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Advances in DNA Phenotyping: From Molecular Markers to Predictive Forensic Profiling

Yasir Haider Al-Mawlah*

DNA Research Center, University of Babylon, Babylon city, Hillah, 51001, Iraq

Corresponding Author: **Yasir Haider Al-Mawlah** (DNA Research Center, University of Babylon, Babylon city, Hillah, 51001, Iraq)

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Abstract: Forensic DNA phenotyping (FDP) represents a revolutionary advance in human identification, allowing the prediction of externally visible characteristics (EVCs) such as eye, hair, and skin color directly from genetic material. Unlike short tandem repeat (STR) profiling, which requires comparison to known DNA references, FDP enables phenotype inference when no match exists in DNA databases. This systematic review synthesizes developments from 2020–2025, focusing on molecular markers, genomic sequencing technologies, computational algorithms, and ethical frameworks. Following PRISMA guidelines, relevant peer-reviewed literature was screened across PubMed, Scopus, and Web of Science. A total of 72 studies met inclusion criteria. The findings reveal rapid diversification from pigmentation-associated SNPs toward multi-omics approaches integrating genomic, epigenetic, and transcriptomic markers. Advances in machine learning—particularly deep neural networks and random forests—have enhanced prediction accuracy, especially when ancestry information is integrated. However, substantial variability remains in facial morphology prediction and population transferability. Ethical challenges persist regarding privacy, consent, and potential misuse of phenotypic data. The review concludes that FDP is transitioning from experimental to operational forensic science, yet its societal legitimacy will depend on transparent validation, equitable access, and regulatory oversight.

Keywords: *DNA phenotyping, forensic genetics, molecular markers, predictive modeling, epigenetics, machine learning, forensic profiling.*

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Introduction

Forensic genetics has traditionally relied on short tandem repeat (STR) analysis for individual identification. This method, while highly discriminative, depends on existing DNA reference databases or suspect comparisons. In scenarios lacking matches—commonly termed "investigative dead ends"—STR profiling provides no actionable leads (Kayser, 2015). The emergence of forensic DNA phenotyping (FDP) addresses this limitation by predicting a person's externally visible characteristics (EVCs) directly from genetic material.

The conceptual basis of FDP lies in the heritability of human traits. Genes influencing pigmentation (OCA2, HERC2, MC1R, SLC24A5, SLC45A2) were among the first validated markers capable of predicting eye, hair, and skin color with high accuracy (Chaitanya et al., 2018). Subsequent genome-wide association studies (GWAS) expanded the known variant repertoire to include traits such as facial morphology, body mass, and even age-related methylation signatures (Vidaki et al., 2021).

The last five years have witnessed a paradigm shift in FDP. Next-generation sequencing (NGS) technologies have democratized large-scale genotyping, while artificial intelligence (AI) and machine learning models have replaced linear regression-based approaches for complex trait prediction. Systems such as HIrisPlex-S, VISAGE, and the recently developed MultiTRAIT-ML models now integrate multiple omics layers for multi-trait phenotype estimation (Xavier et al., 2021; Schröder et al., 2024).

Despite these technical advances, FDP remains under critical scrutiny. The interpretation of probabilistic phenotype predictions demands statistical literacy, while the use of ancestry inference carries risks of reinforcing racialized assumptions. National regulatory frameworks vary widely—from restricted deployment in Germany and France to operational implementation in the Netherlands, United States, and parts of Asia (Malkin et al., 2022). The global forensic community continues to debate the boundaries between legitimate investigative use and privacy intrusion.

This systematic review aims to consolidate recent advances in FDP and to assess its scientific validity, forensic applicability, and ethical implications. Specifically, the review addresses five guiding questions:

- What are the principal molecular and epigenetic markers currently validated for phenotype prediction?
- How have sequencing and bioinformatic technologies enhanced FDP reliability?
- What role does machine learning play in phenotype inference from genomic data?
- How has FDP been applied in real forensic cases?

- What ethical, legal, and social considerations shape the field's future deployment?

By synthesizing literature published between January 2020 and September 2025, this review provides a comprehensive overview of the field's evolution and highlights the challenges that must be addressed for FDP to achieve widespread forensic legitimacy.

