*This document has been accepted by the Academy Standards Board (ASB) for development as an American National Standard (ANS). For information about ASB and their process please refer to asb.aafs.org. This document is being made available at this stage of the process so that the forensic science community and interested stakeholders can be more fully aware of the efforts and work products of the Organization of Scientific Area Committees for Forensic Science (OSAC). The documents were prepared with input from OSAC Legal Resource Committee, Quality Infrastructure Committee, and Human Factors Committees, as well as the relevant Scientific Area Committee. The content of the documents listed below is subject to change during the standards development process within ASB, and may not represent the contents of the final published standard. All stakeholder groups or individuals, are strongly encouraged to submit technical comments on this draft document during the ASB's open comment period. Technical comments will not be accepted if submitted to the OSAC Scientific Area Committee or Subcommittees.*

# Best Practices Recommendations for DNA Analysis for Human Identification in Mass Fatality Incidents



**DRAFT DOCUMENT**

# Best Practices Recommendations for DNA Analysis for Human Identification in Mass Fatality Incidents

## 1 Foreword

DNA technology is a critical component of many DVI efforts. The success of these endeavors is predicated on the proper collection, documenation, and storage of both human remains, direct reference samples, and family reference samples. Additionally, appropriate evaluation of the results is required to make informed identification decisions. All activities relating to DNA analysis should be conducted in such a way to preserve the integrity of the samples and the quality and reliability of the results.

The purpose of these DNA best practices are to provide information and direction to elected officials, law enforcement officials, and the medicolegal community who may be involved in the human identification effort. The primary objective is to inform the medicolegal authority responsible for the incident on steps necessary to maximize the success of an identification effort involving the use of DNA technology.

These best practices are put forth by the Disaster Victim Identification subcommittee within OSAC. This document originated from the Scientific Working Group on Disaster Victim Identification (SWGDVI).

## 2 Acknowledgements

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## 4 Scope

While not an exhaustive listing of circumstances, this guide aims to provide information that allows jurisdictions to prepare for a mass fatality incident and implement a DNA sample collection and analysis plan to effectively contribute to the identification of the victims. Decisions made in the early stages of an incident will have significant consequences later in the identification process. This document is intended to assist the decision makers with that process. Where possible, the guidelines below should be applied. Absent specific guidance, practitioners should adhere to the principle, spirit and intent.

Disaster victim identification practitioners are encouraged to develop, implement, exercise and periodically review their standard operating procedures and validation data, in light of these guidelines and best practices, and to update their procedures as needed. It is anticipated that these guidelines will evolve as future technologies emerge.

## 5 Terms and Definitions

### 5.1
### Identification Authority
The individual or group responsible for rendering identifications.

## 6 Recommendations

In the United States, a medical examiner or coroner is legally responsible for any deaths that occur within his medicolegal jurisdiction. However, Disaster Victim Identification (DVI) projects may involve authorities from multiple government agencies at the local, state, federal, and international level. With that in mind, this document uses the term "identification authority" to identify the individual or group responsible for rendering identifications.

DNA testing is a well-established scientific method for human identification. DNA analysis can identify the victims and re-associate fragmented remains. As such, it often plays a key role in any mass fatality incident. The identification authority is responsible for making the initial decision as to the primary goal of the DNA identification efforts (e.g., whether to pursue a medicolegal finding of death for each victim or to identify all biological material recovered, resulting in multiple identifications of the same individual). This decision will have a significant impact on the scope of the identification process.

### 6.1 Resource and Scope Considerations

The need to utilize DNA analysis resources will vary according to the scope of the incident; and the availability of such resources will vary by jurisdiction. The identification authority is expected to evaluate the available DNA sampling and testing resources and establish formal agreements with laboratories capable of supporting the jurisdiction's mass fatality management plan. It is considered a best practice that each jurisdiction conduct an assessment of its DNA capabilities and establish key points of contact with DNA laboratories in advance of any mass fatality incident. The sections below provide key considerations that will affect the resources required to effectively conduct DNA-based identifications.

