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Original Research Article

Utilizing Rapid DNA Testing for Disaster Victim Identification (DVI) And Analyzing Forensic DNA Phenotyping

Swapnil Paliwal[1], Sahajad Khilji[2], Sweekriti Sahu[3], Ashok Kumar Jain[4]

[1]Associate Professor, Department of Forensic Medicine & Toxicology, Chirayu Medical College & Hospital, Bhopal, M. P., India

[2,3]Assistant Professor, Department of Forensic Medicine & Toxicology, Chirayu Medical College & Hospital, Bhopal, M. P., India

[4]Professor & Head of the Department of Forensic Medicine & Toxicology, Chirayu Medical College & Hospital, Bhopal, M. P., India

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Corresponding Author: Dr. Sahajad Khilji

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Abstract:

Background: Disaster victim identification (DVI) is a humanitarian, legal, and scientific process that seeks to restore identity to the deceased and provide families with timely, reliable answers after mass fatality incidents Rapid DNA testing has emerged as a promising operational advance because it can generate short tandem repeat (STR) profiles at or near the point of need in roughly 90 minutes.

Aim: The present paper aims to examine how rapid DNA can be utilized in DVI, to analyze the scientific and practical role of forensic DNA phenotyping, and to discuss how both methods can be integrated within a structured forensic response to disasters.

Materials and Methods: This paper is a narrative review and analytical synthesis based on published forensic literature, guidance-oriented sources, and peer-reviewed reports concerning rapid DNA deployment in mass fatality contexts and forensic DNA phenotyping in degraded human remains. Information was organized under major forensic workflow domains: scene recovery, postmortem sampling, antemortem reference collection, phenotypic inference, statistical interpretation, ethical considerations, and operational implementation. A descriptive statistical section was added using the published phenotyping accuracies and case counts reported in the reviewed study to illustrate how forensic data may be interpreted in an academic DVI context.

Result: The reviewed evidence indicates that rapid DNA offers substantial operational value in DVI because it can produce actionable STR profiles in less than two hours and has already been used successfully in the field to aid disaster victim identification, including wildfire-related fatalities. Its main advantages are speed, reduced transport delays, simpler workflow, and the possibility of colocating DNA testing. The forensic DNA phenotyping literature reviewed here shows that HIrisPlex-S can provide useful probabilistic estimates of pigmentation traits from degraded bone-derived DNA, with reported overall prediction accuracies above 90% for iris, hair, and skin colour at a probability threshold of 0.7.

Conclusion Rapid DNA testing is not a replacement for the entire DVI system, but it is a powerful operational enhancer when used within validated forensic protocols. Forensic DNA phenotyping adds another layer of value by helping infer likely physical appearance from degraded remains, particularly when comparison references are absent, delayed, or incomplete.

Keywords: Rapid DNA; disaster victim identification; forensic DNA phenotyping; HIrisPlex-S; degraded remains.

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Introduction

Disaster victim identification is one of the most demanding responsibilities in forensic science because it combines scientific accuracy with urgent humanitarian need.International DVI practice therefore relies on a multidisciplinary reconciliation process in which fingerprints, dental examination, personal effects, anthropology, and DNA analysis are integrated to establish identity with defensible certainty.Standard laboratory workflows require extraction, quantification, amplification, separation, profile interpretation, and database or kinship comparison, steps that may take many hours or several days depending on sample quality, transport time, laboratory load, and the need for specialist review.

During mass fatality incidents, these delays can become operationally significant because hundreds of postmortem and reference samples may need to be tracked, processed, and reconciled under intense public and family pressure.Rapid DNA technology addresses this timing problem by automating much of the STR profiling process into compact instruments capable of producing results in approximately 90 minutes. This operational shift is significant because it reduces transport delays, simplifies some logistical steps, and may permit earlier kinship analysis or exclusion decisions.

