Iraqi Journal of Medical and Health Sciences, ISSN: 3078-8722, Vol. 3, No. 1 2026, Pages 7- 13
DOI: 10.51173/ijmhs.v3i1.80

Iraqi Journal of Medical and Health Sciences
Journal Homepage
https://ijmhs.mtu.edu.iq/ijmhs/index.php/home

RESEARCH ARTICLE – GENERAL BIOCHEMISTRY, GENETIC AND MOLECULAR BIOLOGY

Two Sets of DNA, One Body: A Multidisciplinary Review of Human Chimerism from Biological Mechanisms to Clinical and Forensic Challenges

Israa M. Ali Alameen[1*], Nabil Amin[2]

[1]Department of Biology, Faculty of Sciences, Yarmouk University, Irbid, Jordan

[2]Deutsche Ärztekammer, Landesärztekammer Hessen, Hessen Deutschland Hofgeismar, Germany

*Corresponding author E-mail: Israa.m.ali.alameen@gmail.com

Article Info.

Article history:

Received
20 Jan. 2026

Revised
28 Fab. 2026

Accepted
10 March.2026

Publishing
10 May. 2026

Abstract

Background: One person, one genome; this is the foundation of the biological axiom, nowadays it is exposed to a big challenge due to the human chimerism phenomenon. The appearance of genetically distinct lineages in one person. It was rare in the past, but nowadays it has become more common due to Multifactorial causes. In this narrative review, we will expose a different aspect and different Implications of these phenomena.

Methods: We adopted a narrative approach to collect the newest studies and reports published between 2018 and 2026, related to this phenomenon. The data were collected and analysed from 18 article review, from academic data base (PubMed, NCBI).

Results: The review revealed that there is a comprehensive shift in these couple of years, 2025-2026, where the chimerism has evolved from a diagnostic complication into a therapeutic tool to achieve the immunological tolerance in organ transplantation and bioengineering human organs within interspecies hosts, which triggered to create a gap in the forensic aspect, due to the limitation in the traditional (STR-PCR) test which failed to account for genomic plurality and that led to legal paradoxes in parentage and criminal identification.

Conclusion: The science and forensic fields have to standardise all concepts and protocols about the chimerism, which include the medical terms and the procedures of collecting samples and tissue from the body and using advanced DNA technologies like NGS. We have to accept that biological identity is not always a single profile or a static code; instead, it can be a complex and changing mosaic.

Publisher: Middle Technical University

Keywords: Human Chimerism; Micro Chimerism; Forensic DNA; Next-Generation Sequencing (NGS); Vanishing Twin Syndrome.

1. Introduction

One person, one genetic code" is the core of the forensic and genetic science [1]. Contrary to the common belief, Recent studies revealed that the human body is almost a (genetic mosaic), nowadays some techniques have a high resolution reaching to 0.3 % which revealed new sequences weren't noticed before [2– 10]. The presence of more than one sequences in one human body is called, human chimerism [11, 12]. There are two types of chimerism, we should to distinguishing between them the first one is a Gross chimerism (resulting from extensive embryonic fusion,) and the second one is micro chimers, (resulted low level cellular integration [13, 14]. The recent studies have helped the scientific community to expand the understanding of the "Communicatee." This theory explains the bidirectional cellular dialogue, which continues throughout the lifespan, that has a crucial role in helping to repair the maternal tissues and immune system [15, 16]. It's worth mentioning that research done in 2025 has expanded the concept the Milk-derived Micro chimerism, where it has been suggested that the maternal T-lymphocytes integrated in the newborn during breastfeeding potentially shape neonatal immune maturation [17, 18].

Over time, the chimerism concept has improved from being just a visible characteristic, such as eye color, into therapeutic tool, in which the clinical studies reported positive results in the "immunological tolerance." which gives the patient who receives the transplanted organ immunosuppressive drugs the option of discontinuing that drug for the rest of his life [19- 22]. This new field requires strict and clear global ethical rules to prevent the neural integration and to protect the moral status of chimeric models by setting strict developmental limits [23]. The rise of the assisted reproductive technologies (ART) has significantly increased the prevalence of the chimerism, and that hurts the genomic plurality, introducing profound forensic crises, as we see in the parentage exclusion cases like Lydia Fairchild [24]. To resolve the forensic gap, this review assesses the shift from traditional STR-PCR to a "Two-Tiered Forensic System," using the NGS and "Multi-Tissue Profiling" as essential protocols for navigating the collapse of genetic absolutism [25]. This narrative review aims to collect and explain all biological mechanisms and identify forensic gaps. It will address the lack of comprehensive protocols and explain the advantages of shifting toward using

chimerism as a therapeutic strategy for autoimmune diseases and organ failure, as reported in the most recent studies in 2026 [26]. Search strategy include comprehensive review was conducted about human chimerism and its forensic implications to ensure a thorough and up-to-date understanding of this phenomenon, using multiple electronic databases, such as PubMed, Scopus, NCBI, and Google Scholar. We attempted to cite the most recent literature as much as possible, but some basic fact found in older sources due to the relative scarcity. The priority was given to the peer-reviewed articles, the high-impact case studies (e.g., the Lydia Fairchild case), and the reports of the clinical involving hematopoietic stem cell transplantation (HSCT) and assisted reproductive technologies (ART) as shown in Fig. 1. This timeline shows how the chimerism phenomenon changed over time from a rare forensic problem into an important therapeutic too.