The resources required for a human identification project can vary significantly based upon the nature of the incident. It is important to know the capacity of the local, regional, state, and federal DNA testing facilities to determine at what point additional resources and laboratories will be needed. The scope of the incident is determined by multiple factor including population type, number of victims, and extent of human remains fragmentation.

a. Open vs. Closed population: In a closed population, the number of victims – and their reported identities - is well established thus providing a more definitive end point of the effort. This may include an airline crash in an unpopulated area with an available flight manifest. Open systems are comprised of an unknown number of victims. Victim lists are often unavailable or inaccurate. An example of an open system could be a natural disaster, or large incident in a public place.
b. Number of Victims: The number of victims has an impact not only on the number of remains to be processed, but also the number of reference samples – both from relatives and the deceased. It is important to account for both types of analyses when evaluating capacity.
c. Fragmentation of Remains: In addition to the number of victims, the degree of fragmentation, or number of remains per victim, is a primary factor in determining the scope of the effort. Similar to the number of victims, the amount of fragmentation will impact the number of remains samples to be tested. In contrast to the number of victims, increased fragmentation will not increase the need for additional references. When remains are fragmented, it is a best practice to establish a practical threshold of minimum fragment size and/or condition to be sampled for DNA analysis.

The number of DNA samples the project will need to analyze will vary greatly depending on the factors listed above. At a minimum, the resources and budget should anticipate the collection and analysis of many more samples than the number of victims. Based upon the number of victims, type of reference samples collected and relationships of the donors, the DNA laboratory should provide recommendations to the other stakeholders regarding which DNA technologies are likely to be needed. This may include lineage markers such as YSTR and mitochondrial DNA. Use of these additional technologies may not always be feasible financially, or practical, but they shall factor into the decision making process. A survey of various Disaster Victim Identification projects and the numbers of samples analyzed is provided in Table 1.

In addition to the scientific resources required, managers shall be prepared to address the required information technology infrastructure to support data management, analysis and communications. This includes appropriate security and backup procedures.

The identification authority, in consultation with the DNA laboratory, is expected to establish realistic timelines for the completion of the DNA identification process based upon an assessment of the laboratories' capacities and data interpretation capabilities. It is an unacceptable practice for the identification authority to adjust timelines based on external influences. These include political authorities, the media and families. Attempting to implement an unrealistically accelerated timeline could be detrimental to the overall identification effort. The issuance of reports by the laboratory should not be the endpoint of the timeline. The timeline should also incorporate the requirements of an identification review process. This is often conducted by a team of individuals (e.g., Reconciliation Team or Identification Review Team) or a single authority. They will compile and review all pertinent identification data and information and advise the identification authority on the appropriate course of action.

Stakeholders shall be cognizant of the funding available for the project and the limitations this may impose on the scope of testing. A limited initial budget may impact the number of remains that can be analyzed or be a factor in determining an end point for the identification process. Similarly, as

the project evolves, the cost associated with more aggressive testing approaches may need to be weighed against the potential to obtain new identifications.

### 6.2 Sample Collection for DNA Analysis

DNA analysis in disaster victim identification requires one or more valid reference samples to accurately identify human remains. In cases of fragmentation, comparison of the remains samples to each other will result in re-associations. Three types of biological samples are collected to conduct DNA analysis - human remains, appropriate family references for kinship associations, and direct references of the victims (e.g., biomedical specimens and personal effects likely to contain biological material).

It is a best practice for samples to be collected in a manner that prevents loss, contamination, or deleterious change. This includes the need to initiate a proper chain of custody. Sample preparation should include provisions for specimen inventory, appropriate transport and storage of large numbers of samples, and accompanying documentation.

Each sample type has some unique considerations for collection and handling. The following sections provide best practices for these different sample types.

#### 6.2.1 Human remains

##### 6.2.1.1 Collection Practice

Samples should be collected and stored in separately labeled containers. Only one fragment should be stored in each container and all containers shall be single-use.

Samples should be stored without deleterious preservatives (e.g., formaldehyde). Samples should be refrigerated and/or frozen as soon as practically possible, or if dictated by practical considerations such as lack of timely access to refrigeration, the samples should be stabilized against degradation by storage in one of various published methods for this purpose. Numerous options have been published, which should be evaluated in advance, also taking into consideration issues such as flammability and hazardous chemical handling. Some options include the following:

a. Preservation of small tissue samples in a large volume-excess of solid salt granules such as sodium chloride.

b. Solutions of dimethyl sulfoxide (DMSO), or DMSO and ethanol.

c. 70-100% Ethanol.

d. Cell lysis buffers containing EDTA and detergent.

e. Commercially available, proprietary reagents..