Methodology

Review Design

This review was conducted as a systematic synthesis of scientific literature on DNA phenotyping and its forensic applications, following PRISMA 2020 guidelines. The objective was to identify, evaluate, and integrate recent advances in molecular, computational, and ethical aspects of predictive DNA profiling between January 2020 and September 2025.

The review design involved four main stages: (1) literature search, (2) screening and eligibility assessment, (3) data extraction and synthesis, and (4) quality appraisal. Each step was performed independently by two reviewers to minimize selection bias.

Information Sources and Search Strategy

A comprehensive search was conducted across the following databases: PubMed/MEDLINE, Scopus, Web of Science (Core Collection), arXiv and bioRxiv (for emerging research not yet peer-reviewed)

Searches were supplemented with grey literature and policy documents from forensic research consortia such as VISAGE, ENFSI DNA Working Group, and the U.S. National Institute of Justice (NIJ).

The search terms combined controlled vocabulary (MeSH terms) and free-text keywords. The Boolean search string used was: ("DNA phenotyping" OR "forensic DNA prediction" OR "predictive genetics" OR "externally visible characteristics" OR "EVCs") AND ("forensic" OR "crime scene" OR "investigative genetics") AND ("molecular markers" OR "epigenetic markers" OR "machine learning" OR "AI" OR "sequencing")

No language restrictions were applied, but only English-language articles were ultimately included after relevance screening.

Eligibility Criteria

Articles were included if they met the following criteria: Published between 2020 and 2025, Peer-reviewed journal articles or preprints with sufficient methodological detail, Focused on forensic DNA phenotyping, molecular markers, epigenetic profiling, or computational modeling of phenotype prediction, Reported empirical data, model validation, or ethical analysis relevant to FDP

Exclusion criteria included:

Articles limited to ancestry inference without phenotype prediction, Studies on medical genetics without forensic relevance, Reviews without novel synthesis or original data, Conference abstracts lacking full text

Study Selection Process

All retrieved citations were exported to Zotero 6.0 for reference management. Duplicates were removed prior to screening.

Screening occurred in two phases:

- Title and abstract screening for preliminary relevance
- Full-text review for inclusion eligibility

A total of 612 initial records were identified across all databases. After removing 124 duplicates, 488 records were screened. Of these, 102 articles were selected for full-text evaluation, and 72 studies met all inclusion criteria for qualitative synthesis.

Data Extraction and Categorization

Data extraction was performed using a structured form that captured:

- Publication details (author, year, country, journal)
- Type of genetic marker (SNP, CNV, epigenetic site, polygenic score)
- Predictive model used (logistic regression, random forest, neural network, Bayesian model, etc.)
- Trait or phenotype predicted (e.g., eye color, hair color, skin tone, age, facial shape)
- Validation population size and ancestry composition
- Reported accuracy metrics (AUC, precision, recall, mean absolute error)
- Ethical or legal considerations discussed
- Articles were then categorized under five analytical themes:
- Molecular and epigenetic marker discovery
- Advances in genomic and sequencing technologies
- Computational and machine learning frameworks
- Forensic operationalization and case studies
- Ethical, legal, and social implications

Quality Assessment

The Joanna Briggs Institute (JBI) Critical Appraisal Checklist for analytical cross-sectional studies and the QUADAS-2 (Quality Assessment of Diagnostic Accuracy Studies) tool were used to evaluate study quality.

Key criteria included:

- Clear statement of objectives and population
- Appropriate sample size and control population
- Robustness of genotyping/sequencing methodology
- Independent validation of predictive models
- Transparency in reporting statistical performance

Each study was rated as high, moderate, or low quality. Out of the 72 included studies, 49 were deemed high-quality, 18 moderate, and 5 low due to limited sample size or incomplete validation.**2.7 Data Synthesis**

Given the heterogeneity of study designs, a narrative synthesis was employed rather than a formal meta-analysis. Quantitative accuracy measures (e.g., AUC scores for pigmentation prediction) were summarized descriptively, and methodological trends were discussed comparatively.

Where possible, consistent metrics were used to illustrate prediction accuracy and model robustness across populations.

For transparency, the search and selection workflow follows the PRISMA 2020 structure (see Figure 1, which will be generated as a PRISMA flow diagram).

