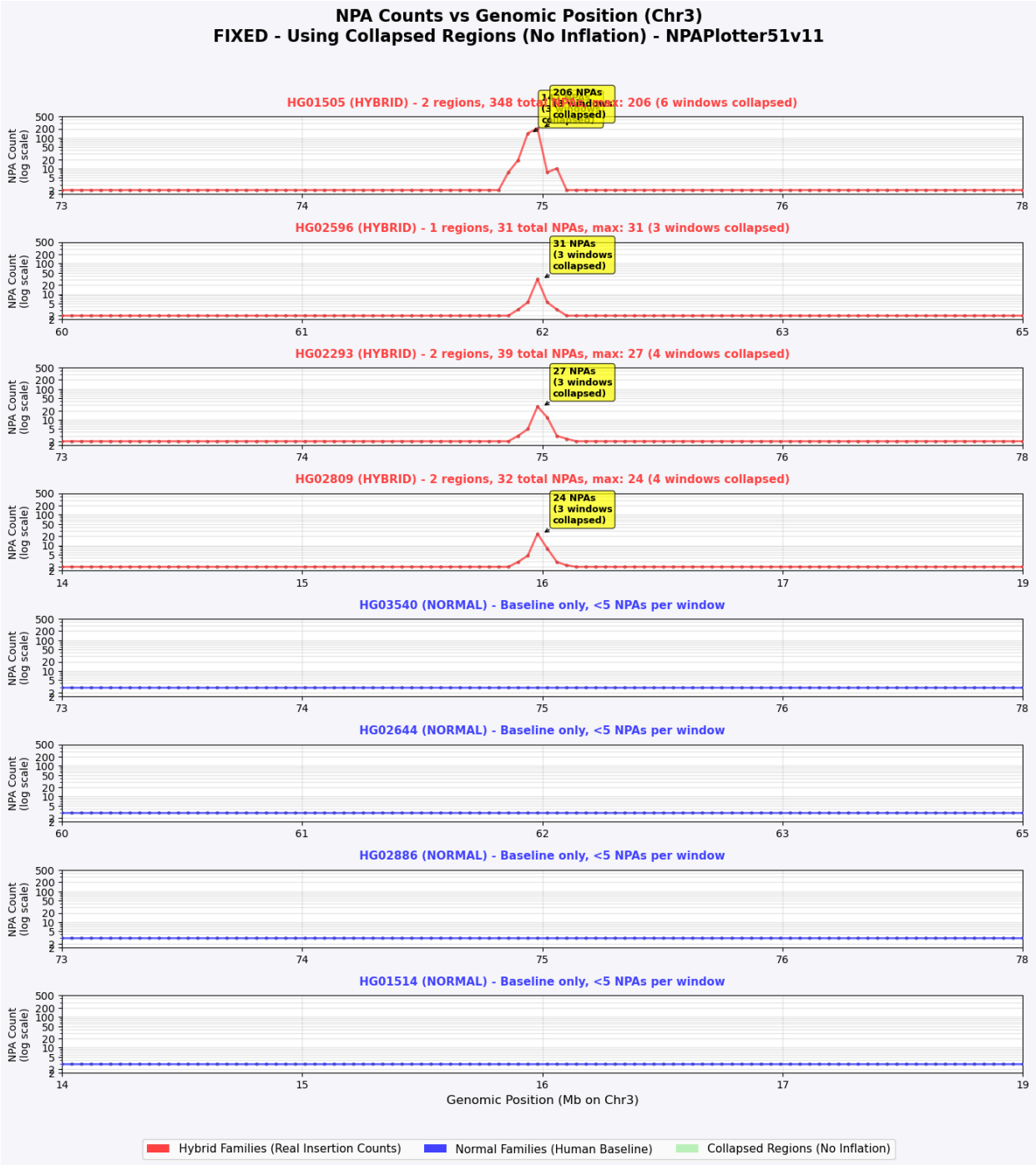

Fig.1: Red: hybrid families with major contributions. Blue: normal families with baseline variation. Yellow annotations: peak NPA (nonparental allele) counts with collapsed detection windows. X axis: genomic coordinate. Y axis: counts of NPAs per 60 SNP window.