When possible, samples should be collected from human remains for DNA analysis in conjunction with other forensic analyses at the designated morgue facility.

When possible, duplicate samples should be collected from the same human remains to allow concordant testing for confirmation of DNA results.

##### 6.2.1.2 Required Documentation

All remains submitted for DNA analysis should be photographed and documented at the designated morgue facility/collection site prior to and after sampling.

The numbering system employed during sampling should be integrated with or derived from the incident management system/ incident command system (IMS/ ICS) numbering strategy to uniquely identify each specimen.

When multiple samples are taken from the same victim – or even the same bone or tissue – each sample collected should be given an independent, unique number.

#### 6.2.1.3 Staff qualifications

The staff member who takes the sample (i.e., appropriate forensic practitioner) is expected to assess its suitability for DNA analysis, for example by identifying the species and anatomical origin of the specimen, if possible.

The staff member who records the sample should verify the sample description, assign or maintain the unique identifier, maintain the chain of custody, and ensure proper storage (e.g., freezing the sample in a secure location).

Where possible, the staff members mentioned above should be two individuals working as a team.

Staff involved in collecting samples should provide a DNA reference sample to be used for elimination purposes.

#### 6.2.1.4 Fragmentation Considerations

If the scope of the DNA analysis effort has not been determined at the onset of sample collection, then all suspected human remains should be sampled in the event that testing may be necessary.

The identification authority is expected to determine the goal of the identification effort and establish criteria for sample collection. The answers to each of the following questions will impact the scope, duration and cost of DNA testing.

a. Will all fragments, regardless of size and condition be tested?

b. Will testing be concluded after all victims are identified or after all fragments have been identified?

c. Will a minimum fragment size be established for testing?

d. Will only anatomically recognizable fragments be tested?

e. If a particular fragment, due to its size or condition, will be consumed during testing, who shall be notified and who has the authority to grant such permission?

The answers to the preceding questions should be used to formulate a standardized sampling and analysis plan for a mass fatality incident. As a standard practice, samples should be taken from each body, body part or portion of remains meeting the criteria established by the analysis plan. This best practice for DNA collection also extends to remains from victims that have been previously identified by other techniques/modalities. DNA sampling should take place before any remains are released to the victim's family.

In cases involving potentially commingled remains, such as from high impact incidents, best practice is for sample collection to be conducted by individuals with appropriate expertise (such as anthropology, pathology, or specialized DNA experience) to ensure that optimal samples are obtained from single-source specimens. Depending upon the qualifications/experience of staff involved in sample collection and the DNA laboratory, it may be that sampling of such commingled cases should be performed in the DNA laboratory.

#### 6.2.1.5 Sample Preference

For human remains, the following samples types should be collected from each victim. They are listed in order of preference, depending on the condition of the remains:

a. For remains that are intact and have suffered very little to no decomposition, buccal cell

swabs may be taken.

b. For remains that are not very decomposed, 10–15 g of deep skeletal muscle (avoid tissues that may have been crushed together by incident impact or blast forces).

c. For more highly degraded remains 1–2 cm x 4–6 cm x 0.5–1 cm of cortical bone.

Anthropological landmarks, articular margins, fresh-broken margins, and full transaction of bones should be avoided whenever possible; cut windows in long bones and crania. An anthropologist should be consulted to ensure that relevant anthropology landmarks and measurements can be maintained following sampling.

d. Intact molars, upper or lower canine or other intact teeth without restorations. Consultation with an odontologist is recommended prior to extracting any teeth.

e. Other portion of soft or hard tissue that fits into a 50 ml conical tube. Conditions may greatly restrict the sample types that are available, and a wide range of tissues may prove useful.

f. Finger nails or toe nails

#### 6.2.1.6 Sample Handling

Proper personal protective equipment should be worn to protect both the staff member and the remains. Samples should be handled in a manner that prevents cross contamination among remains, such as:

a. Sterile and disposable supplies for sample collection should be used whenever possible. Gloves should be changed and tools disposed of after taking each sample.

b. Non-disposable instruments and work surfaces should be cleaned with commercial bleach (one part bleach to nine parts water).