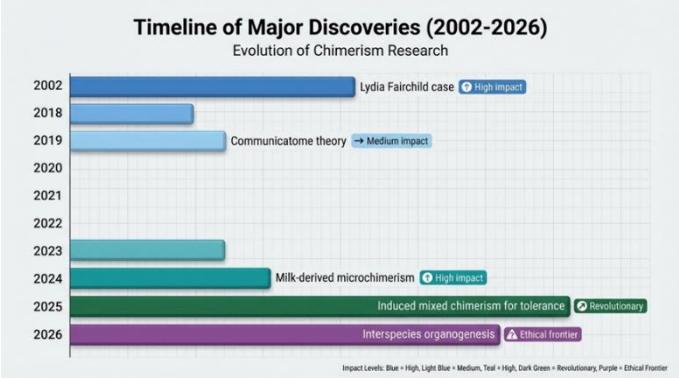

Fig. 1. Evolution of chimerism research (2002–2026)

2. Classification and Biological Mechanisms

The Genetic plurality is divided into two basic phenomena, each of them arising from different embryological mechanisms, so it is very important to distinguish between the biological origins of cell lineages, that will help to understand how the individual can have two different sets of DNA in their body.

2.1. Distinction between chimerism and mosaicism

To distinguish between Chimerism and Mosaicism, we have to look at the number of zygotes which are involved at the inception of life. Genetic Mosaicism occurs when there is just one fertilized egg (one zygote) exposed to a spontaneous mutation or if the chromosomes fail to disjoin during the early mitotic divisions. that leads all cell lines share the same ancestral origin. Large-scale genomic studies conducted in 2024 revealed that mosaicism is a universal feature of human development. It reported that the healthy tissues usually had a significant chromosomal variation without pathological outcomes [2].

In contrast, Human Chimerism occurs when two or more zygotes fuse. In an individual with chimerism, what happens is that two or more different cell populations, whether they are "siblings" or "strangers", coexist within the same host. This can manifest as disparate sex chromosomes (XX/XY), or different blood types or even distinct HLA profiles [11]. From a forensic statistical perspective, it is important to distinguish between "Micro chimerism," which is present in about 90% of women with a history of pregnancy, and "gross/tetra gametic chimerism," which remains an extremely rare clinical case, with fewer than 100 documented cases around the world. This method shows that minor genetic differences are normal, but the major differences are rare, and it also identifies the cases where forensic analysis might completely fail [4] as shown in Fig. 2. This pie chart illustrates the statistical hierarchy of genomic plurality as synthesized from the 2018–2026 literature review.

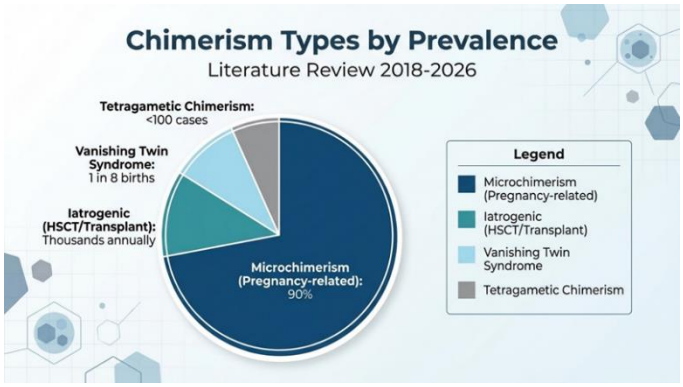

Fig. 2. Distribution of chimerism types by prevalence based on 2018-2026 literature synthesis

Microchimerism is related to pregnancy, is a very common type, found in about 90% of pregnant women, and represents a nearly universal "communicatome"(biochemical communication between these cells and the mother's body). Iatrogenic chimerism reflects the prevalence-increasing range of HSCT and organ transplantation, resulting in thousands of cases annually, where individuals possess a permanent dual genetic profile. Vanishing twin syndrome (VTS) occurs in 1 to 8 % of single births, triggering "cryptic" multi-genomic states that are often undetectable through the traditional detection methods. Tetragametic Chimerism remains an extremely rare clinical case with <100 documented cases, and it poses the most significant threat to forensic "genetic absolutism" in parentage exclusion scenarios.

