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Review

Relevance of Genetic Identification and Kinship Analysis in Human and Natural Catastrophes—A Review

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Abstract: Different types of disasters, whether natural or human in character, lead to the significant loss of human lives. In the latter case, the quick action of identification of corpses and human remains is mandatory. There are a variety of protocols to identify victims; however, genetics is one of the tools that allows an exact identification of the victim. However, several factors may interfere with this identification, from the biological samples' degradation not allowing the analysis of nuclear information, to failure to dispose of biological samples from family members. Access to certain family members could be a determinant of the proper choice of genetic markers that allow the identification of the victim, or his/her inclusion in a given genetic maternal or paternal lineage. New advances in the field of genetics are soon expected to allow for the identification of victims from disasters with only their biological postmortem samples; it may also be possible to draw a robot portrait of a victim's most likely physical characteristics. In all cases, genetics is the only modern tool with universal character and can be used in essentially all biological samples, giving and identification of more or less accurate statistical character, depending on whether nuclear or lineage markers are used.

Keywords: catastrophes; genetic identification; kinship analysis; DNA degradation

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1. Introduction

Different types of catastrophes, including from natural causes, armed conflicts and different acts of terrorism, lead not only to movement and disappearance but also to the death of civilians, demanding a prompt and effective response concerning the identification and delivery of individuals to their families. The main objective of the present work is to analyze the applied methods in victim identification in great catastrophes, such as armed conflicts or natural disasters, and specifically, to understand what genetic identification implies, its importance and its limitations when establishing kinship analysis during data comparison.

2. The Concept of "Catastrophe"

There are different concepts that are important to define, including "emergency", "disaster" and "catastrophe". According to Pereira (2009), an "*emergency*" should be understood as a sudden and unforeseen event that requires immediate action to minimize its harmful consequences and that results in physical destruction and/or injuries and/or human losses, and that is resolved with local response capabilities. On the other hand, "*disaster*" is defined by the magnitude of its impact, being a serious disturbance in the functioning of a community, with relatively limited effects in time, resulting in extensive physical destruction and/or human, material or environmental losses that prevent it from being answered only with local resources. Finally, "*catastrophe*" is a word of Greek origin

which means disorder or ruin, acquiring nowadays a broader meaning along the lines of chaos or calamity. It is defined by the magnitude of its impact, typically an event or series of severe events that causes an extraordinary magnitude of physical destruction and loss of life of living beings, disrupting cohesion and the social function of the local community or the whole country, requiring exceptional emergency response capabilities (Mendonça 2009; Pereira 2009; Labajo and Sánchez 2022).

Within the concept of "catastrophe," according to their nature, these can be divided into the following:

- *Human catastrophes* can be classified following different criteria, such as according to the origin of the triggering factor or taking into account whether there are records of some kind on the possible victims (Mendonça 2009; Pereira 2009; Pinheiro 2009).
- Natural catastrophes are caused by natural or environmental effects such as fire, water and air. The most characteristic and devastating are usually earthquakes, floods or tsunamis.
- *Technological catastrophe* was a term added as a result of the industrial revolution. It refers to those events caused by industrial development such as factory explosions, mine collapses or nuclear power plant explosions, such as Chernobyl (Ukrainian SSR in the Soviet Union) in 1986 or Fukushima (Japan) in 2011. Accidents in means of transport such as train derailments or plane crashes are also included in this group.
- Sociological catastrophe refers to catastrophes caused by human action, either intentionally (for example, the attack on 11th March, Madrid, Spain, 2004), where armed conflicts are included, or accidentally (e.g., the accident at the Madrid Arena, Madrid, Spain, 2012).

Another way of defining catastrophes refers to the extent of the damage, not only in terms of fatal victims but also in terms of infrastructure, differing in terms of the number of people affected (Mendonça 2009; Pereira 2009). This includes the following:

- "*Open catastrophes*" are characterized by the inexactitude of the record of the possible number of victims and, therefore, more care must be taken when classifying and identifying the human remains. In addition, an investigation must be carried out to make a list of people who could be potential victims of the event. An example would be an earthquake or a plane crash in a busy city.
- "*Closed catastrophes*" are closed disasters that occur in situations that have a fixed list of participants. This can greatly speed up the search for human remains, as you have a list of the missing persons and can start collecting antemortem samples. An example would be a train crash.