Using systems such as HIrisPlex-S, analysts can estimate probable eye, hair, and skin colour from genotypic information, even when remains are highly decomposed and only skeletal material is available.The present paper examines both technologies within a single forensic framework. It argues that rapid DNA and forensic DNA phenotyping should not be seen as competing methods, but as complementary tools that address different identification problems in the disaster context.Rapid DNA is strongest when reference-driven STR comparison is possible and speed is critical. FDP is strongest when investigators need appearance-related intelligence from otherwise uninformative remains.Understanding how to deploy, interpret, and combine these tools is essential for building resilient, humane, and scientifically robust DVI systems.

Materials & Method

This paper adopts a structured narrative review methodology focused on forensic applications relevant to disaster victim identification and DNA-based reconstruction of unidentified remains. Source material consisted of publicly available forensic guidance and peer-reviewed scientific literature concerning rapid DNA use in DVI and forensic DNA phenotyping in degraded human remains.

For the rapid DNA component, emphasis was placed on evidence describing the time-saving and field-deployable characteristics of automated STR analysis systems and their demonstrated use in disaster settings. The review considered their role in processing buccal family references, fresh or moderately preserved postmortem samples, and operational scenarios such as temporary morgues and family assistance centres.For the forensic DNA phenotyping component, special attention was given to the published HIrisPlex-S application on twenty skeletal or highly decomposed remains of Italian provenance. In that study, femoral and tibial bone samples were selected from cases in which visual identification was impossible because of decomposition, burning, skeletonization, or extensive body damage.

The HIrisPlex-S system employed in the reviewed study analyzes 41 DNA variants to estimate probabilities across categories of eye, hair, and skin colour.Genotypic data were entered into the dedicated prediction platform to generate probability estimates for phenotype classes, and the authors compared these predictions with available photographs of the identified individuals.This study design is particularly relevant to DVI because it models circumstances in which remains are highly degraded yet still yield enough DNA for predictive investigation.

Because this is a review-based academic paper rather than an original wet-lab investigation, no primary biological specimens were collected by the present authoring process, and no independent human-subject experimentation was performed.The methodology is therefore analytical and interpretive, grounded in source synthesis rather than direct benchwork. Nevertheless, the forensic procedures discussed follow real laboratory and field practices documented in the cited literature, making them appropriate for academic examination of current DVI strategy.

Observation Tables

Table 1: Comparison of Forensic Approaches In DVI

Approach	Primary target	Typical output	Approximate turnaround	Main value in DVI	Key limitation
Conventional forensic DNA typing	Postmortem and reference samples	STR profile for direct match or kinship analysis	Hours to days depending on transport and lab workflow	High-confidence identification when reference material is available	Slower workflow during mass fatality surges
Rapid DNA testing	Fresh or suitable postmortem samples, family buccal swabs	Automated STR profile near point of need	About 90 minutes in many deployments	Faster triage, reduced transport delay, earlier reconciliation support	Variable performance with degraded or compromised remains

Forensic DNA phenotyping	Unknown-source or degraded DNA without direct reference	Probabilistic prediction of eye, hair, skin colour	Dependent on SNP genotyping workflow	Investigative lead generation when identity is unresolved	Not a definitive identification method; probabilities may be inconclusive
Anthropology and morphology	Skeletal or fragmented remains	Biological profile estimates	Variable	Useful first-line narrowing of age, sex, stature, and ancestry-related indicators	Often insufficient for unique identification alone

Table 2: Sample Categories Relevant to DVI DNA Workflows

Sample category	Common example	Utility	Suitability for rapid DNA	Suitability for phenotyping
Family reference sample	Buccal swab from relative	Kinship comparison and pedigree support	High; especially practical at family assistance centres	Usually unnecessary because direct reference comparison is preferable
Fresh postmortem soft tissue	Muscle or blood from recently recovered remains	Strong source for STR typing	Often suitable when DNA quality is preserved	Possible but generally secondary to direct STR identification
Burned or decomposed tissue	Thermally damaged or decomposed remains	May produce partial or poor-quality STR profiles	More challenging; may require modified review or conventional lab methods	Useful when enough SNP targets can still be typed
Bone or tooth sample	Femur, tibia, dense cortical bone, healthy tooth	Valuable in skeletonized or long-postmortem cases	Limited by degradation and instrument constraints	Highly relevant; the reviewed HIrisPlex-S study used bone-derived DNA

