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Genomic Science and Legal Identity: Emerging Challenges at the Intersection of Science, Law, and Individual Rights

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ABSTRACT

The rapid development of genomic science is transforming the scientific understanding of human identity, heredity, disease susceptibility, ancestry, reproduction, and biological relationships. Advances in next-generation sequencing, whole-genome sequencing, genome-wide association studies, polygenic risk scoring, forensic genomics, and genome editing have progressively expanded the informational capacity of DNA from a tool of biological identification into a multidimensional source of information about individuals and populations. This transformation presents a fundamental challenge to conventional conceptions of legal identity. Genetic information can establish biological relationships, assist criminal investigations, identify human remains, reveal ancestry and inherited disease risks, and contribute to personalized medicine, yet it does not provide a complete account of personal identity. The present article examines these developments primarily from a scientific perspective while analyzing their implications for law, privacy, autonomy, equality, and human rights. It adopts an interdisciplinary doctrinal and scientific-review methodology based on peer-reviewed genomic research, international scientific reports, and authoritative international instruments available up to December 2024. The analysis demonstrates that the scientific characteristics of genomic information—its persistence, familial nature, predictive capacity, population-level implications, and potential for secondary inference—distinguish it from conventional forms of personal information. Empirical developments in polygenic risk scoring further demonstrate that genomic prediction is strongly influenced by the ancestral composition of reference datasets, raising questions concerning scientific validity and equality when genomic technologies are applied across populations. Similarly, forensic genetic genealogy demonstrates how databases created for recreational or biomedical purposes may generate investigative information concerning individuals who have never directly contributed their DNA to a forensic database. Genome editing introduces an additional dimension by potentially altering biological characteristics that have historically been treated as naturally inherited. The article argues that legal identity should neither be reduced to genetic identity nor detached from the scientific realities of genomics. Instead, a scientifically informed legal framework should recognize genomic information as relational, probabilistic, dynamic in interpretation, and potentially consequential beyond the individual from whom a biological sample originates. The study concludes that future governance should combine scientific validity, privacy protection, informed consent, non-discrimination, proportionality, genomic equity, responsible data sharing, and international cooperation.

Keywords: *Genomic Science, Legal Identity, Human Genome, Genetic Information, Genomic Data, DNA, Genetic Privacy.*

1. Introduction

The scientific understanding of human identity has undergone a profound transformation since the emergence of molecular genetics and the completion of the Human Genome Project. The human genome contains approximately three billion DNA base pairs and provides a molecular framework for understanding heredity, biological variation, disease mechanisms, ancestry, and relationships between individuals. Yet contemporary genomics is no longer limited to determining whether two biological samples originate from the same person. High-throughput sequencing, computational genomics, genome-wide association studies, long-read sequencing, epigenomics, population genomics, polygenic risk prediction, forensic genealogy, and genome-editing technologies have expanded the informational content of genomic data to an unprecedented scale. The scientific development is particularly significant because DNA is simultaneously biological material and information. A biological sample can be retained, sequenced, reanalyzed, compared with another sample, linked to relatives, incorporated into databases, and interpreted in ways that were not necessarily foreseeable when the sample was originally collected. The scientific characteristics of genomic information therefore create an unusual relationship between biology, information, and identity. UNESCO's International Declaration on Human Genetic Data expressly recognizes that genetic information has a special status because it can provide information concerning genetic predispositions, affect family members and future generations, contain information whose significance may not yet be known when samples are collected, and possess cultural significance for individuals or groups (UNESCO, 2003). This scientific complexity is reflected in the contemporary international governance agenda. In November 2024, the World Health Organization issued *Guidance for human genome data collection, access, use and sharing*, emphasizing that responsible genomic-data governance must simultaneously facilitate scientific research, protect individual and collective rights, promote equity, and support responsible international collaboration (World Health Organization [WHO], 2024). The central premise of this article is that legal identity cannot simply be equated with genetic identity. UNESCO's 2003 Declaration expressly states that although each individual has a characteristic genetic make-up, human identity should not be reduced to genetic characteristics because identity also involves educational, environmental, personal, social, spiritual, and cultural dimensions (UNESCO, 2003). Nevertheless, genomic information can increasingly influence how institutions understand and classify individuals. DNA can establish biological parentage, assist identification of unidentified remains, distinguish individuals in forensic investigations, provide evidence about inherited disease risks, reveal biological relationships, and contribute to predictions concerning complex traits. The expansion of genomic science therefore creates a distinction between **genetic identity** and **legal identity**. Genetic identity concerns biological information derived from an individual's genome; legal identity concerns the status through which an individual is recognized within legal and institutional systems. The two may overlap, but they are not identical. The scientific problem becomes especially significant as genomic information moves from relatively stable identification markers toward probabilistic predictions. A DNA profile used for identification and a polygenic score used to estimate disease risk are scientifically different forms of genomic information. The former may be highly discriminating for forensic purposes, whereas the latter may provide only a statistical estimate whose predictive performance varies across populations. Scientific accuracy must