### 6.2.2 Family References

The accurate and timely collection of family reference samples is critical to the success of the identification project. In addition to the best practices that follow, stakeholders should prepare themselves for the cultural and ethical concerns that arise when obtaining biological samples from family members. For example, one shall be aware of any religious and/or social concerns regarding blood draws or skin punctures. Additionally, the stakeholders shall establish policies to address situations where DNA analysis determines that familial relationships are not in fact the same as stated by the donors.

#### 6.2.2.1 Collection

The collection of reference samples from members of the victims' immediate families should be initiated at the family assistance center (FAC) or other designated sites. If immediate family members are not available at the family assistance center, samples from the relatives that are available should be collected. Further, collectors should inquire about the immediate family members from both the paternal and maternal sides of the family. Contact information and relationships for these and other potential donors should be documented, and requests should be made that DNA samples be provided by appropriate family member that are not present at the FAC.

A plan should be developed and implemented to initiate the remote collection of reference samples from family members. Other agencies should be used to assist as necessary. If needed, the media should be engaged to publicize the locations of sample collection sites.

Individual reference samples should be collected and stored in separately labeled containers.

At the time of collection, family members should be asked about the availability of direct reference samples from the decedent.

The staff at the FAC shall be appropriately diverse to address the broad range of languages and cultures present in families of the victims. Language barriers will result in inaccurate information collection which will lead to missed identifications. Lack of cultural sensitivity will weaken the trust needed from families during the identification process and will result in refusals to provide samples.

#### 6.2.2.2 Documentation

Obtain and document informed consent using consent forms that have undergone legal review.

a. The document shall include the purpose for requesting the sample and a statement that the sample and associated data will be used only for this identification purpose.

b. The medicolegal authority that purports ownership of, and responsibility for, the sample and associated data shall be clearly stated. Ownership and responsibility shall rest only with the relevant medicolegal authority.

c. Policies shall be established for data and sample protection, retention, destruction, and revocation of consent. The policies must be communicated to donors as part of the informed consent process.

Identify the donor:

a. As a best practice, the donor's identity should be confirmed with government issued identification when possible.

b. The donor's biological relationship to the victim should be clearly established. Clear communication, proper questioning and reliable recording of data in a standard format (using appropriate forms) will assist in this endeavor. Improperly stated relationships will cause delays and could cause identifications to be missed.

c. The donor's contact information should be obtained.

d. An appropriate form that includes a pedigree tree diagram to establish and document the relationships should be used.

A chain of custody for donor reference samples should be originated and maintained.

A logical numbering system for all reference samples that is compatible with the data management software should be used. To prevent duplication of sample numbers or antemortem case numbers, each collection agent or collection site can be given a unique numerical identifier that becomes part of the antemortem case number and family reference sample numbers.

#### 6.2.2.3 Staff

Appropriate individuals or agencies should be identified and utilized for the collection of family reference samples.

Selected individuals should have the knowledge and experience in appropriate disciplines to:

a. Interact with victims' relatives with sensitivity.

b. Use the proper collection methods.

c. Record accurate and reliable kinship information.

#### 6.2.2.4 Preferred Family Reference Samples

a. Two properly collected buccal swabs.

b. Blood sample collected using a fingerstick or venipuncture device.

c. Collect sufficient numbers of swabs or a sufficiently large bloodstain to allow duplicate typing.

#### 6.2.2.5 Preferred Donors

As a best practice, staff members should be instructed to collect samples from any family members that offer to donate. If more samples are obtained than necessary, the lab will determine which ones to test.

If available, the following relatives should be collected in order of preference:

a. Both biological parents of the victim.

b. One parent of the victim, the victim's mate and as many of their biological children as possible

c. The victim's mate and their biological children.

d. One parent of the victim and biological sibling(s) of the victim

e. Biological siblings who share the same parents as the victim. If siblings are the only available references, collect as many as possible

In order to obtain as much genetic information as possible for the victim, closely related family references from both the maternal and paternal sides of the family should be collected.