2.2. Natural chimerism mechanisms and pathways

Natural chimerism occurs through spontaneous biological events, categorized by the extent of cellular integration. This include tetra gametic chimerism that involves the fusion of two distinct embryos at the early blastocyst stage. The resulting person possesses a "patchwork" of tissues; for instance, the hematopoietic system may belong to one genome while the reproductive organs belong to another different genome, a phenomenon underpinning legal paradoxes in parentage cases [27]. Vanishing twin syndrome (VTS) refer to the normal estimated of vanishing twin syndrome occur as 1 in 8 single births, it involves the reabsorption of a non-viable embryo by the surviving twin. recent study conducted in 2025 suggest these "vanished" genomes persist in specialized "host niches," effectively creating a cryptic multi-genomic state that remains hidden by standard testing [28]. Micro chimerism bidirectional exchange shown the 2024 "Communicatome" theory redefines micro chimerism as a complex immunological regulatory system rather than a transient byproduct. Fetal micro chimerism explain fetal cells (FMc) integrate into maternal organs, so it participating in tissue repair or potentially contributing to autoimmune pathologies [29,30]. Maternal micro chimerism include maternal cells (MMc) cross into the fetus. A breakthrough in March 2025 identified that maternal T-lymphocytes transferred through human milk establish lifelong maternal micro chimerism, and have a main role in shaping the neonatal immune maturation. Future research must develop algorithms that can distinguish between the external accidental contamination and endogenous microchimeric, which is known as "noise" (consisting about 1-2% in certain tissues), and use them in bioinformatics [31].

3. The Effect of the Medical Interventions and ART

In nature, the biological mechanisms of chimerism usually occur spontaneously; despite this, modern medical progression lead to a significant shift in its status from a rare case to a clinical commonality. This section explains how is the human intervention leads to an increase in the prevalence and clinical utility of the chimeric state [31].

3.1. Assisted reproductive technology (ART) as a catalyst

The introduction of ART into the reproductive technology field has created an environment with high potential that facilitates genomic plurality. Multiple embryo transfer (MET) and fusion is placing multiple embryos in limited space (the woman's uterine) increases the potential of Tetra gametic Chimerism [32]. Increased "vanishing twin" events explain prevalence of using the ART technique to increase the pregnancy potential rate also has a negative side, which is increasing the frequency of early twin loss, which means the persistence of reabsorption of the lineages in "host niches". Adopting the protocol of "Informed Disclosure" in a forensic setting will help to detect the presence of micro chimerism; therefore, individuals convicted by ART techniques should be prompted to disclose this history during forensic sampling to avoid "phantom suspect" errors in DNA databases [33].

3.2. Iatrogenic chimerism

Acquired genetic duality, iatrogenic Chimerism, acquired due to medical procedures, leads to the creation of a permanent "split" in biological identity. Allogeneic hematopoietic stem cell transplantation (HSCT) this process include Monitoring of the (HSCT) via NGS-based analysis becomes mandatory according to the 2025 UK and Belgian Guidelines. The forensic protocol must take into consideration the period of “transition phase," during the diagnosis, which is the period during which patient analysis revealed mixture of DNA profiles directly after receiving the stem cells from the donor, before achieving full donor chimerism in the peripheral blood [34]. Solid organ transplantation and induced tolerance the most innovative shift in 2025–2026 is Induced Mixed Chimerism. By performing a partial bone marrow transplant from the organ donor, the recipient's immune system is "educated" to recognize the foreign organ as "self" [35] emerging frontiers Interspecies Chimerism Growing human-derived organs within porcine hosts using blastocyst complementation is the frontier of 2026.

4. Forensic and Legal Challenges

The collapse of genetic absolutism the fundamental principle of forensic DNA profiling is based on the assumption that an individual’s DNA is unique and uniform across all biological tissues. However, the phenomena of chimerism and micro chimerism introduce a "genomic plurality" that threatens the reliability of DNA as an absolute legal truth [36].

4.1. The crisis of maternal exclusion

Lessons from case law historically, high-profile cases like lydia fairchild (2002) alerted the legal community to the dangers of chimerism [8]. Fairchild was nearly stripped of her parental rights when blood DNA tests excluded her as the biological mother of her children, despite having given birth to them. To resolve such "parentage exclusion" paradoxes, this review proposes the adoption of "Mandatory Multi-Tissue Sampling”. Legal systems must ensure that a "negative" result from a single tissue (e.g., blood) is insufficient to invalidate parenthood if chimerism is suspected; instead, samples from secondary embryonic lineages, such as cervical cells or hair follicles, must be legally required [37]. Historical contrast the Case of Alun Keeler (1953).

4.2. Chimerism in criminal investigations and evidence interpretation

In criminal forensics, multiple DNA profiles within a single suspect can lead to catastrophic misinterpretations: Post-transplant forensic discrepancies the blood of an HSCT recipient reflects the donor's DNA, while the skin or hair save or retains the recipient’s genome [4]. This creates a "suspect-evidence mismatch" if the reference sample is taken from the wrong tissue. The "phantom" suspect in Vanishing Twin Syndrome, a suspect may leave biological evidence matching a "non-existent" person—the absorbed twin. This creates a forensic "phantom" whose profile exists in the survivor's tissues but not in any external database [38].