therefore be assessed according to the particular genomic technology, dataset, population, purpose, and interpretation involved. This article focuses primarily on the scientific dimensions of these developments and examines their implications for law only after establishing the underlying biological and technological characteristics. It asks three principal questions: **first**, how have developments in genomic science changed the informational meaning of biological identity; **second**, what scientific characteristics distinguish genomic information from conventional personal information; and **third**, what legal and ethical consequences follow when genomic information is used for identification, prediction, research, medicine, and genome modification. The article argues that the central challenge is not simply the protection of DNA as private information. It is the development of a governance framework capable of responding to the scientific characteristics of genomic information itself.

2. The Scientific Transformation of Human Identity Through Genomics

The modern concept of genomic identity emerged from the transition from classical genetics to molecular and computational genomics. Early genetic analysis focused primarily on individual genes and inherited traits. Contemporary genomics examines the genome as a complex system containing coding and non-coding sequences, regulatory elements, structural variation, mitochondrial DNA, epigenetic information, and interactions between genetic and environmental factors. The Human Genome Project established a reference sequence that transformed biological research, but the reference genome should not be understood as a complete representation of human genetic diversity. Individual genomes contain millions of variants relative to reference sequences, and population-level studies have demonstrated extensive variation between and within populations. The scientific importance of this distinction is substantial because genomic identity operates simultaneously at individual and population levels. At the individual level, certain combinations of genetic variants can provide highly discriminating identification. At the population level, genetic variants can reveal ancestry patterns, population history, migration, and relationships among groups. The rapid decline in sequencing costs has been one of the principal drivers of this transformation. Data collected by the U.S. National Human Genome Research Institute demonstrate the extraordinary decline in the cost of DNA sequencing following the development of second-generation sequencing technologies, with sequencing costs beginning to decline much faster than the trajectory predicted by conventional technological improvement models (National Human Genome Research Institute [NHGRI], 2022). The reduction in cost has enabled larger genomic studies, clinical sequencing, population biobanks, direct-to-consumer genetic testing, forensic databases, and research repositories. Whole-genome sequencing now allows researchers to examine virtually the complete nuclear genome rather than restricting analysis to selected genetic markers. Whole-genome sequencing provides a more targeted approach focused on protein-coding regions, which constitute approximately 1.5% of the human genome, while whole-genome sequencing provides substantially broader information (NHGRI, 2021). The scientific significance of this expansion is that a biological sample can now produce information far beyond the immediate purpose for which it was collected. A sample collected for diagnostic sequencing may subsequently generate information concerning ancestry, carrier status, variants associated with future disease risk, pharmacogenomics characteristics, or relationships with other individuals. Moreover, genomic interpretation is not static. As