Chr3:75.5Mb Insertion Hotspot

The biggest nonparental substitution hotspot was located at chromosome 3:75.5Mb. Two independent families (HG01505 and HG02293) showed major nonoverlapping nonparental

substitution regions within 68kb of each other in this region, suggesting a genomic hotspot for nonparental haplotype substitution. One trio, HG01505, has two separate nonparental substitution regions with 142 and 206 nonparental alleles, respectively (348 total), while family HG02293 showed insertions with 27 nonparental alleles.

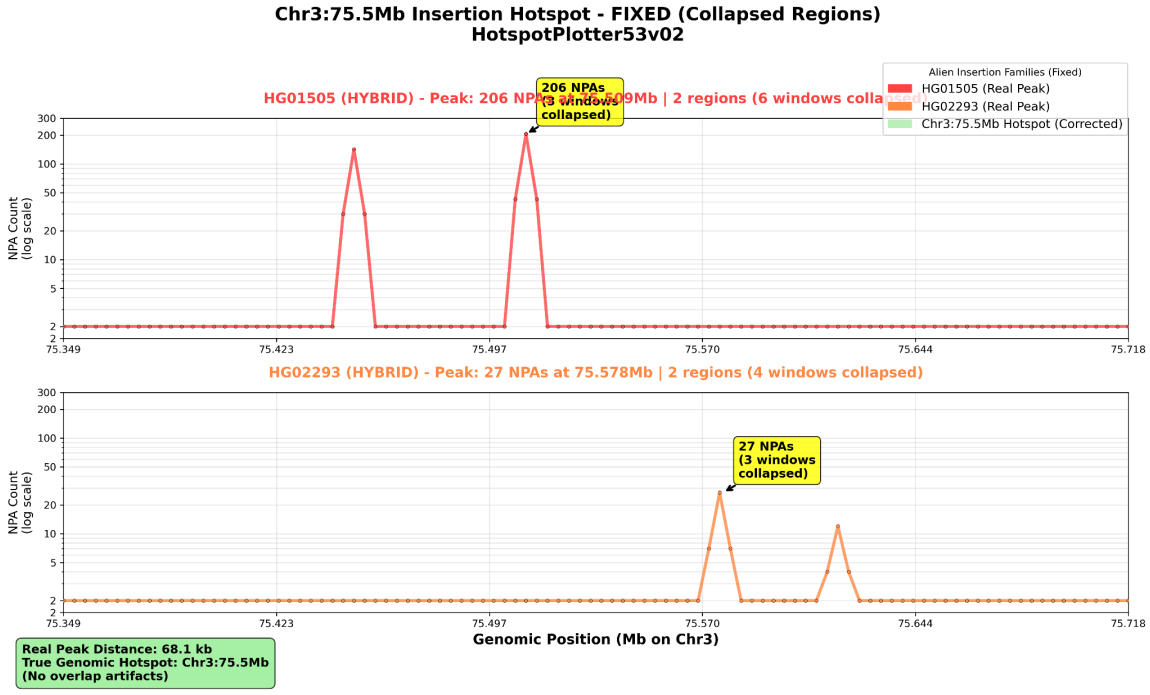

Fig.2. Chromosome 3:75.5Mb insertion hotspot analysis showing two independent families with major nonparental haplotype substitutions. Family HG01505 displays two insertion regions (142 and 206 nonparental alleles) totaling 348 nonparental variants, while family HG02293 shows a 27-allele insertion 68kb away.

Double-Strand Substitution in HG01505

Normally, we would expect that a substitution of a sequence would happen only in one of the paired chromosomes. Just in case, I checked the alleles in the largest substituted fragment (child HG01505). I looked at the inheritance pattern at 252 positions in family HG01505, shown as the top right red peak in Fig.2. At each SNP position, I compared the child's two chromosome copies against all four parental chromosome copies. The analysis revealed that 100% of violations involved both of the child's chromosome copies carrying alleles that were completely absent in both parents. In genetic terms it could be called biallelic or double nonparental haplotype replacement. This means that in a child's DNA, both parental fragments were replaced with non-parental copies. The nonparental fragment length is 16 kb. This type of anomaly is very unusual, and it eliminates technical contamination as an explanation because contamination would create mixed inheritance violations where some positions show normal inheritance from one parent. The complete absence of single-parent inheritance violations

demonstrates that both chromosome copies were systematically replaced with foreign genetic material across the entire 16 kb region, indicating precise artificial genetic manipulation.