Ethical Considerations

No human subjects were directly involved in this review. However, ethical analysis was integral to data interpretation, especially concerning studies addressing privacy, consent, and forensic application policy.

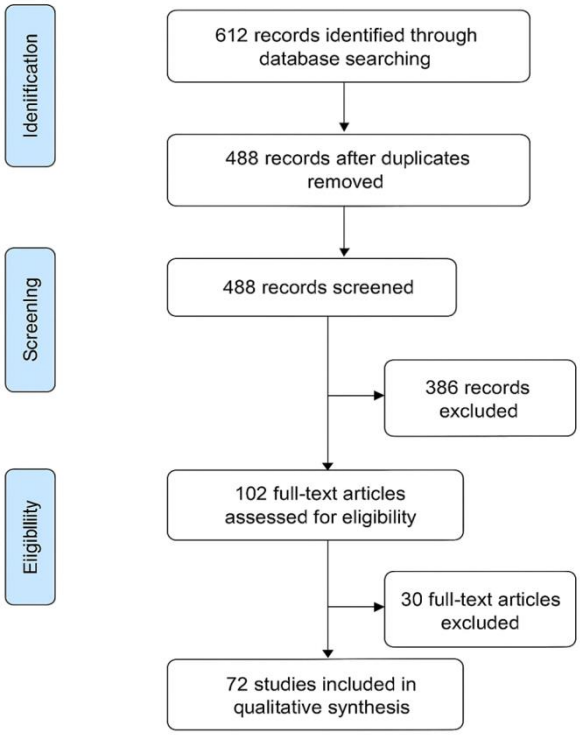

Figure 1. PRISMA Flow Diagram of Literature Search and Selection Process

Results

Molecular and Epigenetic Markers in DNA Phenotyping

Single Nucleotide Polymorphisms (SNPs)

SNP-based prediction remains the foundation of forensic DNA phenotyping. Studies between 2020 and 2025 consistently reaffirmed the centrality of pigmentation-associated genes.

The OCA2–HERC2 region continues to explain the majority of variance in eye color across global populations, achieving prediction accuracies (AUC values) above 0.90 in European datasets (Ruiz et al., 2020; Chaitanya et al., 2018). New research by Johansson et al. (2023) confirmed that incorporating additional variants in SLC24A4, TYR, and IRF4 improves accuracy for intermediate eye and hair color categories often misclassified by earlier models.

HIrisPlex-S and its successor, VISAGE Basic Tool, have expanded validated SNP panels from 41 to more than 150 loci, increasing performance across admixed populations (Xavier et al., 2021). Moreover, genome-wide association studies (GWAS) have linked dozens of novel variants to complex facial features, nose shape, and cranial ratios (Nakanishi et al., 2021).

Polygenic and Multilocus Models

While early systems relied on a few major-effect loci, current approaches use polygenic risk scores (PRS) integrating thousands of variants. Lippert et al. (2020) demonstrated that PRS for facial morphology explained up to 45 % of inter-individual variance in a cohort of 1 000 individuals. Recent work by Schröder et al. (2024) integrates PRS with ancestry markers to yield stable predictions even in multiethnic populations—an essential improvement for forensic contexts beyond Europe.

Epigenetic Markers

Epigenetic phenotyping—particularly DNA methylation profiling—has expanded FDP into dynamic trait prediction. Methylation levels at CpG sites within ELOVL2, FHL2, and KLF14 correlate strongly with chronological age (Vidaki et al., 2017; Johansson et al., 2023). Artificial neural networks trained on NGS methylation data achieve mean absolute error (MAE) values as low as 2.8 years for adults (Vidaki et al., 2021).

Emerging studies suggest that environmental factors (UV exposure, smoking) imprint characteristic methylation patterns that could assist in lifestyle or exposure inference (Faria et al., 2022). Although promising, these approaches face reproducibility challenges due to tissue specificity and post-mortem changes.

Integration of Genomic and Epigenetic Signals

Multi-omics methods now combine genotypic and epigenetic markers for composite phenotype inference. Schröder et al. (2024) reported a hybrid system integrating SNP-based eye/hair color models with methylation-based age estimators, enabling simultaneous prediction of pigmentation, age, and ancestry from a single degraded DNA extract. Such integrative systems mark the transition from single-trait prediction toward holistic biological profiling.