4.3 Technological solutions

From STRs to NGS usually the traditional Short Tandem Repeat (STR) analysis fails to detect the microchimerism, that leads to false exclusions. But the Next-Generation Sequencing (NGS) offers about 0.3% of sensitivity, but the disadvantage is that the high cost, its remains a barrier for universal adoption. As illustrated in Figure 3, the tenfold price difference between STR-PCR and NGS justifies the proposed targeted approach to ensure the laboratory budget sustainability. To bridge this economic-technical gap, this review advocates for a "Two-Tiered Forensic

System"[39]. Tier 1 (Routine): STR-PCR occupies the first place and remains the primary tool for standard cases due to its speed and the suitable cost. Tier 2 (Confirmatory): NGS is mandated only in special cases, such as those involving ART history cases, bone marrow transplantation, or when there is a conflict in the results across different tissues as shown in Table 1.

Table 1. Comparative Analysis of Forensic Accuracy (2026 Models)

Feature	Traditional STR-PCR (Blood Only)	Proposed 2026 Protocol (NGS + Multi-Tissue)
Detection Threshold	~5-10% (Low Sensitivity)	<0.3% (High Sensitivity)
Paternity/Maternal Result	False Exclusion (Paradox)	Confirmed Inclusion (True Genetic Identity)
Bioinformatic Filter	None (Raw Data)	Deconvolution Algorithms Applied
Legal Outcome	Potential Wrongful Charge	Accurate Biological Verification

This comparative analysis shows limitations that hinder the use of the high-sensitivity next-generation sequencing (NGS), as shown There is a significant gap in the cost (10x price difference) between the STR-PCR and (NGS), in addition to the long time (8-24 hours) required, these limitation were taken into count, even with the accuracy (<0.3\%) provided by this technique necessary for resolving chimeric paradoxes a hypothetical chimeric case table to explain the necessity of the proposed protocols by comparing the traditional methods with the 2026 NGS-based standard.

5. Ethical Dimensions and Research Gaps

Ethical dimensions and research gaps include several unresolved questions and research gaps have been revealed as a result of chimerism transitions from a biological curiosity to a cornerstone of forensic science. The ethics of interspecies chimerism and organogenesis the most ethical issue related to interspecies chimaera is that results from the development of human-derived organs in porcine hosts. Neural and germline integration neural and germline Integration one of the most significant concerns is the risk resulting from the migration of human stem cells to the animal's brain or reproductive system, which could potentially lead to the creation of a "human-like" consciousness or gametes [23]. To prevent that, "Neural and Germline Barriers" should be applied, which mean knocking out certain genes before injection by using CRISPR-Cas9 as mentioned in the 2026 ethical roadmap, in that way. The scientists can ensure the localisation contribution of human cells to the targeted organ (e.g., heart or kidney), and prevent any "humanisation" of animal consciousness as shown in figure 3 [39,40]. Note about CRISPR Fidelity: even if CRISPR-Cas9 serves as a safeguard against neural humanisation in the interspecies models, it is still theoretically, and it should take the "off-target" mutations in consideration. As of 2026, the scientific community emphasises that chimeric models must remain under strict "Ethical Moratoriums", until achieving to absolute precision in cellular homing.

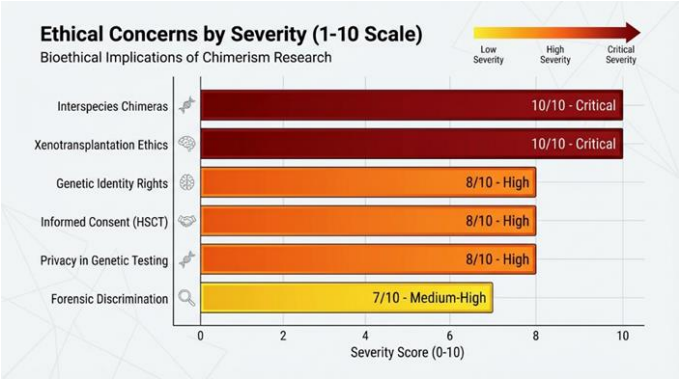

Fig. 3. Bioethical impact assessment of chimerism research

This chart shows the ethical concerns based on the severity scale. where Interspecies chimerism and xenotransplantation represent the highest ethical frontier, which requires immediate regulation and supervision. Moreover, other issues, such as genetic identity rights and forensic discrimination, come in the second place in severity.