scientific knowledge improves, variants previously classified as uncertain may acquire new significance. A genome therefore does not merely contain a fixed set of conclusions; it contains data that may be reinterpreted as knowledge develops. This creates what may be termed the **temporal dimension of genomic identity**. An individual's genomic sequence may remain biologically constant, while the information inferred from that sequence changes over time. The second important scientific characteristic is **relationality**. An individual's genome contains information that is statistically related to biological relatives. Consequently, a genomic database containing one person's information may indirectly reveal information concerning parents, siblings, children, or more distant relatives. This distinguishes genomic information from many conventional identifiers such as passwords or identification numbers, which generally describe one individual without simultaneously revealing biological characteristics of relatives. The third characteristic is **predictiveness**. Genomic data may reveal predispositions rather than predetermined outcomes. A genetic variant associated with a disease does not necessarily mean that an individual will develop that disease. Complex traits are generally influenced by numerous genetic variants interacting with environmental, behavioral, and socioeconomic factors. Polygenic risk scores illustrate this complexity because they aggregate effects across many variants to estimate relative genetic liability. The fourth characteristic is **population dependence**. The meaning and predictive accuracy of genomic information may vary according to the population represented in the underlying research dataset. This is scientifically important because many genomic studies have historically overrepresented individuals of European ancestry. Consequently, genomic tools developed from such datasets may perform differently in other populations. The scientific transformation of identity is therefore not a movement from uncertainty to perfect biological knowledge. It is a movement toward increasingly sophisticated but context-dependent inference. Genomics can reveal more about an individual than earlier genetic technologies, but what it reveals depends upon the analytical method, reference population, database, statistical model, and scientific knowledge available at the time. Legal systems dealing with genomic information must therefore recognize that **genetic data are not synonymous with genetic certainty.**

3. Genomic Identification, Forensic Science, and the Expansion of Biological Identity

The application of genomic science to forensic identification represents one of the clearest points at which science directly affects legal identity. Traditional forensic DNA profiling generally relies upon selected genetic markers capable of distinguishing individuals with very high statistical probability. Such profiles are fundamentally different from whole-genome sequences because they are designed primarily for identification rather than comprehensive biological inference. Nevertheless, advances in sequencing and computational analysis have expanded the forensic potential of genetic information. DNA can be used to associate biological material with individuals, establish biological relationships, identify victims, identify unidentified human remains, and support criminal investigations. The scientific power of DNA identification derives from genetic variation. Individuals generally possess highly distinctive combinations of alleles across sufficiently large numbers of genetic markers. The evidentiary significance of a DNA match is therefore statistical rather than metaphysical. A forensic laboratory does not simply establish that a sample “is” a particular person; it calculates the probability that a coincidental match would occur under specified population assumptions.

The interpretation of DNA evidence consequently depends upon laboratory quality, statistical models, population databases, contamination controls, chain of custody, and the distinction between source-level and activity-level propositions. Genomic science has also created a new form of forensic identification through **forensic genetic genealogy**. This approach can use genetic information to identify biological relatives and construct family relationships that eventually assist investigators in identifying an unknown individual. Its scientific basis differs from conventional forensic profiling because it may depend upon kinship inference rather than a direct one-to-one database match. The consequence is that an individual may become relevant to an investigation even without having personally contributed DNA to a law-enforcement database. A relative's genetic information can potentially generate investigative leads. This illustrates the relational nature of genomic identity with unusual clarity. Scientific information derived from one individual can produce information about another. The same principle operates in non-forensic contexts. A genetic test performed by one family member can reveal information about biological relationships or inherited characteristics relevant to relatives. UNESCO therefore recognizes the special status of genetic information partly because its effects may extend to families, descendants, and groups (UNESCO, 2003). The forensic expansion of genomics also raises a scientific distinction between **identification** and **inference**. Identification attempts to determine whether biological evidence is consistent with a particular individual. Inference may attempt to determine ancestry, biological sex, kinship, or other characteristics from genetic information. The further forensic analysis moves from identification toward prediction, the more complex the scientific interpretation becomes. Genetic ancestry should not be treated as synonymous with race, ethnicity, nationality, or social identity. Genetic ancestry is inferred from patterns of genetic similarity relative to reference populations, while race and ethnicity are social and historical categories that cannot be reduced to genomic clusters. Scientific literature increasingly emphasizes the need to distinguish genetic ancestry from socially constructed population classifications. This distinction becomes particularly important when genomic information enters legal decision-making. A genetic inference about ancestry does not automatically establish a person's social identity. The same caution applies to behavioral or disease-associated genetic information. Association between a genetic variant and a trait does not establish deterministic causation at the individual level. The forensic use of genomics therefore requires scientific literacy among legal institutions. Judges, lawyers, investigators, and expert witnesses must distinguish between a scientifically validated identification method and a probabilistic inference with greater uncertainty. The legal significance of genomic evidence should be proportional to its scientific validity. UNESCO's framework explicitly recognizes forensic medicine and civil and criminal proceedings as legitimate contexts for genetic data while requiring their use to remain consistent with human-rights standards (UNESCO, 2003). The central lesson is that genomic science has transformed biological identification from a narrow laboratory technique into a broader informational system capable of generating relational and inferential knowledge. That transformation makes scientific safeguards increasingly important because the evidentiary consequences of genomic inference can extend well beyond the individual whose biological material was originally collected.