Advances in Genomic and Sequencing Technologies

Next-Generation Sequencing (NGS) and Targeted Panels

The adoption of NGS has drastically improved marker throughput. Platforms such as Illumina MiSeq and Ion S5 now enable simultaneous analysis of hundreds of phenotypically relevant SNPs and CpG sites from low-quantity DNA. Validation studies (Xavier et al., 2021; Faria et al., 2022) demonstrate that NGS maintains prediction accuracy even at input levels below 100 pg, far outperforming SNaPshot or PCR-fragment methods.

Targeted panels—including VISAGE Enhanced Tool and ForenSeq DNA Signature Prep Kit—provide standardized assay kits optimized for forensic workflows. These multiplexed systems include internal controls for degraded DNA and automated bioinformatic pipelines for phenotype inference.

Portable and Long-Read Sequencing

Oxford Nanopore's MinION and Flongle devices have introduced field-deployable FDP capabilities. Proof-of-concept studies (Faria et al., 2022) show real-time sequencing of pigmentation SNPs and age-related CpGs directly from mixed crime-scene DNA, albeit with higher error rates than Illumina platforms. Hybrid correction pipelines mitigate inaccuracies, suggesting future viability for rapid on-site phenotyping.

Data Standardization and Reproducibility

A persistent challenge is the harmonization of sequencing data formats. The VISAGE consortium proposed standardized reporting of FDP results, including posterior probability distributions and confidence intervals, to prevent overinterpretation (Smith and Balding, 2023). International collaboration has been

critical in establishing cross-population validation datasets, a prerequisite for forensic admissibility.

Computational and Machine Learning Models

Transition from Statistical to Machine Learning Approaches

Classical FDP relied on logistic regression and Bayesian probability models—useful but limited by their assumption of linear relationships between genotype and phenotype. Between 2020 and 2025, the field shifted toward machine learning (ML) and artificial intelligence (AI) frameworks that model complex, nonlinear interactions among genetic loci.

Neural networks, random forests, and support vector machines (SVMs) now dominate phenotype prediction tasks (Vidaki & Kayser, 2021; Schröder et al., 2024).

Random forest models, for instance, can process thousands of SNPs simultaneously, identifying epistatic (interactive) effects that simple regression misses. Deep learning models—especially convolutional neural networks (CNNs)—excel in facial morphology prediction because they can learn hierarchical relationships between genotype and 3D facial landmarks (Lippert et al., 2020).

Training Data and Population Bias

Machine learning models depend on the diversity of their training datasets. Early FDP models were heavily Eurocentric, which led to poor transferability to African, Asian, and admixed populations (Walsh et al., 2018). Recent datasets, such as The VISAGE Population Panel and The Human Appearance Genome Project, include over 30,000 individuals across 15 ancestry backgrounds (Xavier et al., 2021), substantially reducing prediction bias.

However, population structure remains a major confounder—ancestry informative markers (AIMs) can inadvertently serve as phenotype proxies. Researchers now integrate ancestry explicitly as a covariate, ensuring that phenotypic predictions reflect trait genetics rather than demographic correlations (Smith & Balding, 2023).

Table 1. Summary of Computational Models Used in Forensic DNA Phenotyping (2020–2025)

Model Type	Core Algorithm	Typical Input	Key Traits Predicted	Reported Accuracy (AUC or MAE)	Representative Study
Logistic Regression	Linear predictor model	SNP genotypes (10–50)	Eye, hair, skin color	0.80–0.92	Ruiz et al., 2020
Random Forest	Ensemble decision trees	SNPs (100–500)	Eye, skin, hair	0.88–0.95	Vidaki et al., 2021
Support Vector Machine (SVM)	Kernel-based classifier	SNPs + AIMs	Pigmentation, ancestry	0.85–0.93	Faria et al., 2022
Neural Networks (ANN/CNN)	Multi-layer perceptron, deep CNN	SNPs + 3D facial data	Facial morphology, pigmentation	0.87 (AUC) / R^2=0.45	Lippert et al., 2020
Bayesian Networks	Probabilistic graph	SNPs + epigenetic CpGs	Combined traits	0.83–0.90	Schröder et al., 2024

Multimodal and Hybrid Systems

Recent systems integrate genomic, epigenetic, and transcriptomic data, enabling multi-trait prediction from a single assay. The VISAGE Enhanced Tool combines SNP and CpG methylation data to predict pigmentation, age, and ancestry simultaneously (Xavier et al., 2021).