6. Discussion

The results of this review showed that the "one-genome" theory is no longer viable in forensic or even in clinical settings. Today, in 2026, several points are raised for discussion here. The most important one is the concept of Normalisation Chimerism. Due to the expansion of using ART and where the mothers of milk can derive micro chimerism, we have to ask: Is anyone truly genetically uniform? Moreover, 90% of mothers carry their fetal cells, so we have to redefine the "standard" DNA profile as it must evolve from a single code to a statistical range. In this context, it is recommended that legal definitions of "Biological Identity" be updated to reflect a dynamic mosaic state, protecting chimeric individuals from genetic discrimination in insurance or employment. Case study: the lydia fairchild paradox (2002) include: Case overview: Lydia Fairchild, a mother of two (and pregnant with a third), applied for public assistance in Washington State. As a routine part of the application process, she should have done a maternity confirmation test. The conflict: The Conflict: The results confirmed their father and exclude the mother; that triggered to accused her of fraud and an attempt to remove the children from her custody. The turning Point: The court directed to repeat the test, therefore another DNA sample was taken from Lydia's developing fetus during the birth. again, the result of the fetus's DNA did not match Lydia's blood DNA, but matched her cervical tissue. Scientific conclusion: Scientific Conclusion: Lydia was a Tetragametic chimerism. She absorbed the cells of her fraternal twin, when they were in her womb. Another DNA copy ws in her ovaries from her "unborn sister," which later she passed on to her children, while her blood already carried her own primary DNA. Legal precedent: lydia's case is considered a primary reference for the "collapse of genetic absolutism." It proved that the single DNA test is legally insufficient and can lead to biologically misleading results [30- 32].

Regarding Privacy vs. Public Safety, technical disclosure creates tension due to the conflict between patients' privacy and the necessity of forensic accuracy, which requires a new legal framework to protect people who disclose their status. Forensic intake forms should include questions about bone marrow or organ transplantation and fertility treatments. Also, courts should take into consideration multiple tissue types, such as cheek swabs, hair roots, or cervical cells not only blood, in paternity testing before ruling out a biological parent or in chimerism suspected cases. To prevent that, it should apply the "Neural and Germline Barriers", which mean knocking out certain genes before injection by using CRISPR-Cas9 as mentioned in the 2026 ethical roadmap, in that way the scientists can ensure the localisation contribution that human to the target organ (e.g., heart or kidney), and prevent any "humanisation" of animal consciousness. Note about CRISPR Fidelity: even if CRISPR-Cas9 serves as a safeguard against neural humanisation in the interspecies models, it is still theoretically, and it should take the "off-target" mutations in consideration. As of 2026, the scientific community emphasises that chimeric models must remain under strict "Ethical Moratoriums", until achieving to absolute precision in cellular homing [40]. Privacy vs. forensic utility there is a conflict between two important needs: the forensic need, which is the knowledge of a person's ART or HSCT history, leading to the correct interpretation of DNA evidence, and the privacy need, which means that someone is forced to disclose such personal medical history, which may violate their legal rights under laws like GDPR [40].

The NGS Transition remains a pivotal point; while this review advocates for Next-Generation Sequencing (NGS), the economic barrier is still real. The global "Justice Gap" remains a concern; as long as developing country rely only on STR-PCR, the risk of false genetic exclusions remains a systemic threat. To mitigate this, a Two-Tiered Forensic System should be implemented: STR-PCR for routine casework and mandatory NGS for "high-risk" profiles, such as individuals with a history of ART or bone marrow transplants. Parallel to this, funding should be prioritized for developing Deconvolution Algorithms capable of distinguishing "environmental noise" from true endogenous micro chimerism (The Signal-to-Noise Challenge). Given these challenges, this review argues for the standardisation of forensic protocols. Refined Medical History Disclosure refined Medical History Disclosure: The forensic forms filled out by the patients should be updated to include information about ART or HSCT, and it should be considered as a necessary laboratory parameter, rather than a social inquiry, while ensuring the protection of the patients' privacy and ensuring that the correct application of bioinformatic filters during DNA analysis. Comprehensive tissue profiling a "multi-tissue profile" must be considered as a mandatory requirement in an individual who's suspected as chimeric case to detect the full mosaic of their identity. To achieve justice, it must rely on Next-Generation Sequencing (NGS) as soon as possible to resolve these crises. with due consideration of the technical and ethical challenges [38- 40].

On the clinical and ethical levels, the long-term studies play a crucial role in drawing a map for what can be called the "communicatome", which is essential to understand how mothers' breast milk-derived microchimeric maternal cells affect the development of the neonatal immune system and vaccine responses. To appreciate the evolution of chimerism in forensics, one must reference the first documented human chimerism, Alun Keeler. Unlike modern cases identified via NGS, Keeler was identified through simple blood typing which revealed two distinct blood groups. Contrasting this with the Fairchild case highlights how chimeric detection has transitioned from accidental serological findings to complex genomic deconvolution, necessitating the multi-tissue protocols proposed in this review. Clinically, inducing Mixed Chimerism may help eliminate the need for lifelong immunosuppressive therapy following organ transplantation. However, a clear ethical and regulatory foundation is needed to govern such advances. For example, in interspecies research models, it must mandate the use of CRISPR-based gene knockouts to prevent human cell migration into the animal neural or reproductive tissues. Finally, the Genetic Barcoding system has become a standard requirement and is now mandated to ensure transparency and to prevent illegal organ trafficking.