Samples from self-reported self-suspecting abductee families

In addition, we did a preliminary analysis of 2 families from self-reported self-suspecting abductee families. The families were invited via a webinar and provided informed consent. The DNA was genotyped by 23andMe and analyzed by me. In the older version of the analysis pipeline, one family showed a number of NPAs (nonparental alleles), and another family did not show unusual NPA enrichment. Yet, I plan to reanalyze these 2 families with the new version of the analysis pipeline, which was optimized on a large number of families. Since the new version is much more sensitive, it might show more NPAs. The initial analysis demonstrated that commercial genotyping services such as 23andMe and MyHeritage are suitable for genotyping and, later, with my pipeline, finding traces of genetic manipulation in full families.

Discussion

Surprisingly, nonparental insertions were not described before. Most likely, researchers didn't take them seriously since alien hybridization was not considered. Otherwise, nonparental insertions are unlikely to occur. None of the known natural biological mechanisms can explain such dense clusters of nonparental substitutions with over 20 NPAs in a cluster. Genomic duplications and rearrangements can not cause the anomaly since they still have parental alleles. Natural transmission of genetic material from one human to another hasn't been discovered. It would be especially unlikely since the genetic material from an unrelated human should not only get into the germline (sperm or eggs) but also needs to substitute the original piece of parents' DNA in its exact location and orientation. This excludes transmission by viruses, which can transfer small pieces of DNA but would insert them elsewhere in the genome. The explanation that a parent has a mosaicism (mixed genetics) is also unlikely since mosaicism would produce a lot of mixed genotypes all over the genome and not clean genotypes in a small spot as seen on the graphs (Fig.1). The idea that autism is a result of alien hybridization is discussed by Barbara Lamb (Lamb & Piérre 2015) and Mary Rodwell (Rodwell 2017). Considering that the prevalence of autism is 1 in 30 children under 10 years old, and it doubles every 10 years, that might be in agreement with the prevalence of alien hybridization.

Conclusion

Large nonparental haplotype substitutions were identified in public trio genome data and in self-suspecting abductee families, suggesting alien genetic manipulation. These results show that current genotyping can reveal nonparental genetic substitutions. Further expansion of this research with long-read sequencing and abductee family genotyping is needed.

References

Anon, 2018. He Jiankui affair. *Wikipedia*. Available at: https://en.wikipedia.org/wiki/He_Jiankui_affair.

Cong, L. et al., 2013. Multiplex genome engineering using CRISPR/Cas systems. *Science*, 339(6121), pp.819–823. Available at: http://dx.doi.org/10.1126/science.1231143.

Cooper, W., 1991. *Behold a Pale Horse*, Light Technology Publications.

Doniger, W. (translator), 1981. *The Rig Veda*, Penguin Classics.

Gordon, J.W. et al., 1980. Genetic transformation of mouse embryos by microinjection of purified DNA. *Proceedings of the National Academy of Sciences*, 77(12), pp.7380–7384. Available at: http://dx.doi.org/10.1073/pnas.77.12.7380.

Howe, L.M., 1989. *Alien Harvest: Further Evidence Linking Animal Mutilations and Human Abductions to Alien Life Forms*, LMH Productions.

Jacobs, D.M., 1998. *The Threat: Revealing the Secret Alien Agenda*, Simon & Schuster.

Lamb, B. & Piérre, M.M., 2015. *Meet the Hybrids: The Lives and Missions of ET Ambassadors on Earth*, Amazon Digital Services / Lisa Hagan Books.

Mack, J.E., 1994. *Abduction: Human Encounters with Aliens*, New York: Scribner.

Rempel, M.M., 2011. *Celestial Science*, United States: Amazon Digital Services LLC. Available at: https://www.amazon.com/dp/B006O2OXBK.

Rempel, M.M., 2023. *Welcome to Earth! A Guide for Aliens*, Independently Published. Available at: https://www.amazon.com/dp/B0DH4GFXVV.

Rodwell, M., 2017. *The New Human: Awakening to Our Cosmic Heritage*, New Mind Publishing.

Sitchin, Z., 1976. *The 12th Planet*, New York: Stein and Day.

Wangerin, W., Jr, 1993. *Branta and the Golden Stone*, Simon & Schuster.