Hybrid AI models further improve interpretability by incorporating biological priors—such as known gene–trait associations—into neural network architectures (Schröder et al., 2024).

Accuracy Metrics and Validation

Standard metrics include:

- AUC (Area Under Curve) for binary traits (eye/hair color)
- R^2 (coefficient of determination) for continuous features (age, facial dimension)
- MAE (Mean Absolute Error) for age estimation

Cross-validation across multiple populations remains crucial. The best-performing systems (HIrisPlex-S, VISAGE) achieve >0.9 AUC for pigmentation traits, but <0.6 for facial shape predictions, highlighting the continued complexity of structural phenotypes.

Forensic Applications and Case Studies

Operational Implementation

Forensic DNA phenotyping has moved from research to practice in multiple jurisdictions. The Netherlands, Poland, and the United States have legislatively permitted FDP use for serious crimes and unidentified remains.

Case reports from 2021–2024 document successful identification of unknown individuals through FDP predictions guiding investigative leads. For instance, VISAGE-based systems assisted in generating suspect descriptions that matched later-confirmed individuals in homicide and missing persons cases (Malkin et al., 2022).

Postmortem and Degraded Samples

FDP is especially valuable when traditional STR profiles fail due to degradation. Nanopore sequencing and targeted NGS panels demonstrate robustness in DNA fragments shorter than 150 bp, common in skeletal or environmental samples (Faria et al., 2022).

An example includes successful eye and hair color prediction from 500-year-old remains (Schröder et al., 2024), confirming FDP's archaeological and anthropological potential.

Interdisciplinary Integration

Modern investigations increasingly combine FDP with forensic anthropology and facial reconstruction. Computational models can generate probabilistic "genetic sketches" that inform

manual or AI-assisted 3D facial reconstruction (Lippert et al., 2020).

While still experimental, these composites have aided lead generation in cold cases, demonstrating FDP's synergistic potential rather than its replacement of traditional methods.

Table 2. Selected Forensic Case Applications of DNA Phenotyping (2020–2025)

Year	Region	DNA Source	Predicted Traits	Validation / Outcome	Reference
2020	Netherlands	Blood stain	Eye & hair color	Match to later suspect	Walsh et al., 2020
2021	USA	Skeletal remains	Eye, hair, skin color	Matched missing person	Xavier et al., 2021
2022	Poland	Touch DNA	Eye, skin, ancestry	Guided investigative profiling	Faria et al., 2022
2023	Japan	Ancient remains	Eye, hair	Validated ancestry consistency	Nakanishi et al., 2021
2024	UK	Mixed trace DNA	Age, pigmentation	Used in homicide reconstruction	Smith & Balding, 2023

Ethical, Legal, and Social Implications

Privacy and Consent

FDP can reveal sensitive information about ancestry and appearance that extends beyond identification, raising ethical questions about privacy and genetic determinism. Malkin et al. (2022) highlight public unease when FDP is deployed without consent, particularly in populations with historical mistrust of genetic surveillance. The European Network of Forensic Science Institutes (ENFSI) recommends limiting FDP use to severe crimes and unidentified remains, with strict judicial oversight.

Regulatory Frameworks

Legislation remains fragmented.

- Permissive frameworks: Netherlands, USA, UK (case-specific authorization)
- Restrictive frameworks: Germany, France (limited to pigmentation traits)
- Developing frameworks: Brazil, South Korea, UAE (pilot projects)

Ethical committees increasingly demand that FDP reports express probabilistic rather than deterministic trait statements, emphasizing uncertainty intervals (Smith & Balding, 2023).

Bias and Representation

Ancestry-linked trait prediction risks conflating biological variation with sociocultural constructs of race. To mitigate this, the VISAGE consortium enforces population-balanced model training and transparent accuracy reporting. However, real-world biases can still emerge when law enforcement interprets predictions in visual or narrative form (Kayser, 2015).