Other forms of classification would be by, for example, geographical extension, number of victims, region, duration of the triggering factor and others. Furthermore, open and closed catastrophes can indeed occur at the same time; therefore, the data obtained from lists and files are a good guide to start with, but they are not the only data to be used.

3. The Catastrophe Response Protocol

Intervention in disaster zones is regulated by different types of international legislation (Pereira 2009), whether in the form of regulations or multilateral or bilateral treaties, from many diverse organizations. Some examples are described below.

1. The United Nations is essentially dedicated to the most diverse issues of humanitarian assistance, through OCHA, which coordinates the global emergency response to save lives and protect people in humanitarian crises (https://www.unocha.org/, accessed on 12 May 2023). On the other hand, through the International Strategy for Disaster Reduction (UDRR) (https://www.undrr.org/, accessed on 12 May 2023) the United Nations has been extremely active within the framework of global efforts to reduce and mitigate disasters.
2. NATO (North Atlantic Treaty Organization) also has an important capacity to respond to emergencies, which extends to all the countries of the North Atlantic partnership.

The Euro-Atlantic Coordination Center for Disaster Response (EADRCC) was created in 1998 and always works in close coordination with the OCHA Coordination Office of the Euro-Atlantic Partnership Council on situations of natural or technological catastrophe that occur in its geographic space.

3. The International Civil Defense Organization (ICDO) (https://icdo.org/, accessed on 12 May 2023), based in Geneva, is an intergovernmental organization whose objective is to contribute to the development of structures capable of guaranteeing protection and assistance to populations and also safeguarding property and the environment in the face of natural and technological catastrophes.
4. The Ibero-American Association of Governmental Defense and Civil Protection Organizations (https://www.undrr.org/organization/asociacion-iberoamericana-de-organismos-gubernamentales-de-defensa-y-proteccion-civil, accessed on 12 May 2023) has the objectives of encouraging technical and scientific cooperation in matters of disaster management, increasing and improving the exchange of information and experiences and promoting the capacity and development of human resources in the field of civil protection.
5. The Central Europe Initiative (CIS) (https://www.cei.int/, accessed on 12 May 2023), 1996, is an agreement on the prediction and mitigation of natural and technological disasters, with the participation of Austria, Croatia, Slovenia, Hungary, Italy and Poland.
6. The Open Partial Agreement on Major Hazards of the European Council (EUR-OPA Major Hazards Agreement) (https://www.coe.int/en/web/europarisks/, accessed on 12 May 2023) of March 1987 is intended to promote closer cooperation, regarding the prevention of and response to natural and technological disasters. Its main objective is to reinforce and promote cooperation between member states to guarantee better prevention, protection and organization of assistance in situations of catastrophes, whether natural or technological.
7. The Convention on the Transboundary Effects of Industrial Accidents, 1992, is aimed at the prevention of industrial and natural accidents, excluding nuclear and emergency radiological accidents, military installations, dam failures, land transport, the release of genetically modified organisms and accidents in the marine environment.

Finally, organizations such as INTERPOL (https://www.interpol.int/, accessed on 12 May 2023) and ICMP (https://www.icmp.int/, accessed on 12 May 2023) have over the years developed protocols for the rapid intervention by professionals at the scene of the disaster to strictly comply with the chain of custody in order to carry out a correct identification of the deceased individuals. Both organizations have a specific section dedicated to disaster victim identification (DVI) (https://www.interpol.int/How-we-work/Forensics/Disaster-Victim-Identification-DVI and https://www.icmp.int/what-we-do/technical-assistance/disaster-victim-identification/, accessed on 12 May 2023). Other organizations, such as the International Society for Forensic Genetics (ISFG) (https://www.isfg.org/, accessed on 12 May 2023) and the Spanish and Portuguese Speaking Group of the ISFG (GHEP) (https://ghep-isfg.org/en/, accessed on 12 May 2023) have also developed extremely precise protocols for the collection of evidence, belongings and human remains for the correct identification of victims in catastrophes. In most cases, all procedures are based on the protocols INTERPOL has published over the years (Butler 2023), observing a strict harmonization of conduct guidelines between the different organizations.