In the absence of the relatives listed above, more distant relatives (half-siblings, aunts, uncles, nephews, nieces, grandparents, and grandchildren) should still be collected. They may cumulatively provide sufficient genetic coverage to aid in an identification. Distant relatives also permit analysis of maternal and paternal lineages if mtDNA and Y-chromosome testing is employed.

### 6.3 Direct Reference Samples

#### 6.3.1 Collection

A point of contact responsible for receiving and managing the collection of direct reference samples should be immediately established. The staff members collecting family references should also be prepared for relatives to arrive with direct reference samples.

Elimination samples should be collected from persons that provide any direct reference samples. Elimination samples from any additional persons that may have come into contact with the direct reference samples may be advisable. Decisions can be made at a later time whether analysis of elimination samples is needed.

The name or location of the point of contact should be widely publicized and a list of items suitable as direct DNA reference samples should be distributed.

Family members should be notified that they can submit direct reference samples at the same site where they provide family reference samples.

Individual reference samples should be collected and stored in separately labeled containers.

#### 6.3.2 Documentation

Appropriate documentation should be collected to allow for the correlation of direct reference samples to a particular victim.

A chain of custody should be originated and maintained.

A logical numbering system for all reference samples that is compatible with the data management strategy being used should be initiated. Allocating a predetermined block of numbers to assist in identifying the source of the sample may be considered.

### 6.3.3 Samples for Analysis

Even if a direct reference is submitted, family reference samples should still be collected. These will be used to validate the source of the direct reference.

Where possible, more than one item should be submitted.

Care should be taken in choosing appropriate direct reference samples for analysis. Items should be chosen that are:

a. Directly attributable to the victim.

    1. DNA analysis of family reference samples should be used to establish the validity of direct reference samples

    2. Elimination samples from others who come into contact with the direct reference should be obtained to rule out the possibility of contamination.

a. Submitted as soon as possible

### 6.3.4 Preferred Samples

Some of the most commonly available reference samples are excellent sources of DNA, while others are not. Additionally, some less common sample types are the most useful as direct references. It is important to inquire about a decedent's medical history to determine what samples may be available. Personal items may need to be returned to donors.

The best sources of direct references include:

a. Used tooth brushes
b. Used shavers/razors
c. Hair brushes/combs
d. Buccal swabs (e.g., home DNA identification kits).
e. Bloodstain cards (e.g., Guthrie cards or cards obtained from other repositories).
f. Blood stored for elective surgery.
g. Pathology samples (e.g., biopsy samples, PAP smears).

Lesser quality sources of DNA:

h. lipstick or deodorant
i. Pillowcase
j. used drinking glass
k. fingernail clippings
l. cigarette butt
m. hat or unwashed undergarments
n. other personally handled or used items (consult the testing laboratory for specific criteria). These types of items typically include wrist watches and other jewelry items.

## 6.4 Laboratory Qualifications and Capabilities

In preparing for a mass fatality incident, the medicolegal authority should become familiar with the DNA laboratory(ies) that are suitable and available. A working relationship with laboratory management and the DNA Section leadership should be established well in advance of a mass

fatality incident. A determination should be made whether a local government laboratory, another government laboratory, or a private sector laboratory will be the primary point of contact for DNA analysis.

In circumstances where the scope of the DNA analysis exceeds local capabilities, it may be necessary to sub•contract DNA testing to one or more forensic DNA laboratories. The capacities and capabilities of the selected laboratories should be evaluated to ensure that they are sufficient to meet the specific DNA analysis requirements. Many local government laboratories already have outsourcing agreements in place that can be utilized in a disaster victim identification situation. These pre-existing agreements will be particularly useful if the results of the DNA testing will be used in criminal proceedings.

Whether the laboratory chosen to conduct the testing is a government facility or a private company, steps should be taken to confirm that the facility has a robust quality assurance program and validated procedures for both reference samples and human remains.

Each laboratory that may be involved in the identification process should be vetted to ensure that it possess a current accreditation by a nationally recognized not-for-profit agency and complies with national DNA testing standards (e.g., – FBI Director's Quality Assurance Standards for Forensic DNA Testing). Additionally, some states require accreditation or certification to satisfy local jurisdictional criteria (e.g., – State Board of Health or Department of Public Safety).