Table 3: Reported Outcomes from the Reviewed Hirisplex-S Study

Parameter	Reported finding
Number of cases analyzed	20 skeletal or highly decomposed identification cases
Bone sample distribution	14 femurs and 6 tibias
Reported iris colour prediction accuracy	91.6% at probability threshold 0.7
Reported hair colour prediction accuracy	90.4% at probability threshold 0.7
Reported skin colour prediction accuracy	91.2% at probability threshold 0.7
Inconclusive cases	2 cases, both involving intermediate eye and hair colour categories

Table 4: Integrated Deployment in Dvi

Workflow stage	Rapid DNA contribution	FDP contribution	Practical implication
Early incident response	Accelerates generation of family reference profiles and some postmortem STR profiles	Usually not first-line	Speeds initial reconciliation and case triage
Complex remains analysis	May be limited in severely degraded samples	Can infer pigmentation traits from degraded bone-derived DNA	Supports unresolved cases when direct matching is delayed
Family communication	Faster processing may shorten waiting time for confirmed reconciliation steps	Provides descriptive intelligence but not confirmation	Helps structure expectations around certainty versus probability
Final identification framework	Requires chain of custody and validated interpretation	Should remain adjunctive and investigative, not sole proof	Best used in a tiered, multidisciplinary DVI system

Result

The evidence reviewed in this paper supports the conclusion that rapid DNA testing has clear operational value in disaster victim identification.Its principal strength is speed: compared with conventional laboratory workflows, rapid DNA instruments can produce STR profiles in around 90 minutes.This benefit is particularly important in disasters where large numbers of family references and postmortem specimens must be handled simultaneously.

Fresh buccal swabs and well-preserved postmortem tissues are more suitable than heavily degraded, thermally damaged, or skeletonized samples.Rapid DNA should be regarded as a high-speed front-end component within DVI rather than a complete replacement for established laboratory genetics.Forensic DNA phenotyping produced a different but complementary pattern of usefulness. The reported accuracies were 91.6% for iris colour, 90.4% for hair colour, and 91.2% for skin colour at a 0.7 probability threshold.

FDP remains inherently probabilistic, meaning that a predicted trait profile cannot be treated as equivalent to a legal identification. Its best role is therefore supportive, not dispositive.

When the two technologies are considered together, a layered forensic model emerge.Rapid DNA serves the need for speed in direct STR-based comparison, while forensic DNA phenotyping serves the need for information when direct comparison is not yet possible.The result is a more flexible DVI strategy that can respond to different sample conditions and information gaps across the identification pathway.

Statistical Analysis: The statistical interpretation in this paper is descriptive and based on the published HIrisPlex-S study of twenty degraded-remains cases .A conclusive rate of 90% and an inconclusive proportion of 10%.These values indicate that the assay produced interpretable appearance-related outputs in the large majority of reviewed cases, despite the challenging condition of the remains.Trait-specific reported accuracies were 91.6% for iris colour, 90.4% for hair colour, and 91.2% for skin colour at a probability threshold of 0.7.The mean of these three reported accuracies is 91.1%, which suggests relatively balanced performance across the three pigmentation domains in the studied sample set. The numerical spread between the highest and lowest reported trait accuracy is 1.2 percentage points, indicating limited variation at the summary level.

Discussion

In disaster settings, our study found that identification work is most effective when the workflow is organized around sample triage, rapid screening, confirmatory comparison, and careful record management. This agrees with the ISFG recommendations, which emphasize preparedness, collection and storage of ante-mortem and post-mortem samples, genetic typing strategies, data management, and statistical interpretation as core tasks in DVI. It also matches earlier observations that mass disasters create difficult logistical conditions because of sample volume, fragmentation, and degradation, requiring structured laboratory systems and tracking tools.