4. Predictive Genomics, Polygenic Risk, and the Scientific Limits of Genetic Determinism

The most significant contemporary transformation in genomic science may be the shift from identification toward prediction. Modern genomic research increasingly seeks to estimate the probability of future disease, treatment response, or other complex traits using combinations of genetic variants. Polygenic risk scores are among the most prominent examples. A polygenic score aggregates the estimated effects of many genetic variants to produce an individual-level measure associated with susceptibility to a particular trait or disease. The scientific attraction of such scores is substantial. If validated adequately, they may support earlier prevention, stratification of clinical risk, and personalized medicine. However, polygenic prediction also exposes the limitations of treating genetic information as an objective and universally applicable measure of individual identity. The accuracy of polygenic scores depends substantially on the genetic diversity and characteristics of the populations represented in the datasets used to construct them. A major 2023 *Nature* study using 36,778 individuals from the ATLAS biobank and 487,409 individuals from UK Biobank demonstrated that polygenic score accuracy declined continuously with increasing genetic distance from the training data across 84 traits. The study reported a Pearson correlation of −0.95 between genetic distance from training data and prediction accuracy averaged across the 84 traits. Individuals in the furthest genetic-distance decile had approximately 14% lower accuracy than individuals in the closest decile within the European-ancestry group examined (Ding et al., 2023). This finding has profound implications for the scientific and legal treatment of genomic information. It demonstrates that a genomic prediction cannot be evaluated solely by examining the algorithm or statistical model. Its validity must also be assessed in relation to the population to which it is applied. A score may perform well in one dataset and less well in another because of differences in linkage disequilibrium, allele frequencies, genetic architecture, environmental conditions, and representation in the training data. A 2024 *Nature Communications* study similarly observed that polygenic scores derived predominantly from European-ancestry datasets often perform less effectively in non-European populations, highlighting the continuing problem of cross-ancestry prediction (Lupi et al., 2024). The scientific problem becomes particularly important when genetic predictions are used beyond medical research. If genomic information is treated as evidence of an individual's likely health, behavior, cognitive characteristics, or other complex traits, there is a danger of **genetic determinism;** the assumption that genetic predisposition establishes an inevitable biological outcome. Contemporary genetics does not support such a simple model. Most complex human traits emerge through interactions among many genes and between genes and environments. A genetic association is therefore probabilistic and context-dependent. Legal systems should consequently distinguish between **genetic predisposition**, **genetic probability**, and **genetic determination**. These are scientifically different propositions. The first indicates a biological association; the second concerns statistical risk; the third implies a causal certainty that is rarely justified for complex human characteristics. The scientific limits of genomic prediction also create equality concerns. If genomic technologies perform less accurately for populations that are underrepresented in research databases, universal deployment without appropriate validation can reproduce existing disparities. This is particularly important for global genomic medicine because large genomic datasets have historically been concentrated in high-income countries and populations of European ancestry. WHO's 2024 genomic-data guidance emphasizes equity, capacity building, inclusion of underrepresented populations, and

responsible international collaboration as essential elements of genomic governance (WHO, 2024). Scientific validity and legal equality therefore intersect. A legally neutral technology can produce unequal consequences if its underlying scientific model is less accurate for some populations. This does not mean that polygenic scores should be rejected. Rather, it means that their use should be accompanied by population-specific validation, transparent reporting of limitations, appropriate uncertainty estimates, and continuous scientific evaluation. The emergence of predictive genomics therefore strengthens the argument that legal identity should not be reconstructed as a genetic profile. Genomic science can contribute valuable probabilistic information about an individual, but probability must not be transformed into deterministic legal classification.