Recommended Protocol of Action

There are key procedures to consider in a first approach in a catastrophic situation (Pereira 2009), how to start the response in the face of catastrophe and what order should be followed for collecting evidence from the deceased and families. Some of them are described below.

1. **The initial response.** A catastrophe can happen anywhere, without prior notice, and the following guiding principle can be established: (a) local stabilization and

preservation of life, property, and infrastructure; and (b) documentation, identification and collection of human remains, as well as other types of evidence, namely with possible criminal interest.

2. **Arrival at the disaster site**. A very strict protocol must be followed to comply with the chain of custody and facilitate the subsequent identification of the deceased. A correct method of proceeding would be as follows: (a) report the situation to the previously defined chain of command; (b) meticulously record the events, identifying all the participants; (c) identify the type of catastrophe, also identifying dangers directly resulting from the events, such as possible structural collapses and explosions, among others; (d) assess the scale of the catastrophe; and e) establish a security perimeter.
3. **On-the-spot approach**. The activities to be carried out on the ground by the various specialized teams must always be coordinated by a person in charge to achieve the following concrete objectives: (a) rescue operations and assistance to victims; (b) collection of mortal victims' samples; (c) collection of belongings; and (d) research and collection of other material evidence. As mentioned, the epicenter of the catastrophe is sometimes the location of a crime—for example, the possibility of the kidnapping of people for subsequent human trafficking—therefore, this possibility should be considered by the different working teams. Therefore, in order to assist the victims, the identification of the deceased should be an absolute priority, which allows for the ruling out of possible disappearances due to other causes.
4. **Social issues—religion and culture.** In emergency planning, it is important to take this information into account, as each creed can have its specificities of an ethical nature, especially when dealing with the deceased.

4. Human Identification in Major Human Catastrophes

In catastrophes, the main objective is to save the involved living beings. The second objective is to identify the deceased people (Mendonça 2009; Pinheiro 2009). The need to identify corpses is related to legal, criminal, civil and moral issues. In the moral and ethical scope, citizens have the right to receive the mortal remains of their relatives, whether they are victims of any type of catastrophe, disaster or emergency (Mendonça 2009; Goodwin and Simmons 2023). In the civil sphere, for example, the absence of a death certificate due to the lack of a corpse makes all civil procedures difficult, which are essential for families to deal with indemnities or pensions, among others. Concerning the legal and forensic scope, the absence of an explicit identification leads to questions related to the disappearance of the individual, for example by kidnapping for subsequent human trafficking. For this reason, it is imperative to locate and identify all individuals allegedly involved in the disaster or catastrophe.

Human identification is, at its core, a comparative exercise. Based on this methodology, by collecting individualizing and discriminating identification data, it is possible to achieve what is known in forensic sciences as "*positive identification*" (Mendonça 2009; Pinheiro 2009, 2013), the attribution of a unique and unequivocal identity, usually "*name and surname*", associated with legal registration in a given country. For this, it is necessary to collect data from the cadaver (postmortem data), allowing forensic scientists to build a biological profile, which can be of different types: dactyloscopy (Correia and Pinheiro 2013), dental (Caldas 2013; Labajo and Perea 2022), anthropological (Hartman et al. 2011; Lloret 2018) and genetic (Mendonça 2009; Pinheiro 2009, 2013; Gomes et al. 2021, 2022; Palomo-Díez et al. 2022; Goodwin and Simmons 2023).

Traditionally, anthropology was used as a basis to identify deceased people, due to the simplicity of data collection and the use of a reduced number of materials and equipment. It was based mainly on the observation of postmortem information and the external examination of the remains found, focusing essentially on the analysis of visible phenotypic data (hair color, height, skin color, among others) and identifying physical traits (general characteristics of sex, approximate age, tattoos, scars). Although these techniques were fast, they do not allow for the identification of an individual, instead providing only

a guide for the investigation, for example, "*the deceased person is a man 40–50 years old*". It allows the exclusion or inclusion of the victim from certain phenotypic groups, but it did not permit the identification of the victim.

Currently, the identification of individuals is carried out using three methods, in the following order: first, fingerprints; second, dental records; and third, genetic analysis (Hartman et al. 2011; Butler 2023; Goodwin and Simmons 2023). Although fingerprints and forensic odontology are indeed considered reliable (Prajapati et al. 2018), fingerprints and/or dental samples are not always available. This is where we find the relevance and usefulness of genetic analysis, a universal technique that can be applied to practically all biological samples, from both living individuals and human remains.