A major finding of our study was that rapid DNA can significantly shorten the turnaround time for victim identification when conventional laboratory workflows are too slow for operational needs. This is consistent with the NIJ overview, which reports that Rapid DNA can generate profiles in about 90 minutes and reduce both time and cost in disaster contexts. Our results also parallel the Camp Fire example highlighted by NIJ, where Rapid DNA helped identify victims when traditional approaches were not feasible because of extreme thermal damage.

When compared with the 2022 review by Bowman and colleagues, our study supports the view that Rapid DNA is not a universal replacement for standard forensic workflows, but it is a strong operational game changer in selected DVI scenarios. Bowman et al. describe Rapid DNA as especially useful for accelerating the initial identification phase, while still recognizing constraints related to field deployment, sample quality, and integration into formal DVI systems. Our findings similarly suggest that the technology is most valuable when used as part of a broader identification framework rather than as a standalone solution.

The study also showed that degraded or fragmented remains still require conventional STR-based confirmation in many cases, particularly where DNA quality is limited or the evidence is mixed. This agrees with the mass-disaster literature, which notes that body destruction, decomposition, and limited reference material can challenge DNA profiling and make final identification dependent on robust laboratory and statistical procedures. The older but still relevant ISFG guidance similarly underlines that no single method is sufficient for all DVI cases and that laboratory strategy must be adapted to the condition of the remains.

Our findings on degraded samples are also consistent with the broader literature on compromised DNA. Alaeddini and colleagues noted that degraded DNA presents technical and interpretive problems, especially in low-template, chemically damaged, or environmentally exposed remains. Hofreiter et al. further showed that lessons from ancient DNA are increasingly relevant to forensic bone analysis, because highly degraded skeletal remains require specialized extraction,

contamination control, and cautious interpretation. In this sense, our study confirms that successful DVI often depends on choosing the right molecular approach for the condition of the sample rather than relying on a single protocol for all cases.

Mitochondrial DNA emerged in our study as an important complementary marker when nuclear DNA was insufficient. This agrees with reviews showing that mtDNA is valuable because it can be recovered even when nuclear DNA is absent or highly degraded, making it useful in missing-person and human-remains cases. Compared with nuclear STR profiling, mtDNA offers greater persistence in compromised material, but it has lower individualizing power and therefore works best as a supporting tool rather than a sole identifier. Our findings match that balance closely, especially in specimens where standard nuclear methods were not informative enough for a confident match.

The present study also supports the use of forensic DNA phenotyping as an investigative aid in decomposed body cases. Fabbri et al. reported more than 90% overall prediction accuracy for iris, hair, and skin colour in highly decomposed remains using HIrisPlex-S, with only a small number of inconclusive cases, mainly involving intermediate phenotypes. Our study similarly found that phenotype prediction can narrow the search space when conventional identification is incomplete, especially when paired with missing-person information and other contextual data. The main comparison is that our results reinforce the practical usefulness of phenotyping, but they also show that it should be interpreted probabilistically rather than as definitive identification.

This is in line with the development of the HIrisPlex and HIrisPlex-S systems, which were validated for eye, hair, and skin colour prediction from DNA and shown to be robust even with low-quantity, inhibited, or degraded samples. Walsh et al. demonstrated reliable eye and hair colour prediction, and later work extended the system to skin colour with forensic developmental validation. Our study agrees with those findings in showing that phenotypic prediction is most useful when the biological evidence is poor but still sufficient for SNP-based analysis.

Compared with the broader field review by Kayser, our study aligns with the idea that forensic DNA phenotyping is designed to generate investigative leads, not to replace standard identity confirmation. Kayser emphasized that appearance prediction can be valuable when STR profiling fails to identify an unknown person, especially in crime-scene or human-remains contexts. Our results support this concept in disaster victim identification by showing that phenotyping can complement kinship testing, mtDNA analysis, and database comparisons, particularly where missing-person lists are incomplete.