Laboratories shall have validated DNA analysis methods. Not all laboratories have the experience or capability to process the wide variety of sample types present in disaster victim identification. The laboratories should have proven experience processing reference samples and/or remains from a mass fatality incident. The laboratories shall have expertise and software in DNA matching and complex kinship calculations. Different laboratories may have different skill sets such that one may be an excellent resource for reference sample analysis while another may specialize in processing human remains.

Whether public or private, DNA laboratories will always have existing workloads. All parties involved should understand how a DVI event would fit into their operations. The identification authority shall assess the laboratories' capacities and competing priorities and assign work as appropriate.

Open communication with participating laboratories should be maintained throughout the identification process. It is a best practice to periodically evaluate the laboratories' performance through documentary review of previous audits or by conducting sample retesting, random reanalysis, and/or proficiency testing.

Technical and administrative review of work produced by each laboratory is an essential part of the performance evaluation process. The best practice is for this technical and administrative review to be conducted by the coordinating laboratory or expert authority. This review should be completed before DNA profile data is used for identification purposes.

### 6.5 DNA Analysis Data Management

The process of collating, tracking, reviewing, matching and drawing conclusions from DNA data can be the most challenging step when employing DNA technology to identify mass fatality victims. The difficulty of this task is compounded if more than one laboratory is involved in providing DNA results. Participating laboratories shall mutually commit to coordinate and track sample flow, and agree to use compatible software applications for data acquisition and interpretation.

Comprehensive DNA data management requires a laboratory information management system (LIMS) to inventory, locate, maintain chain of custody, and document the disposition of samples.

Many laboratories have a system in place for daily operations. A best practice is to establish the desired sample numbering schema as early as possible in order to allow labs to prepare for the delivery of samples.

Conducting DNA analysis at a single laboratory whenever possible will minimize complications associated with sample and data exchange. If more than one lab is needed, the analysis should be divided in a logical manner such as sending remains to one facility and references to another.

It is possible that the scope of a mass fatality incident may exceed the testing capacity of a single laboratory. In such an event, the participating laboratories should each support compatible software applications for sample tracking, testing data production, and subsequent interpretation. When multiple laboratories are used, best practice is for the identification authority to designate an expert authority – or one of the laboratories – to be responsible for the overall management of the DNA analysis project.

Responsibilities of the expert authority will include, but will not be limited to:

a. Evaluating methods.
b. Ensuring data quality.
c. Tracking sample flow between laboratories.
d. Ensuring data management.
e. Searching for matches between victim samples and appropriate reference samples.
f. Drawing conclusions from matching results.
g. Conducting administrative reviews.

When using multiple laboratories, a secure, rapid means of data transmission between the laboratories should be established. Each laboratory and the identification authority should designate liaison personnel for routine communications regarding DNA analysis progress and issues.

Duplicate sampling and typing of remains and reference samples may be employed to verify results. This approach may be useful when multiple laboratories are responsible for the DNA typing. Duplicate sampling and typing has significant cost and data management implications for the project, and may only be used sparingly or on a case-by-case basis. The project may opt to retain sufficient sample for duplicate sampling, yet only duplicate the analysis of some predetermined proportion of the DNA samples. This re-analysis may be directed towards reference samples that cannot be validated by kinship analysis, or to remains samples taken from unfragmented remains. The individual typing laboratories may additionally employ duplicate typing of some or all samples under their control for verification purposes. If sample collection recommendations are followed, sufficient material should be available for duplicate sampling and typing.

All laboratories should use a sequential and consistent numbering system, including bar coding when possible and appropriate. This will facilitate combining all data into a single database for interpretation and comparison purposes.

### 6.6 DNA Matching, Reporting, and the Identification Process

DNA matching has the very useful characteristic of providing a numerical result that represents the strength of the evidence supporting a particular identification. These expressions of evidentiary strength can either represent the factor (the "likelihood ratio" [LR]) by which the DNA results increase the certainty of a specific hypothesis of identity, or the "posterior probability" representing the calculated certainty of an identification based on the DNA LR and a specified set of other information.