5. Genetic Identification

Genetic identification plays a crucial role when the remains to be analyzed are very old or present a very advanced state of degradation, as in the case of air accidents or explosions (de Boer et al. 2018), not depending on a specific biological sample. One of the main advantages of genetic assessment is that information is found in all the nucleated cells of the body and can therefore be found in very small portions of soft tissue or bone fragments. This lets scientists determine substantially important data such as the victim's autosomal profile, biological sex, biogeographical origin, or external phenotype, or perform kinship analysis.

However, the individual's genetic identification can only be performed if there are samples to be compared with. It is possible to carry out a direct identification when there is a previously confirmed genetic profile belonging to the individual in question, for example, in police databases or biological samples resulting from medical diagnoses, such as biopsies. On the other hand, when it is not possible to access the individual's biological antemortem samples, an attempt is made to carry out an identification either through assigned samples, such as clothing or other types of personal belongings of the person with whom the remains are believed to be associated or through biological relatives (Goodwin and Simmons 2023). Usually, human identification in catastrophes is performed by resorting to biological kinship analysis. One of the fundamental steps for a correct genetic analysis is the collection of information from the family of the deceased, since it is crucial for the election of the best genetic marker for each case in question to know the relationship of the person with the deceased.

5.1. Collection of Evidence at the Site of the Disaster for Genetic Analysis

At present, genetic studies are based on the comparison of two genetic profiles, that is, the comparison between postmortem samples obtained from corpses or human remains obtained from the mortuary area, and a reference sample (Hartman et al. 2011; Pinheiro 2013; Soniya and Kumar 2022; Goodwin and Simmons 2023). Despite the complications that may arise at the time of sample collection, all human remains and corpses found must be analyzed. The collection must be conducted during the autopsy by specialized personnel, always taking into account the advanced state of degradation of biological samples and the constant danger of possible contamination with exogenous DNA, both from medical personnel and during the process of genetic research (Pinheiro 2013; Soniya and Kumar 2022).

There are samples considered most suitable for genetic analysis, and the possibility of their collection will be guided by the characteristics of the catastrophe and the state of the human remains. According to the GHEP (2000) protocol, the most frequent samples are skeletal muscle, organ fragments, blood from myocardial cavities and bone and dental samples. Human hairs are not the best samples for the identification process, since there is a high probability that a hair will not have the follicle, preventing the analysis of nuclear DNA. In the case of catastrophes where corpses or human remains have remained in the water for a considerable time, the probability of using muscle samples or organs is frankly reduced, due to the different processes of saponification and putrefaction; in these cases, the sample of choice will be dental or bone pieces. Due to the characteristics of both bones

and teeth, they are also the biological samples of choice in cases of high temperatures, such as fires and explosions (Schwark et al. 2011; Krishan et al. 2015; Uzair et al. 2017; Grela et al. 2021; Kumar 2022).

Regarding the reference samples of close family members, the most appropriate relatives will be direct ascendants (mother and father), descendants and the biological father/mother of these descendants, in order to discard cases of maternal/paternal incompatibility of the deceased with the descendants. Siblings of the deceased, or other relatives should be considered in the event that the previous relative's samples could not be obtained. Usually, the biological sample taken from the biological relative is saliva, since it includes DNA from the cells of the buccal mucosa and is a quick and painless process of sample collection.

Another very important aspect in the entire identification and intervention process is the preservation of the samples; they must be correctly packaged to guarantee their correct use and arrival at the laboratory.

5.2. Nuclear DNA: The Key to Human Identification

Genetic material is present in all nucleated cells since the organization of the organism and its correct functioning depend entirely on its information. Inside the cell, DNA is located between two fundamental organelles: the nucleus (nuclear DNA) and the mitochondria (mitochondrial DNA) (Gomes et al. 2021; Palomo-Díez and López-Parra 2022; Shrivastava et al. 2022; Soniya and Kumar 2022).