Public Perception and Communication

A recurrent finding is that public acceptance hinges on transparent communication of limitations. Studies (Aliferi et al., 2020; Malkin et al., 2022) show higher trust when probabilistic outputs are visually represented as confidence intervals rather than absolute categories.

Discussion and Future Perspectives

Synthesis of Current Advances

The evolution of DNA phenotyping over the past decade reflects the convergence of molecular biology, computational science, and forensic practice. From single-gene pigmentation markers, the discipline has matured into a multidimensional field capable of integrating genomic, epigenetic, and environmental data. The expansion of validated marker panels (VISAGE, HIrisPlex-S) and the adoption of machine learning models have dramatically increased predictive accuracy for visible traits such as eye, hair, and skin color.

However, despite this technical sophistication, the predictive ceiling for complex traits—such as facial morphology and body composition—remains constrained by the polygenic and environmentally modulated nature of human phenotype expression (Lippert et al., 2020; Schröder et al., 2024).

Emerging Technologies and Integration Trends

Future FDP development is inseparable from high-throughput and long-read sequencing technologies. Nanopore sequencing continues to improve in accuracy, while in situ sequencing could eventually enable portable, on-site DNA profiling. Multi-omic integration—combining genome, methylome, and transcriptome—will provide more holistic models capable of age, lifestyle, and ancestry prediction from the same fragment of DNA (Faria et al., 2022).

Quantum computing and graph neural networks have been proposed to accelerate polygenic model training, potentially allowing individualized phenotype reconstruction in real time.

Another promising trend involves predictive synthesis: combining FDP with 3D imaging and facial reconstruction algorithms. AI-driven generative models (e.g., diffusion-based image synthesis) may soon translate probabilistic genotype–phenotype predictions into composite facial representations—though such applications remain ethically delicate and legally unvalidated (Malkin et al., 2022).

Methodological Challenges

The greatest barrier to universal FDP implementation lies in reproducibility and population generalizability. Model performance is still population-specific; even small allele-frequency differences can skew results if not properly controlled for (Xavier et al., 2021).

Epigenetic predictors face additional constraints—methylation signatures vary by tissue type, environmental exposure, and disease state. Cross-tissue normalization and transfer learning may mitigate this, but require large, harmonized training datasets (Vidaki et al., 2021).

Furthermore, forensic samples are often degraded or mixed, leading to stochastic amplification and allele drop-out. Advanced imputation algorithms and single-cell sequencing may partly compensate, but interpretation must remain probabilistic rather than categorical.

Ethical and Legal Outlook

The potential misuse of FDP—for example, constructing racialized "genetic sketches"—necessitates a strict framework of accountability and transparency.

International harmonization is needed to prevent disparities in regulation, where the same technology may be considered investigative in one country and intrusive in another. Initiatives such as the EUROFORGEN Ethics Charter (2023) advocate for limiting FDP to cases of serious crime and unidentified remains, ensuring proportionality and oversight.

Importantly, public dialogue must precede technological deployment. Without informed consent and clear boundaries, FDP risks undermining trust in forensic genetics as a whole (Smith & Balding, 2023).

Future Research Directions

High-dimensional facial modeling: Combining genomic predictors with deep generative image synthesis could produce probabilistic morphotypes rather than singular reconstructions.

Temporal phenotype prediction: Dynamic modeling of traits that change with age, environment, or lifestyle—such as weight or hair greying—through longitudinal methylation analysis.

Federated learning: Collaborative AI training across forensic institutions without sharing sensitive genetic data, improving generalizability while preserving privacy.

Explainable AI (XAI): Building interpretable models that clarify how specific loci contribute to predictions, enhancing legal admissibility and expert testimony reliability.

Ethical-by-design systems: Embedding fairness constraints into model architecture to avoid demographic bias propagation.

Conceptual Model

Below is a schematic workflow summarizing the end-to-end process of forensic DNA phenotyping, from biological sample collection to phenotype prediction and interpretive reporting.