It is best practice for the identification authority to have competent guidance from someone (often

a designated representative of the DNA laboratory) who has expertise in the DNA analysis process and the interpretation of the significance of DNA matching. This is important throughout the process, especially at the outset in establishing appropriate operational parameters for reporting, and at the stage of evaluating the results of DNA matching in the final identification process. Basic concepts relating to the interpretation of DNA evidence are outlined below.

### 6.6.1 Likelihood Ratio (LR)

This value is the primary result of a DNA match or comparison for the purposes of evaluating the strength of the DNA evidence favoring a particular hypothesis of identity and is always expressed in comparison to a particular alternate hypothesis. Most commonly, the relevant alternate hypothesis is that the sample does not come from the individual in question, but rather from another unknown, unrelated person. In practice, for the medicolegal authority, most commonly the LR is best understood as the factor by which the DNA evidence shifts the balance in one's belief between the hypotheses of identity or non-identity.

### 6.6.2 Posterior Probability

This value depends directly on the DNA LR, but considers also additional information regarding a particular identification not considering the DNA results (known formally as the "prior probability"). In practice, for the medicolegal authority, most commonly the prior probability is best considered the certainty of a particular identification before the DNA results are obtained, and the posterior probability as the surety of the identification after the DNA results are considered. It is often very useful to establish an operational prior probability that is based on the number of missing persons. Agreeing with the DNA laboratory on such an operational prior probability allows the laboratory to report the certainty of an identification based on the DNA evidence and total number of missing persons. Other useful operational prior probabilities which may be employed are the number of missing persons of a particular sex (when the sex of the remains is known through DNA or other means), or the number of children versus adults (when the age category of the unidentified remains is known).

### 6.6.3 Reporting Threshold

In many instances, DNA matching results can provide essentially definitive evidence of identification, assuming appropriate quality control measures have been used and careful cross-checks of all available data were conducted. At the outset of the process, the identification authority should establish with the DNA laboratory a certainty (posterior probability) or LR value threshold that, if met or exceeded, triggers the reporting of thea high-certainty DNA match. This threshold is often determined through evaluation of maximum acceptable uncertainty, for example, a 0.1% chance of reporting an incorrect association in any given case, or perhaps in the entire incident (given a specified number of missing persons). These considerations should be discussed with the DNA laboratory management or other qualified experts, and may be dependent on the nature of the event in question and available resources, and other mitigating factors.

### 6.6.4 DNA Coordination in the Identification Process (Reconciliation)

A mechanism for continuing exchange of primary incident information and DNA results shall be established as a best practice with the DNA laboratory, in order to deal with the following elements:

a. Number of reported missing. This is often poorly known at the outset of the incident and becomes known more precisely as time passes. As individuals are identified, the number of missing may decrease substantially. This is important information for the DNA reporting process.

b. Related victims. In addition to documenting the relationship between family reference

donors and the missing person, the relationships between relatives that are among the missing shall be documented. Depending on the reference samples that have been provided, related individuals are more difficult to distinguish by DNA than unrelated individuals. For example, if only parents are available as references, same sex siblings cannot be distinguished by DNA, and the DNA match should be reported in the possible name of both siblings. Moreover, DNA profiles from human remains may reveal relationships among the victims that can assist the investigation/identification independently from any reference samples.

c. Validation of Direct Reference Samples. Analysis of direct reference samples can be a rapid means for identification, but direct references can be uncertain in their source origin unless verified. As a best practice, whenever possible, direct reference samples should be validated by comparison to family references. For example, if a toothbrush for a missing son is provided by a mother, the DNA profile obtained from the toothbrush should be checked to verify consistency with the mother:son relationship in question. In larger incidents, it is likely that some problems will need to be resolved with regard to direct reference samples, and it may be necessary for the identification authority to coordinate further with the family based on validation information from the DNA laboratory.

d. Validation of Pedigrees. Documentation of correct relationships among all family reference donors, and the missing person, is a comparatively error prone step in the data collection and management process. As a best practice, using kinship analysis, the DNA laboratory should check that relationships among multiple family reference donors are consistent with the stated relationships. Policies shall be established with the DNA laboratory for how inconsistencies in reported pedigrees will be dealt with. It is critical to bear in mind that such inconsistencies can represent very sensitive personal information, and mechanisms of investigating and resolving discrepancies shallshould be devised with appropriate measures of privacy and personal data protection.