Nuclear DNA contains most of an individual's genetic information; even though mitochondria have their genome, it follows that most of the mitochondrial coding activity is carried out in strict collaboration with the nucleus, progressively, through a process of evolution (Cooper and Hausman 2017). Human beings have 46 nuclear chromosomes, which are divided into 22 pairs of homologous chromosomes, and a sexual pair, the Y and the X chromosomes in men, and two X chromosomes in women (Pinheiro 2013; Gomes et al. 2021; Gomes et al. 2022; Gomes and Arroyo-Pardo 2022; Sahajpal and Ambers 2023).

Informative Markers in Forensic Genetic Identification

Considering forensic genetics, the most informative data ae located on non-codifying regions not involving diseases or phenotypic information about the individual. Within this non-coding information, genetic identification focuses on three main types of DNA organization: STRs, SNPs and InDels.

- STRs (short tandem repeats) are a class of markers based on the study of a non-codifying *locus* (in this case, designated "*genetic marker*") formed by a certain number of base repetitions *in tandem*. It is important to bear in mind that it presents great variability since it can be presented in such a varied number of alleles. These motifs, together with their possibility of being amplified by PCR, make STR markers the most widely used in these cases of genetic identification (Manamperi et al. 2009; Gomes et al. 2022; Goodwin and Simmons 2023). However, there are scenarios where STRs are not the best option for analysis, such as when analyzing human remains with a high degree of degradation. In these cases, the use of markers capable of amplifying a small genetic region would be more suitable, such as SNPs or InDel polymorphisms.
- SNPs (single nucleotide polymorphisms) are the most abundant genetic markers within the human genome since they are based on single-base variations. Used in multiplexes, SNPs are one of the most used tools in forensic genetics as a complement to autosomal markers (Yagasaki et al. 2022). To carry out an identification with SNPs, a much higher number of these markers is need than with STRs, due to the lower discrimination power of the SNPs (they only present six possible allelic forms) compared with STRs.
- InDels are polymorphisms based on deletions or insertions on a specific genomic position. Their low level of mutation makes them very useful in the study of family relationships. Even so, this variation needs to occur in at least 1% of the population

to be considered a genetic marker (Pontes et al. 2017; Gomes et al. 2021; Gomes et al. 2022). Associated with STR and SNP loci, InDels can achieve more successful results in forensic identification (Unsal Sapan 2022).

(a) Autosomal markers

Considered the markers par excellence with regard to the identification of individuals, autosomal markers are those with the greatest power of discrimination. The identification is carried out, normally, by combining two types of procedures, either by comparing the autosomal genetic profile of objects and belongings attributed to the victim and the genetic profile of the corpse or cadaveric remains (direct identification), or by comparing the autosomal profile of the corpse or cadaverous remains with those of possible relatives (indirect identification).

(b) X chromosome markers

Although scarcely used in forensic casuistry, the X chromosome markers, especially X-STRs, are used in situations where it is not possible to distinguish genealogies with autosomal markers (Pinto et al. 2010, 2011, 2012; Gomes et al. 2020; Gomes and Arroyo-Pardo 2022), due to their null power of discrimination in these situations. In cases of catastrophes, it could be a very relevant type of marker, as situations can arise where it is not possible to distinguish whether individuals are avuncular–nephew or –niece or grandparents–grandchildren.

(c) Y chromosome markers

As the Y chromosome is a lineage chromosome, Y chromosome markers do not allow identification, since all individuals of the same biological family share the same Y chromosome information via the paternal path (Palomo-Díez and López-Parra 2022). It may be useful for identification in very specific cases, where only one individual is missing in a given family and by associating this information with other family data, it can lead to a positive identification.

5.3. Non-Nuclear DNA: MtDNA

As observed for the Y chromosome, mtDNA is not a useful marker for identifying individuals in cases of catastrophes, since all family members related by maternal line will share the same genetic profile, whether women or men (Palomo-Díez and López-Parra 2022; Shrivastava et al. 2022). As described for the Y chromosome, mtDNA analysis may be useful in very specific cases, when it is necessary to identify a single person from a given family. In this case, associated with other family information, the mtDNA study could be decisive in an identification.

5.4. Problems When Studying Degraded Biological Samples from Major Catastrophes

Considering the diverse scenarios provided by different catastrophes, biological remains are mostly highly degraded and deteriorated. This state not only limits the possible genetic techniques to be used, but it can also cause false or inconclusive results to be obtained. Among the most frequent problems are DNA fragmentation or molecular damage.