7. Conclusion

In this era, the biological paradigm of "one person, one DNA" has lost its value in faced of high-resolution genomics and advanced biotechnology. This narrative review has demonstrated that human chimerism is not a medical anomaly, as once thought, but a phenomenon with multifaceted implications, ranging from the natural embryonic processes, such asVanishing Twin Syndrome, to cutting-edge clinical interventions. Biological identity must be redefined as a mosaic, requiring a nuanced approach to define what constitutes an individual's 'genetic truth' to ensure justice in the face of this evolving science.

Acknowledgements

We would like to thank to Department of Biology, Faculty of Sciences, Yarmouk University, Irbid, Jordan. Also thank full to Deutsche Ärztekammer, Landesärztekammer Hessen, Hessen Deutschland Hofgeismar, Germany for help and support.

Nomenclature & Symbols			
HSCT	hematopoietic stem cell transplantation	MMc	maternal cells
ART	assisted reproductive technologies	FMc	fetal cells
VTS	Vanishing twin syndrome	NGS	Next-Generation Sequencing

References

[1] Grimes, K., Jeong, H., Amoah, A., Xu, N., Niemann, J., Raeder, B., ... & Korbel, J. O. (2024). Cell-type-specific consequences of mosaic structural variants in hematopoietic stem and progenitor cells. Nature Genetics, 56(6), 1134-1146. https://doi.org/10.1038/s41588-024-01754-2.

[2] Cosenza, M. R., Rodriguez-Martin, B., & Korbel, J. O. (2022). Structural variation in cancer: role, prevalence, and mechanisms. Annual Review of Genomics and Human Genetics, 23, 123-152. https://doi.org/10.1146/annurev-genom-120121-101149.

[3] Sano, S., Horitani, K., Ogawa, H., Halvardson, J., Chavkin, N. W., Wang, Y., ... & Walsh, K. (2022). Hematopoietic loss of Y chromosome leads to cardiac fibrosis and heart failure mortality. Science, 377(6603), 292-297. DOI: 10.1126/science. abn3100.

[4] Sanz-Piña, E., Santurtún, A., & Zarrabeitia, M. T. (2019). Forensic implications of the presence of chimerism after hematopoietic stem cell transplantation. Forensic Science International, 302, 109862. https://doi.org/10.1016/j.forsciint.2019.06.020.

[5] Shao, D. D., Kriz, A. J., Snellings, D. A., Zhou, Z., Zhao, Y., Enyenihi, L., & Walsh, C. (2025). Advances in single-cell DNA sequencing enable insights into human somatic mosaicism. Nature Reviews Genetics, 26(11), 761-774. https://doi.org/10.1038/s41576-025-00832-3.

[6] Geiger, H., Furuta, Y., van Wyk, S., Phillips III, J. A., & Tinker, R. J. (2024). The clinical spectrum of mosaic genetic disease. Genes, 15(10), 1240. https://doi.org/10.3390/genes15101240.

[7] Truty, R., Rojahn, S., Ouyang, K., Kautzer, C., Kennemer, M., Pineda-Alvarez, D., ... & Aradhya, S. (2023). Patterns of mosaicism for sequence and copy-number variants discovered through clinical deep sequencing of disease-related genes in one million individuals. The American Journal of Human Genetics, 110(4), 551-564.https://doi.org/10.1016/j.ajhg.2023.02.013.

[8] An, J., Nam, C. H., Kim, R., Lee, Y., Won, H., Park, S., ... & Ju, Y. S. (2024). Mitochondrial DNA mosaicism in normal human somatic cells. Nature Genetics, 56(8), 1665-1677. https://doi.org/10.1038/s41588-024-01838-z.

[9] Chandler, N. J., Scotchman, E., McKay, F., Ramachandran, V., & Chitty, L. S. (2025). Parental Somatic Mosaicism Detected During Prenatal Diagnosis. Prenatal Diagnosis, 45(2), 171-177. https://doi.org/10.1002/pd.6712.

[10] Tsuchida, N., Uchiyama, Y., Hamanaka, K., Okamoto, N., Fujimoto, A., Enoki, H., ... & Matsumoto, N. (2025). Mosaic deletions detected by genome sequencing in two families. Journal of Human Genetics, 70(6), 307-312. https://doi.org/10.1038/s10038-025-01336-y.

[11] Madan, K. (2020). Natural human chimeras: A review. European journal of medical genetics, 63(9), 103971. https://doi.org/10.1016/j.ejmg.2020.103971.

[12] Mitchell, E., Spencer Chapman, M., Williams, N., Dawson, K. J., Mende, N., Calderbank, E. F., ... & Campbell, P. J. (2022). Clonal dynamics of haematopoiesis across the human lifespan. Nature, 606(7913), 343-350. https://doi.org/10.1038/s41586-022-04786-y.