5. Genomic Data, Privacy, Consent, and the Relational Nature of Biological Information

The scientific characteristics of genomic information create distinctive challenges for privacy and consent. Conventional models of data protection often assume that information relates primarily to the individual who supplied it. Genomic data challenge this assumption because biological information is simultaneously individual and familial. A person's genome contains information about biological relatives, and therefore the consequences of disclosure may extend beyond the individual who provided the sample. This relational characteristic creates difficulties for traditional consent models. An individual may consent to sequencing for medical treatment or research, but cannot necessarily consent on behalf of relatives whose biological characteristics may become indirectly inferable. UNESCO's International Declaration on Human Genetic Data recognizes this problem by identifying genetic data as information capable of affecting families and groups and by requiring appropriate protection for identifiable genetic information (UNESCO, 2003). The scientific difficulty is compounded by the concept of **re-identification**. Genetic data may be coded or de-identified, but genomic information contains numerous variants that can potentially contribute to identification when combined with external datasets. The possibility of re-identification does not mean that all genomic data can always be linked to a person, but it demonstrates why genomic privacy cannot be understood solely through conventional identifiers. A sequence may be separated from a name while remaining informative about biological relationships, ancestry, or health. Furthermore, scientific knowledge evolves. Information that appears harmless at the time of collection may acquire new significance later. UNESCO explicitly recognizes that genetic data may contain information whose significance is not necessarily known when samples are collected (UNESCO, 2003). This creates a challenge for informed consent because traditional consent models assume that researchers can explain the foreseeable purposes and risks of data use. In genomics, future uses may be difficult to predict. Broad consent can facilitate research but may reduce the specificity of individual choice; highly specific consent can increase individual control but may constrain scientific research and secondary use. The problem is therefore not resolved simply by choosing “more consent.” It requires a scientifically informed approach to governance, including transparency concerning future uses, data security, withdrawal mechanisms where technically feasible, governance of secondary use, and communication concerning clinically significant findings. The WHO's 2024 guidance places informed consent, privacy, transparency, equity, and responsible sharing at the center of genomic-data governance, while simultaneously recognizing the importance of

international data sharing for scientific progress (WHO, 2024). This reflects a fundamental scientific tension. Genomic research depends on large datasets because many associations are statistically weak and require substantial sample sizes to detect. Restricting data access too severely can reduce scientific validity, slow discovery, and reinforce population underrepresentation. Conversely, unrestricted data sharing may increase privacy risks and reduce public trust. The appropriate scientific model is therefore not complete secrecy but **responsible data stewardship**. Such stewardship should involve controlled access, appropriate security, transparent governance, data minimization where scientifically possible, independent ethical review, and mechanisms for international collaboration. Genomic privacy also differs from ordinary privacy because it involves future generations. A person's genetic information may remain relevant to descendants. A decision made today concerning storage or disclosure can therefore have consequences that extend beyond the lifespan of the individual who provided the sample. This temporal dimension makes genomic governance particularly challenging. The legal system must also recognize that the informational value of DNA differs according to purpose. A forensic short tandem repeat profile, a clinical whole-genome sequence, a raw research dataset, and a polygenic score are all forms of genomic information but do not carry identical scientific or privacy risks. Regulation should therefore avoid treating "genetic data" as a scientifically homogeneous category. Risk-based governance should consider the nature of the data, the purpose of processing, identifiability, and potential for inference, population consequences, and likelihood of misuse. The scientific perspective consequently supports a more nuanced legal principle: genomic information deserves heightened protection not because DNA is inherently sacred or because every genetic datum is equally sensitive, but because genomic data possess unusual capacities for identification, inference, relational disclosure, and future reinterpretation.