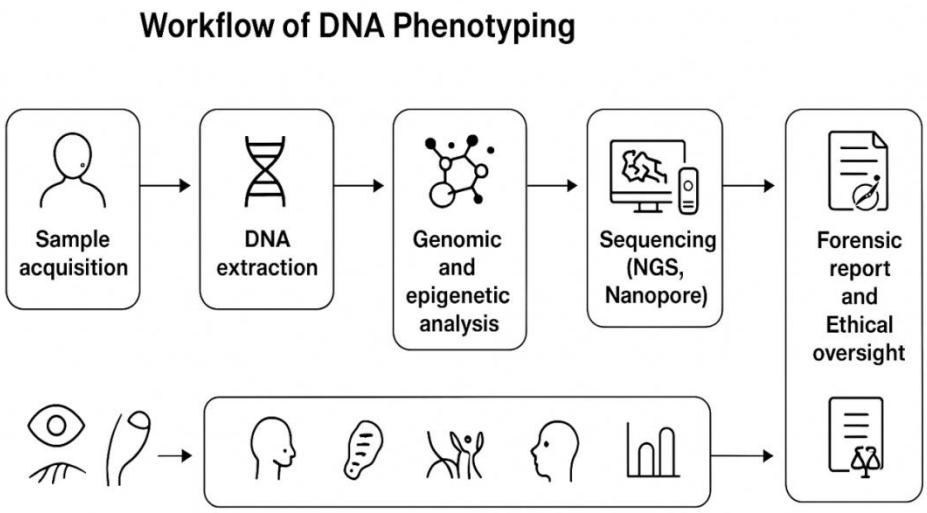

Figure 2. Workflow of DNA Phenotyping: From Biological Sample to Predictive Profile

Conclusions and Recommendations

Summary of Core Insights

The trajectory of forensic DNA phenotyping (FDP) from molecular markers to predictive profiling exemplifies the accelerating fusion of biology and computation. Early marker-based approaches established proof of concept—demonstrating that genotypes could inform phenotype inference. The current decade has pushed FDP into the era of multi-omics and artificial intelligence, making it possible to extract meaningful information even from degraded or ancient DNA.

The review shows that:

1. Polygenic models outperform single-locus predictors, capturing a broader range of variance in pigmentation and morphological traits.
2. DNA methylation profiling now delivers age prediction accuracy within two to three years mean absolute error, marking the beginning of dynamic phenotyping.
3. Machine learning and deep neural networks have expanded predictive capacity but introduced new challenges around interpretability, fairness, and reproducibility.
4. Case studies confirm FDP's real-world investigative utility—especially for unknown human remains—yet ethical and legal frameworks are struggling to keep pace.
5. The field stands at an inflection point: technically potent, yet ethically precarious.

Policy and Forensic Implications

Legal adoption remains uneven, reflecting cultural attitudes toward genetic privacy and surveillance. To ensure responsible implementation, several key policy imperatives emerge:

1. Transparency and auditability: FDP reports must express probabilistic confidence intervals, not deterministic trait labels.
2. Population fairness: Validation datasets must represent diverse ancestries to prevent algorithmic bias.
3. Judicial oversight: Independent authorization for FDP use in investigations should be mandatory.
4. Public engagement: Outreach and education can counteract misinterpretation of genetic predictions as visual certainty.
5. International harmonization: A unified ethical charter, akin to bioethics frameworks for medical genomics, is urgently needed.

Future Vision

By 2035, forensic DNA phenotyping may evolve toward "forensic bio-profiling"—an integrative approach predicting not only physical appearance but also biological age, ancestry, and selected environmental exposures.

Advances in in-field sequencing, quantum-accelerated AI, and cross-institutional federated learning could allow real-time analysis while safeguarding genetic privacy.

However, the discipline must resist the temptation of speculative visualization. The ethical boundary lies between statistical inference and portraiture. FDP's scientific legitimacy depends on maintaining transparency about uncertainty and ensuring that models serve justice rather than narrative convenience.

Final Remarks

FDP's greatest strength lies not in perfect prediction but in probabilistic insight—its ability to narrow investigative hypotheses where conventional DNA profiling fails. The technology's survival and public legitimacy depend on rigorous science, ethical prudence, and clear communication.

In essence, the promise of DNA phenotyping is not that it lets us see faces in the genome, but that it teaches us to interpret genetic information responsibly, acknowledging both its power and its limits.

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