[13] Graf, I., Urbschat, C., & Arck, P. C. (2024). The 'communicatome'of pregnancy: spotlight on cellular and extravesicular chimerism. EMBO molecular medicine, 16(4), 700. https://doi.org/10.1038/s44321-024-00045-x.

[14] Porubsky, D., Höps, W., Ashraf, H., Hsieh, P., Rodriguez-Martin, B., Yilmaz, F., ... & Korbel, J. O. (2022). Recurrent inversion polymorphisms in human's associate with genetic instability and genomic disorders. Cell, 185(11), 1986-2005.https://doi.org/10.1016/j.cell.2022.04.017.

[15] Borges, A., & Irie, N. (2024). Maternal immune activation does not affect maternal microchimeric cells. Biology Open, 13(12), bio061830. https://doi.org/10.1242/bio.061830.

[16] Bigliardi, E., Shetty, A. V., Low, W. C., & Steer, C. J. (2025). Interspecies Blastocyst Complementation and the Genesis of Chimeric Solid Human Organs. Genes, 16(2), 215. https://doi.org/10.3390/genes16020215.

[17] Paul, A., Bui, T., Muelbert, M., & Toldi, G. (2025). T lymphocytes in human milk: Their role in immune system maturation through maternal microchimerism. Journal of Reproductive Immunology, 168, 104451. https://doi.org/10.1016/j.jri.2025.104451.

[18] Doerfler, R., Yerneni, S., LoPresti, S., Chaudhary, N., Newby, A., Melamed, J. R., ... & Whitehead, K. A. (2025). Maternal milk cell components are uptaken by infant liver macrophages via extracellular vesicle mediated transport. The FASEB Journal, 39(2), e70340. https://doi.org/10.1096/fj.202402365R.

[19] Jeong, H., Grimes, K., Rauwolf, K. K., Bruch, P. M., Rausch, T., Hasenfeld, P., ... & Korbel, J. O. (2023). Functional analysis of structural variants in single cells using Strand-seq. Nature biotechnology, 41(6), 832-844. https://doi.org/10.1038/s41587-022-01551-4.

[20] Wolner, L., William-Olsson, J., Podesser, B. K., Zuckermann, A., & Pilat, N. (2025). Tolerogenic therapies in cardiac transplantation. International Journal of Molecular Sciences, 26(9), 3968. https://doi.org/10.3390/ijms26093968.

[21] Bunis, D. G., Bronevetsky, Y., Krow-Lucal, E., Bhakta, N. R., Kim, C. C., Nerella, S., ... & Burt, T. D. (2021). Single-cell mapping of progressive fetal-to-adult transition in human naive T cells. Cell reports, 34(1). https://doi.org/10.1016/j.celrep.2020.108573.

[22] Amoah, A., Keller, A., Emini, R., Hoenicka, M., Liebold, A., Vollmer, A., ... & Geiger, H. (2021). Aging of human hematopoietic stem cells is linked to changes in Cdc42 activity. *Haematologica*, *107*(2), 393. doi: 10.3324/haematol.2020.269670.

[23] Porsdam Mann, S., Sun, R., & Hermerén, G. (2019). A framework for the ethical assessment of chimeric animal research involving human neural tissue. *BMC medical ethics*, *20*(1), 10. 10. https://doi.org/10.1186/s12910-019-0345-2.

[24] Dahiya, B., Gaur, J. R., & Surve, S. (2026). Chimerism and Forensic DNA Profiling in Crime Cases. International Journal of Research and Innovation in Applied Science (IJRIAS), 11(2). doi: 10.51584/IJRIAS.2026.110200031.

[25] Xu, H., Yao, H., Yuan, X., Lan, Q., Lin, Y., Wu, X., ... & Zhu, B. (2025). Forensic utilization of NGS-STRs and evaluation of system efficacy for different kinship identifications. Human Genomics, 19(1), 151. https://doi.org/10.1186/s40246-025-00858-y.

[26] Oisakede, E. O., Olawade, D. B., Bello, O. J., Analikwu, C. C., Egbon, E., Fapohunda, O., & Boussios, S. (2025). Cancer Reversion Therapy: Prospects, Progress and Future Directions. Current Issues in Molecular Biology, 47(12), 1049. https://doi.org/10.3390/cimb47121049.

[27] Dumanski, J. P., Halvardson, J., Davies, H., Rychlicka-Buniowska, E., Mattisson, J., Moghadam, B. T., ... & Forsberg, L. A. (2021). Immune cells lacking Y chromosome show dysregulation of autosomal gene expression. Cellular and Molecular Life Sciences, 78(8), 4019-4033. https://doi.org/10.1007/s00018-021-03822-w.

