Dna use in mass disasters literature reviews examples

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Mass disasters are events that occur without warning and causes large number of deaths. These disasters may be natural, accidental or intentional. Natural disasters include calamities like earthquakes, tsunamis, flooding etc., while accidental disasters include building collapses, train and aircraft disasters. Intentional disasters are observed recently with acts of terror like bombing and other weapons of mass destruction.

The large number of human lives lost in these disasters requires identification. The forensic examination is not only for humanitarian reasons but also for possible criminal investigations. DNA analysis is one of the best methods for identification of individuals from the remains of these disasters. It is of predominance, when there are no physical or characteristic evidence available for complete identification. DNA typing acts as a perfect tool when there are only body parts or the victim's remains are fragmented. DNA analysis can be carried successfully, if a sufficient amount of biological

sample is obtained from the remains (Ladd pp. 244).

Even though, analysis of the DNA is an integral part of the process, there are other important aspects that need to be followed for the precise and correct identification of victims. Attention is given to processes like:

- Sample collection and storage

- Proper shipping and following chain of custody

- Quality assurance (QA/QC) of laboratory conditions and the methods followed in DNA extraction and typing

- Correct interpretation of results

- Automation for expediting the process

- Public education and privacy issues

Therefore, strategies are developed to address these features of DNA identification. Once these strategies are developed and the appropriate software designed and established, it can be also used for identification of missing individuals. Thus, DNA typing is an extremely essential tool in the arson of a forensic laboratory for identification of persons in cases of mass disasters (Budowle pp. 230).

The principal job in these investigations is that of the Medical Examiner (ME). The ME studies the victims for any physical or anthropological determinants like dental records or tattoos. This reduces the time and the resources required in the identification of victims. If the remains do not provide confirmatory evidence, then a sample is collected and sent to the DNA finger-printing laboratory. The DNA analysis process requires:

- Samples from victim and also their kinship samples – these are handled all the way through methodical chain of custody and privacy.

- All the samples are accessioned for documentation purposes and also re-accessioned, if they need to be outsourced.

- The DNA is extracted and genotyped

- The genotyped DNA is then aligned with the matching software and the statistical significance studies are executed.

- After completing the DNA analysis and the ME data the administrations provide the view for the given biological sample.

The DNA analysis report and the forensic examination report are used by ME to justify and declare the identification of the victim and signing the death certificate. DNA analysis is a time-consuming process and requires skilled personnel and specialized tools. It is also prone to cross contamination. However, it has many advantages over traditional methods like birth marks, dental records, tattoos and medical implants. DNA analysis can be carried out on samples, when there are absolutely on other indicators are available. DNA typing is unique and requires very small quantities of the small sample. It is the only technique for identification of severely damaged and fragmented victims. Therefore DNA analysis provides of the ME with significant and strong evidence in the identification of victims in mass fatality incidents (Budowle pp. 230).

In DNA analysis, the DNA is extracted and typed from victims' samples and then is compared to reference samples. The reference samples include:

- Previously obtained DNA fingerprint data

- Victims' personal items like razor, toothbrush or hairbrush

- Biological relatives of the victim

The DNA identification is dependent on quality of the victim's remains and

the reference samples. The reference samples are the most difficult to identify and that too with the certainty of no contamination. Environmental conditions also play an essential role in the quality of DNA sample. In harsh conditions, it is difficult to isolate and quantify the DNA sample from the remains. There is scarcity in finding personal items of the victims, as they might also be lost in the disaster. Samples from biological relatives can also be unavailable if there is no know data. If the biological relatives have not participated in the identification effort or the families are also lost in the disaster, then it DNA analysis is limited significantly. Public awareness thus plays an important role in situations like these and a thorough consideration of all the factors can help in accurate identification of individuals after the mass disasters (Ladd pp. 244).

In mass fatality cases, bulk of the job is to manage, analyse and compare a large number of biological samples. The DNA profiles are mainly of the autosomal short tandem repeats (STR) and in some cases STR of the Y-chromosome. The data requires large amount of bioinformatics tools and electronic information management systems. These bioinformatics tools are required in alignment algorithms and evaluation of match likelihood ratio. There are multiple factors that need to be discussed in the use of DNA in mass disasters. This includes combined effort of DNA sampling, analysis and database searching and that of the member of the disaster management members. The appropriate use of DNA in disaster management needs to be studied in detail (Clayton pp. 7).

DNA Sampling and Information Management

Victim Sample Recovery

The initial analysis is crucial whereby evidence is scrutinised to establish the identity of the victim. This one of the quickest methods of victim identification and therefore the most relied method. The primary task of ME is to try and identify the victim form the human remains recovered. This depends on the circumstances of each mass disaster. However, the ME is trained personnel who studies into the human remains for maximum information of an individual from the body remains. Identification of persons from the remains is one of the most sought after method as it reduces the stress on the DNA analysis process, providing it more time for accurate analysis of very high level of fragmented victims. Recently, as a rule, it is practiced that even though, the victim has been identified, and a sample of DNA is collected from the autopsied body. This is for reference purposes and for future use if necessary (Brenner pp. 173).