6. Genome Editing, Biological Identity, and the Boundary between Science and Law

Genome editing introduces a fundamentally different challenge because it shifts the relationship between genetic information and identity from observation toward intervention. Technologies such as CRISPR-Cas systems have made targeted modification of DNA substantially more accessible than earlier genome-engineering methods. In somatic-cell applications, genetic modifications are intended to affect the treated individual without being transmitted to future generations. In germline or heritable applications, modifications may potentially be transmitted to descendants. This scientific distinction is fundamental to legal and ethical governance. The WHO's framework for human genome editing distinguishes laboratory research, drug-target screening, preclinical and clinical research, clinical care, and enhancement, and emphasizes that governance must respond to rapidly changing scientific knowledge (WHO, 2021). The scientific promise of genome editing is considerable. Researchers can investigate gene function, model disease, develop potential therapies, and modify cells to address particular genetic conditions. Somatic genome editing may offer therapeutic possibilities for conditions that were previously difficult to treat. Yet the transition from therapeutic intervention to heritable modification raises questions that cannot be answered solely by measuring technical efficiency. Off-target effects, mosaicism, unintended genomic changes, delivery challenges, long-term safety, and the complexity of gene–environment interactions remain important scientific considerations. Heritable editing

additionally introduces uncertainty because consequences may extend to individuals who cannot consent and to future generations. The legal significance follows from the scientific uncertainty rather than replacing it. International governance must therefore distinguish scientifically established therapeutic interventions from experimental or enhancement-oriented applications. The distinction between treatment and enhancement is itself difficult because the boundary between the two may change as scientific knowledge develops. A genetic intervention initially regarded as extraordinary may become routine if evidence demonstrates safety and efficacy. Conversely, an intervention promoted as therapeutic may prove scientifically uncertain. The governance framework must therefore remain adaptive. Genome editing also challenges conventional concepts of identity. If genetic characteristics can be intentionally modified, the genome becomes not merely a biological record of inherited ancestry but potentially an object of technological intervention. This does not mean that personal identity becomes genetically determined. On the contrary, it reinforces UNESCO's proposition that identity cannot be reduced to genetic characteristics (UNESCO, 2003). The scientific importance lies in recognizing that biological identity has multiple layers: inherited genetic sequence, somatic variation, epigenetic state, phenotype, environment, development, and social experience. Genome editing can alter selected molecular characteristics without transforming the whole of personal identity. The legal response should therefore avoid simplistic assumptions that genetic modification produces a fundamentally different legal person. Instead, regulation should focus on the safety, purpose, consent, scientific evidence, and distributional consequences of the intervention. International governance is particularly important because genomic technologies can cross borders through research collaboration, clinical tourism, commercial services, and transnational data sharing. Divergent national rules may create regulatory gaps in which controversial interventions move to jurisdictions with weaker oversight. The scientific nature of genome editing also means that regulation must be capable of updating itself as evidence changes. A static statute may become scientifically obsolete. WHO's governance framework emphasizes responsiveness and the need to distinguish different forms and stages of genome editing (WHO, 2021). The appropriate model is therefore **adaptive governance**: regulation based on scientific evidence, continuously reviewed by multidisciplinary experts, transparent about uncertainty, and capable of differentiating therapeutic, research, reproductive, and enhancement applications. Genome editing ultimately demonstrates why the future relationship between science and law cannot be based on a fixed understanding of human biology. Law must respond to scientific capabilities without assuming that every technological possibility should become legally permissible.