[28] van Zeventer, I. A., de Graaf, A. O., Salzbrunn, J. B., Nolte, I. M., Kamphuis, P., Dinmohamed, A., ... & Huls, G. (2023). Evolutionary landscape of clonal hematopoiesis in 3,359 individuals from the general population. Cancer cell, 41(6), 1017-1031. https://doi.org/10.1016/j.ccell.2023.04.006 (2023).

[29] Porubsky, D., Sanders, A. D., Taudt, A., Colomé-Tatché, M., Lansdorp, P. M., & Guryev, V. (2020). breakpointR: an R/Bioconductor package to localize strand state changes in Strand-seq data. Bioinformatics, 36(4), 1260-1261. https://doi.org/10.1093/bioinformatics/btz681.

[30] Malinska, N., Grobarova, V., Knížková, K., & Černý, J. (2024). Maternal-Fetal Microchimerism: Impacts on Offspring's Immune Development and Transgenerational Immune Memory Transfer. Physiological Research, 73(3), 315. https://doi.org/10.33549/physiolres.935296.

[31] McManus, J. F., Nguyen, N. Y. N., Davey, R. A., MacLean, H. E., Pomilio, G., McCormack, M. P., ... & Curtis, D. J. (2020). Androgens stimulate erythropoiesis through the DNA-binding activity of the androgen receptor in non-hematopoietic cells. European journal of haematology, 105(3), 247-254. https://doi.org/10.1111/ejh.13431.

[32] Desterke, C., Bennaceur-Griscelli, A., & Turhan, A. G. (2021). EGR1 dysregulation defines an inflammatory and leukemic program in cell trajectory of human-aged hematopoietic stem cells (HSC). Stem cell research & therapy, 12(1), 419. https://doi.org/10.1186/s13287-021-02498-0.

[33] Magnus, M. C., Ghaderi, S., Morken, N. H., Magnus, P., Bente Romundstad, L., Skjærven, R., ... & Eldevik Håberg, S. (2017). Vanishing twin syndrome among ART singletons and pregnancy outcomes. Human Reproduction, 32(11), 2298-2304. https://doi.org/10.1093/humrep/dex277.

[34] Clark, A., Clouston, H., Rao, K., Folarin, N., De la Fuente, J., Hamblin, A., ... & Snowden, J. (2025). UK recommendations for chimerism testing and monitoring following allogeneic haematopoietic stem cell transplantation (HSCT): Best practice consensus guidelines from the British Society for Blood and Marrow Transplant and Cellular Therapies (BSBMTCT), NHS England Genomic Laboratory Hub (GLH) Haematological Malignancies Working Group, UK Cancer Genetics Group (UKCGG) and the UK National External Quality Assessment Service for Leucocyte Immunophenotyping (UK NEQAS LI). British Journal of Haematology, 207(5), 1802-1814. https://doi.org/10.1111/bjh.70061.

[35] Chen, S., Vedula, R. S., Cuevas-Navarro, A., Lu, B., Hogg, S. J., Wang, E., ... & Abdel-Wahab, O. (2022). Impaired proteolysis of noncanonical RAS proteins drives clonal hematopoietic transformation. Cancer discovery, 12(10), 2434-2453. https://doi.org/10.1158/2159-8290.CD-21-1631.

[36] Bukyya, J. L., Tejasvi, M. L. A., Avinash, A., HP, C., Talwade, P., Afroz, M. M., ... & Srisha, V. (2021). DNA profiling in forensic science: a review. Global medical genetics, 8(04), 135-143. https://doi.org/10.1055/s-0041-1728689.

[37] Szklarczyk, D., Gable, A. L., Nastou, K. C., Lyon, D., Kirsch, R., Pyysalo, S., ... & von Mering, C. (2021). The STRING database in 2021: customizable protein–protein networks, and functional characterization of user-uploaded gene/measurement sets. Nucleic acids research, 49(D1), D605-D612. https://doi.org/10.1093/nar/gkaa1074.

[38] Haney, M. S., Shankar, A., Hsu, I., Miyauchi, M., Pálovics, R., Khoo, H. M., ... & Wilkinson, A. C. (2022). Large-scale in vivo CRISPR screens identify SAGA complex members as a key regulators of HSC lineage commitment and aging. bioRxiv.https://doi. org/10.1101/2022.07.22.501030.

[39] Blouin, A. G., Nelson, W., Geraghty, D., Askar, M., & Ye, F. (2024). Performance Characteristics of Next-Generation Sequencing–Based Engraftment Monitoring and Microchimerism Detection in Allogeneic Hematopoietic Cell Transplantation: A Practical Approach for Clinical Assay Validation. The Journal of Molecular Diagnostics, 26(11), 995-1006. https://doi.org/10.1016/j.jmoldx.2024.07.003.

[40] Sobral, A. F., Dinis-Oliveira, R. J., & Barbosa, D. J. (2025). CRISPR-Cas technology in forensic investigations: Principles, applications, and ethical considerations. Forensic Science International: Genetics, 74, 103163. https://doi.org/10.1016/j.fsigen.2024.103163.