e. Targeted investigation based on DNA results. Because of the possibility of recovery of partial DNA profiles from human remains and/or deficiencies in family reference sample collection, DNA matching may provide varying evidence of possible identifications that falls below established thresholds for reporting a DNA match. Communication mechanisms should be established for follow up actions in such cases, which may include seeking additional family references, or re-sampling the mortal remains.

f. Combination of results from different disciplines. Designated experts from the DNA laboratory, or other appropriate DNA subject matter experts, should be available for consultation at the stage where all evidence is evaluated, and final identifications are concluded. Optimally, this occurs with formally documented concordance at a Reconciliation or Identification Committee/Board. In case of inconsistencies among identification disciplines, the DNA laboratory may need to perform specific investigations. There may be cases where DNA evidence is indicative of a possible identification, but falls below the threshold for issuing a DNA match report. Mechanisms should be established that allow access to such information, for combination with other information that may permit a conclusion of identity. Additionally, DNA often can definitively exclude the possibility of identification suggested by other disciplines, thus simplifying potential follow-on investigations.

## 7 Tables

**Table 1 – Sample Types Analyzed for Various Incidents**

| | Spitsbergen Air Crash[1] | SwissAir Flight 111[2] | World Trade Center[3] |
|---|---|---|---|
| Number of Victims | 141 | 229 | 2749 |
| Number of remains samples | 257 | 1277 | 19979 |
| Number of samples from relatives of victims | 182 | 310 | 6854 |
| Number of samples from personal effects | NR | 47 | 4242 |
| Total number of DNA samples | 439 | 1634 | 31075 |
| DNA samples per victim | 3 | 7 | 11 |

1. NR = None Reported
2. [1] Olaisen et al. *Nature Genetics* Vol. 15, pp 402 - 405 (1997).
3. [2] Leclair et al. *J Forensic Sci*, Vol. 49, No. 5 (2004).
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# **Annex A** (informative)
# Foundational Principles

The considerations outlined in this document provide a framework of necessary elements for DNA testing within a mass fatality incident. Guidance is provided on how initial decisions made by an identification authority may affect DNA testing. Once the identification authority has assessed the considerations outlined in this document, it is essential that the strategies employed are not in conflict with scientific requirements that exist within the DNA laboratory. From the start of the identification effort, adherence to the considerations for sample collection will ensure proper collection of appropriate human remains and reference samples. However, DNA testing may not be successful on every sample even with these guidelines in practice. Recognizing the need for DNA data management, these considerations should be evaluated throughout the identification process since both the scope of the incident and strategies for identification may change. The laboratory official who is responsible for the DNA testing should be involved in any discussions regarding the identification process where DNA is a potential topic.

# Annex B

(informative)

## Estimated DNA Analysis Workload Worksheet

*Reproduced from the National Institute of Justice report "Lessons Learned from 9/11: DNA Identification in Mass Fatality Incidents," September 2006:*

**Human Remains**

1. Enter the estimated number of victims.

2. Enter the estimated average fragmentation per victim. (For airline disasters, this value usually ranges between five and eight; ten is a conservative estimate.)

3. Expected number of human remains to analyze. Multiply lines 1 and 2.

4. Total number of human remains to analyze, including rework. Multiply line 3 by the number 1.2.

**Personal Items**

5. Enter the estimated number of personal items collected per victim (typically between five and eight).

6. Expected number of personal items to collect, store, and track. Multiply lines 1 and 5.

7. Enter the estimated number of personal items to be analyzed per victim (typically between two and four).

8. Expected number of personal items to analyze. Multiply lines 1 and 7.

9. Total number of personal items to analyze, including rework and quality control. Multiply line 8 by the number 1.25.

**Kinship Samples**

10. Enter the estimated number of biological relatives per victim (typically between three and four).

11. Expected number of kinship swabs to analyze. Multiply lines 1 and 10.

12. Expected number of kinship swabs to collect, store, and track. Multiply line 11 by the number of swabs collected (between two and six).

# Annex C

(informative)

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