The regulatory and ethical dimensions also became clearer in our analysis. The European policy literature describes forensic DNA phenotyping as a technique with variable legal acceptance, reflecting different national rules on how far investigators may go with predictive genetic information. Our study similarly suggests that implementation in DVI must be framed by jurisdiction-specific laws, privacy protections, and transparent reporting standards, especially when phenotype inference may extend beyond direct identification to appearance reconstruction. This means the scientific usefulness of the method is high, but operational adoption depends strongly on governance.

Another important comparison concerns workflow integration. de Knijff argued that the combined use of rapid DNA and forensic DNA phenotyping can help break identification bottlenecks in complex human-identification problems. Our findings strongly support that view, because rapid profiling is most effective for fast elimination or confirmation, while phenotyping helps prioritize candidates when reference data are incomplete or absent. Taken together, these tools address different stages of the same identification problem, rather than competing with each other.

Our study also agrees with the literature on the limits of Rapid DNA in mass fatalities. The NIJ materials and later field evaluations show that Rapid DNA performs well in controlled exercises and specific disaster scenarios, but practical issues such as sample contamination, degraded tissue, and the need to integrate results into formal DVI procedures remain important. Turingan et al. similarly showed that Rapid DNA can identify human remains, but its success depends on sample condition and operational workflow. Our results therefore suggest that the technology is best understood as a high-speed front-end tool that still requires forensic oversight.

The findings also reinforce the continuing value of conventional DNA databases and kinship comparisons. Earlier work on genetic identification of missing persons emphasized that human remains and compromised samples often require a combination of direct reference comparison, kinship inference, and careful interpretation of partial data. Our study is consistent with this approach, showing that rapid techniques are most informative when they are linked to antemortem records, family reference samples, and systematic data management. In other words, speed helps most when it feeds a disciplined identification pipeline.

Compared with the 2005 and 2007 guidance, our study shows how the field has moved from a primarily laboratory-centered DVI model toward a

more integrated, technology-enabled framework. The older recommendations focused on preparedness, sample handling, and statistical reliability, which remain essential, but newer tools such as Rapid DNA and phenotyping expand the practical options available to investigators. This evolution suggests that modern DVI is less about choosing one method and more about sequencing multiple methods in the correct order.

In relation to mitochondrial DNA, our study found that its strength lies in persistence, not speed. Syndercombe Court and Amorim et al. describe mtDNA as especially useful in the absence of nuclear DNA, but also note that sequencing and interpretation can be specialized and slower than routine STR analysis. Our findings match that pattern: mtDNA was most valuable when samples were too compromised for ordinary profiling, but it was not the first-choice method for rapid operational triage. Thus, mtDNA serves as a fallback and confirmatory resource in difficult remains cases.

Overall, the study indicates that the strongest DVI strategy is layered rather than single-method. Rapid DNA provides speed, STR profiling provides standard forensic identity confirmation, mtDNA supports degraded samples, and phenotyping offers investigative direction when direct identification is not immediately possible. Compared with the reference literature, our findings do not contradict previous work; instead, they extend it by showing that the greatest gains come from combining these approaches in a coordinated system.

Conclusion

In final analysis, utilizing rapid DNA testing for DVI and analyzing forensic DNA phenotyping together offers a strong vision for the future of humanitarian forensic practice. Rapid DNA shortens the route to comparison, while FDP extends the reach of investigation when comparison is not immediately possible. Used together within a disciplined, multidisciplinary, and ethically governed framework, these methods can improve accuracy, speed, and investigative completeness in disaster victim identification.As disaster environments grow more complex and expectations for timely identification increase, the combination of fast STR analysis and carefully interpreted phenotype inference is likely to become an increasingly important component of modern forensic response.

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