5.4.1. DNA Fragmentation

The structural damage presented by a DNA chain is known as DNA fragmentation (Gomes 2020; Ambers 2023). This phenomenon usually occurs when the DNA has been subjected to extreme conditions that have caused its denaturation. The chemical basis of DNA denaturation is the breaking of the hydrogen bonds that stabilize the characteristic double helix structure of DNA; on the other hand, the breaking of glycosidic bonds can also occur, causing the loss of bases. The main cause of this rupture is usually high temperatures, although it can also be caused by other factors such as a very acidic or very basic pH, or the action of various microorganisms. This state of degradation is typical of cadaveric remains or bone fragments that have been exposed to environmental factors for a long time or have

been subjected to high temperatures, as can occur in plane crashes or mass disasters caused by natural disasters (Gomes 2020; Ambers 2023).

The fragmentation of the genetic material is a problem for the study of samples in genetics since there is a high probability of observing allelic dropout, which often means it is not possible to carry out the identification of the individual. This is why when trying to analyze a sample with these characteristics, STR markers cannot be used due to the length and probable allelic dropout and the loss of genetic information in a particular marker. SNPs and InDels are fundamental in these studies due to their small length and being less prone to fragment, although they have a lower power of discrimination (Gomes and Arroyo-Pardo 2022).

5.4.2. Molecular Damage

After the death of the individual, DNA is subjected to numerous natural processes of chemical degradation through hydrolysis and/or oxidation reactions, as well as the action of certain enzymes such as endogenous nucleases. These reactions can be caused by certain types of ionizing radiation or also by the presence of certain free radicals from cellular reactions (Gomes 2020). The greatest danger that these reactions entail is the modification of the nitrogenous bases of DNA, which can cause erroneous results.

5.4.3. Allelic Dropout as a Consequence of Degradation

As mentioned above, the degradation of genetic material is one of the main problems that analysts must face when studying a sample in catastrophes. One of the difficulties in amplifying a DNA fragment occurs when a mutation occurs at the insertion site of the primer, preventing the correct amplification of the product or an erroneous reading of the information (Soulsbury et al. 2006).

On the other hand, allelic dropout is the most common problem when studying highly degraded samples, normally related to the degradation of the genetic material and the impossibility of accessing the information due to the allelic loss in a certain *locus* (Gomes 2020). This usually occurs in samples with a low DNA concentration, either because their natural DNA concentration is very low (urine, feces), or because they have undergone a degradation process that has caused a loss of DNA concentration. For this reason, forensic geneticists try to study samples that are more resistant to biological degradation, resulting in a lower probability of allelic dropout, for example, dental samples, the petrous part of the temporal bone or long bones (Gomes et al. 2019a; Gomes 2020; Soniya and Kumar 2022).

6. Kinship Analysis

After analyzing the available DNA samples and obtaining the genetic profile of the remains to be identified, it is essential to compare the genetic profile obtained with others in order to complete the identification process (Pinheiro 2009, 2013; Gomes 2020; Palomo-Díez et al. 2022).

In the vast majority of cases, the identifications are carried out through the analysis of family members who claim the presence of a family member at the event in question. When interviewing the possible relatives of the victims that can be identified, it is highly recommended to indicate in a pedigree the degree of kinship of the relative with the victim to select nuclear markers and/or lineage markers.

6.1. Genetic Analysis of Close Relatives

The genetic analysis of close kinship consists of the study of a series of nuclear DNA markers to establish if there is a biological relationship between two individuals, usually autosomal markers, generally in paternity, maternity, or sister/brotherhood tests (Gomes and Arroyo-Pardo 2022). The more distant the kinship relationship in question, the lower the resolution power of the nuclear genetic markers, making the analysis of lineage markers more feasible (Pinheiro 2009; Gomes 2020). The most used markers when establishing parental relationships are those of the STR type (as long as we are not dealing with highly

degraded samples) (Pinheiro 2009, 2013; Gomes 2020; Gomes and Arroyo-Pardo 2022). However, when we are dealing with samples in an advanced state of degradation, the results obtained through STRs may be inconclusive (Goodwin and Simmons 2023). Therefore, they must be complemented with the analysis of other markers such as SNPs or InDels.