The samples collected are preserved properly and handed down to proper chain of custody. In the process of DNA sample collection precautions are taken such that there is minimization of contamination in the sample. Samples are mostly collected from the least affected materials and areas of the body fragments. This reduces the chances of exogenous and cross contamination. Soft-tissues like muscles or organs are preferred when the disasters does not include high level of environmental damage. Hard-tissues like bone and teeth are preserved when there is body putrefaction observed or when the body is exposed to environmental insults. These tissue samples are stored so as to be studied further and are kept in a bar-coded system

which ensures sample information categorization on a centralized database and ease in access for future use (Brenner pp. 173).

Direct DNA References

The references samples – direct and kinship samples are sought in the mass fatality scenarios. All the ante-mortem samples like biopsies or blood samples are of utmost importance in the DNA analysis. The STR multi-locus profile of the victim is matched with these direct ante-mortem samples and used in proving the victim's identity. The problem in direct reference is the sources' attribute errors leading to false exclusions. Contamination by other biological samples is another issue to be addressed in this process. Therefore, once a match is obtained from direct reference it is studied with the biological relative reference. Thus, there is a need for development of repository of DNA databank that shall store the DNA typing information of individuals' beforehand (Clayton pp. 17).

Family DNA References

Kinship references are obtained by using the nuclear STR markers for the biological family. These references can be:

- Either single or both the parents

- Biological mate and their children

- Multiple biological siblings

The analysis of mitochondrial DNA for maternal reference and Y-chromosome marker for paternal references can also be carried for the investigation.

Blood samples or oral (buccal) swabs are collected for the family DNA references. The information available from the kinship DNA references and

the interview forms collected during sampling needs to be catalogued and used for review during identification (Clayton pp. 17).

DNA Analysis

Currently, the autosomal short tandem repeats (STRs) are amplified using multiplex PCR and the used for identification of DNA in the mass disaster victims. This method is simple and sensitive, therefore making it method of choice for identification. Due to the large application of the autosomal STR, there are PCR-multiplex kits available for the 9-15 STR loci. These PCR-kits have high discrimination power, which to assess direct matches between victims and their personal DNA references and also with appropriate discrimination power to their biological DNA references.

The STR profiling has been used since 1993, where a quadruplex STR system is used. It is used in combination with CODIS (Combined DNA Index System). It uses a core set of 13 STR by using two separate multiplexes. Recently, 15 STR loci are used in new commercial STR and are best for DNA analysis in mass disaster incidents with very efficient results (Kruglyak pp. 243).

When the DNA sample is severely degraded into shorter fragments (<150 bp), then 13-15 STR loci (150–400 bp) are not very useful. Therefore, a new method is developed whereby multiplexes for mini-STR primers are redesigned to obtain shorter amplicons (average 69 bp). This has led to DNA identification using single nucleotide polymorphism (SNP) for short DNA segments to be studied. This SNP–DNA typing is a high-throughput technique called as the SNP–UHT (ultra high throughput). It utilizes multiplex PCR in

conjunction with SNP that allows to carryout identification with higher accuracy in shorter time (Butler pp. 1054).

High–throughput analysis and Automation

In cases of mass disaster, the major challenge is the magnitude of DNA sample analysis. There is a large number of human bodies that need identification and therefore high-throughput technologies are essential to decrease the time and cost involved in the DNA analysis. Added to high throughput methods, automation of laboratory and robotic implementation of mechanical processes would increase the productivity of the whole DNA analytical processes significantly. Robotic implementation and high throughput techniques have been successfully implemented in processes like bone testing and are also being used in DNA typing. These high-throughput processes combined with bar-coding and complete chain of command provide one of the most reliable methods in identification of individuals deceased in the aftermath of mass disasters (Gabriel pp. 293).

DNA Database Searching

The use of DNA typing in mass disaster can only be successful if it is paired with bioinformatics and DNA databases. The DNA database building is essential as it would provide data for ' match significance'. The comparison between large STR should be possible and also alignment with SNP databases. As the number of samples in the databases increases, the possibility of perfect match would go on increasing, thus providing more leverage for DNA to be used for identification. These databases can not only be used for direct DNA reference, but also kinship DNA references from

biological family. This would also insure security and privacy of individuals. The software should also provide the significance of the DNA match and provide the rank, thus providing the level of compatibility of the DNA samples (Krenke pp. 773).

Recently, all these methods have been employed in the United States after the World Trade Centre attack. US have also launched the Mass Disaster Kinship Analysis Program (MDKAP) combined with Laboratory Information Management Systems (LIMS) that have enhanced the victim identification using DNA. It has been successfully used in identification of the victims of Swissair Flight 111 disaster (Leclair pp. 293). Another bioinformatic tool called as SQL-LIMS system with GPC (Genetic Profile Comparisons) has been successfully used in the Yakolev-42 aircraft disaster. Similarly, the CODIS database was used extensively in the Madrid terrorist attacks (Meyer pp. 1). Therefore, with all the advances in the DNA technology and automation and bioinformatics, DNA is used extensively in the cases of mass fatality incidents. Disasters are not supposed to occur often, nevertheless if they do occur; then DNA would be used as one of the best methods in identification.

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