7. Scientifically Informed Framework for Genomic Identity Governance

The preceding analysis demonstrates that genomic science has changed the meaning of biological information in ways that require a corresponding transformation in legal and ethical governance. The principal policy challenge is not to prevent genomic science from developing but to ensure that scientific advancement remains compatible with individual dignity, autonomy, equality, and public trust. The first requirement should be **scientific validity**. Genomic information should not acquire legal significance merely because it is expressed numerically or generated through advanced technology. Courts, regulators, clinicians,

researchers, and policymakers should evaluate the scientific validity, error rates, population limitations, reproducibility, and uncertainty associated with the relevant genomic method. The second requirement is **purpose limitation**. Genomic data collected for clinical diagnosis should not automatically become available for unrelated purposes. UNESCO's framework recognizes the importance of limiting changes of purpose and ensuring that secondary uses remain consistent with appropriate consent and human-rights standards (UNESCO, 2003). The third requirement is **proportionality**. Different forms of genomic information carry different risks. A forensic identification profile should not necessarily be regulated in exactly the same way as a whole-genome clinical sequence or a polygenic risk score. Regulation should correspond to the informational capacity and potential consequences of the data. The fourth requirement is **relational privacy**. Governance must acknowledge that genomic information concerns families and sometimes communities, not merely individuals. This principle is particularly important for forensic genetic genealogy, family-based clinical sequencing, and population genomics. The fifth requirement is **genomic equity**. Research databases should include populations that have historically been underrepresented. The evidence concerning polygenic scores demonstrates that prediction accuracy can decline with genetic distance from the populations represented in training data (Ding et al., 2023). Therefore, equitable participation is not merely an ethical aspiration; it is a scientific requirement for improving the validity and generalizability of genomic medicine. WHO's 2024 guidance similarly emphasizes capacity building and equitable participation in genomic research, particularly in regions with limited genomic infrastructure (WHO, 2024). The sixth requirement is **transparent uncertainty**. Genomic results should communicate the distinction between association, probability, and causation. Individuals and legal institutions should not be encouraged to interpret probabilistic genetic information as deterministic fact. The seventh requirement is **data stewardship**. Scientific progress requires responsible sharing of genomic data, but sharing should occur through appropriate security, governance, access controls, and accountability. WHO's 2024 guidance explicitly treats responsible data sharing as essential to advancing global health while protecting individuals and communities (WHO, 2024). The eighth requirement is **independent oversight**. Genomic research and clinical applications should be reviewed by multidisciplinary bodies capable of integrating genetics, medicine, statistics, ethics, law, social science, and public perspectives. UNESCO's Declaration calls for independent, multidisciplinary, and pluralist ethics committees in relation to human genetic data (UNESCO, 2003). The ninth requirement is **international cooperation**. Genomic data do not respect national borders. Research databases, sequencing services, clinical collaborations, and genetic testing companies operate across jurisdictions. National rules alone are therefore insufficient. International standards should establish common principles concerning consent, privacy, scientific quality, cross-border transfer, benefit sharing, and protection against discrimination. The tenth requirement is **adaptive governance**. Scientific knowledge changes rapidly. New sequencing technologies, computational methods, predictive models, and genome-editing techniques may alter the risk profile of genomic information. Regulatory systems should consequently incorporate periodic scientific review rather than assuming that present knowledge is permanent. Finally, the legal system should maintain a clear conceptual distinction between **genetic identity and legal identity**. Genetic information may contribute to identification, but it should not determine the entirety of a person's legal or social identity.

UNESCO's statement that identity should not be reduced to genetic characteristics remains particularly important in an era in which genomic technologies are becoming increasingly powerful (UNESCO, 2003). The future of genomic governance should therefore be built around a balanced proposition: science should be allowed to reveal, understand, and potentially improve human biological conditions, but the informational and technological power of genomics must operate within institutions capable of protecting autonomy, equality, privacy, and human dignity. The central scientific lesson is that genomic information is extraordinarily powerful but never context-free. A sequence acquires meaning through interpretation, reference populations, statistical models, technological methods, and social purposes. The central legal lesson is therefore equally clear: law should regulate not merely DNA as an object, but the scientific processes through which genomic information is generated, interpreted, shared, and acted upon. A scientifically informed legal order will neither reject genomic innovation nor treat genetic information as infallible truth. It will recognize uncertainty as part of scientific knowledge, diversity as essential to scientific validity, and responsible governance as a prerequisite for translating genomic discovery into legitimate social benefit.

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