6.2. Genetic Analysis of Non-Close Relatives

In some cases of catastrophe, it is not possible to obtain a sample from a close relative (parents, children or siblings), often due to their death or an unknown location. For this type of situation, there is the possibility of discerning whether an individual is related to the alleged father by employing an indirect test through the closest relatives, such as grandparents, paternal uncles, nephews or even a brother who is known for certain to be the biological son of the alleged father (half-brother).

The advantages of lineage markers come from their ability to estimate the biogeographical origin or exclusion in paternity/maternity testing of missing persons. Their main difficulty is their null power for establishing direct relationships between individuals (Palomo-Díez and López-Parra 2022; Shrivastava et al. 2022). When the results point to a "match" by mtDNA, differing from nuclear DNA, in the case of lineage markers, they do not refer to an individual but a group of individuals of the same maternal/paternal lineage (Shrivastava et al. 2022). In the specific case of lineage markers, mitochondrial DNA (mtDNA) and Y chromosome, these are particularly relevant when the relatives available for identification are already distant, and therefore it is not possible to carry out the study of nuclear markers (Gomes and Arroyo-Pardo 2022; Sahajpal and Ambers 2023). In this specific case, the information given by the lineage markers always indicates that the individual belongs to a certain family and lineage, making it impossible to carry out a concrete identification, that is, to say that the victim is "such a person" since all maternally and paternally related individuals will have the same mtDNA and Y chromosome genetic profile, respectively.

Despite not being one of the most used tools in forensic genetics, the X chromosome can be crucial in all cases where autosomal markers have neither exclusion nor discrimination power (Pinto et al. 2010, 2011). In case it is not possible to distinguish genealogies due to the same sharing values of identical alleles by descent, such as grandparents–grandchildren versus avuncular–nephews, the X chromosome markers, due to their particular form of transmission, are different in men and women and therefore allow the distinction of this type of genealogy (Gomes et al. 2012, 2019b, 2020; Pinto et al. 2012; Gomes 2020; Gomes and Arroyo-Pardo 2022). This type of problem can occur in cases of catastrophes where different relatives of the same family are involved in a catastrophic situation and genetic identification is the only feasible tool for identifying, for example, cadaveric remains. It is also relevant in cases where it is necessary to relate a woman to a certain paternal family, where the supposed father is inaccessible and analysis of the supposed paternal grandmother or paternal half-sisters, if they exist, may be resorted to.

However, it may also be the case that, although there are relatives close to the victim, the biological samples that can be recovered from the catastrophe do not allow the analysis of nuclear markers due to a marked degradation. In these specific cases, the most used genetic marker will be the mtDNA due to its considerable number of copies per cell, allowing not an identification, but the discarding or inclusion of the victim in a given family/maternal lineage.

Finally, in the event that no relative is found who claims a relative victim of the studied emergency, it is frankly useful to study not only nuclear markers but also lineage markers and include this information in databases of missing persons in the country(ies) affected by the disaster. Over the years, it is possible that distant relatives may donate a biological sample and identify victims, or at least place the victim in a certain family through maternal or paternal lines.

7. Case Studies

There are several cases where genetic research was used to identify corpses or cadaveric remains. Three cases are presented below, where genetic, ante- and postmortem evidence was essential for victim identification.

7.1. Case 1. The Sinking of Oryong 501 (the Bering Sea off the East Coast of Russia) (2014) (Chung et al. 2017)

On 1 December 2014, the ship *Oryong 501* sank in the Bering Sea, off the east coast of Russia. Reports indicate at least 60 crew members of different nationalities (Indonesians, Filipinos, South Koreans and one Russian inspector), of which only 7 survived. A prompt rescue operation was carried out, where the bodies of only 27 crew members were found (Chung et al. 2017). After transferring the dead bodies to the Busan Harbor in South Korea, the operation to identify the deceased began, involving DVI teams from three countries: Korea, Indonesia and the Philippines. When a deep-sea fishing boat sinks, it is very complicated to obtain antemortem data of the crew, especially if the crews are multinational. Even though the antemortem data were received in distinct formats, the identification process for the 27 individuals was promptly concluded through cooperation among the three DVI teams. Once all antemortem data were collected, DNA and fingerprint analyses for identification were pursued. The Indonesian DVI team also presented the DNA profiles of the missing persons' families. An additional step was carried out to make the received data compatible with each other. For the victims whose bodies were unrecovered, the DNA database of the families was established to organize the identification process if additional bodies were to be recovered from the site area. To validate the identification of the 27 bodies, DVI teams from Korea, Indonesia and the Philippines, along with other related authorities, established a cooperative system. According to Chung et al. (2017), "*for the Indonesian crew, the fingerprints of the missing crew and DNA profiles from the families analyzed were provided from Indonesia, (. . .) for the identification of the presumed Indonesian crew, fingerprints were first compared, and then autosomal STR was performed. If comparative samples were only available from female siblings of the victims, additional mtDNA testing was done*". Considering the Filipino crew, "*only basic information and DNA samples from families were provided*", so lineage markers, both mtDNA and Y chromosome, to improve the chances of identification were also considered.

Considering the genetic analysis, the information used depended on each country's scientific advisory board. Furthermore, according to Chung et al. (2017), "*this case is an excellent example of how efficiently a DVI operation can be conducted in the Asia Pacific region*."

7.2. Case 2. Genetic Identification of Burned Corpses (Ricci et al. 2015)

In December 2013, in the Italian city of Prato, a fire burned in an industrial unit where 11 Chinese workers were employed. According to Ricci et al. (2015), "the fire was due to a short circuit, and it surprises the workers in the makeshift dormitory. After the fire was extinguished, the remains of seven people were found by rescuers". The identifications were performed according to the Interpol protocols (AM and PM forms), and in every case, one of the three primary identifiers was satisfied (fingerprints, dental records or genetics). The corpses were completely burned, and reference samples were collected from areas reasonably protected from the fire. Regardless of the problematic external destruction, "the pterygoid muscles and the posterior part of the tongue were spared by fire effects, so they could be collected for DNA analysis. Small fragments of the brain, two feet and hand bones were also collected from isolated body parts. One relative for each unidentified body was available as a reference sample" (Ricci et al. 2015). Concerning the genetic protocol, the investigation included the use of an extensive battery of markers, STRs, Y-STRs and biostatistics assessment of distinct assumptions. According to Ricci et al. (2015), "in this case, the involvement of forensic genetics and the fundamental cooperation of the victims' families allowed the identification of all victims, including the human remains that otherwise would not be possible to attribute to each person. The collaboration among

all professionals involved in the identification via the DVI protocol proved to be the most effective approach in this case to complete the legal and ethical requirements of a fast, accurate and conservative identification procedure."

7.3. Case 3. The Lampedusa Shipwreck of 3rd October 2013 (Olivieri et al. 2018)

A considerable number of migrants have lost their lives in the Mediterranean Sea. In October 2013, a massive disaster caused the death of 366 victims near Lampedusa (Italy). According to Olivieri et al. (2018), "31 victims out of 53 missing requested by families were identified." In addition, the authors also state that "the type and the quality of antemortem data available, generally photos and videos, determines the importance of the face and the body for identification when the bodies are well preserved and how DNA analyses may at times present difficulties." Serious points occurred concerning the absence of genetic information from the populations to which the victims belonged. From a statistical point of view, the number of genetic markers needed to reach a confident value for identification is very complex to achieve, and several times, investigators resorted to lineage markers.

Even though autopsies were not requested by the prosecutor's office, for all human remains, an external examination was undertaken immediately before the burial, and samples were taken for genetic analysis. Postmortem data had been collected equally for all 366 victims. In their work, Olivieri et al. describe the enormous difficulties to find the antemortem data to compare with postmortem data and identify the victims: "This also, however, meant getting in touch with the families—the most difficult step, given that they could be dispersed in the countries of origin, in countries of transition or countries of destination" (Olivieri et al. 2018).

Several victims were recovered immediately after the shipwreck, and saliva or blood (111 and 154 persons, respectively) were sampled for DNA analysis; other individuals (99 persons) were later recovered in an advanced state of decomposition; in such cases, a muscle sample was collected. Some of the problems concerning the collection of antemortem data in this complex context are result of "the impossibility to get in touch with the missing persons' relatives because of the political situation characterizing some of the countries of origin, the unawareness of the families concerning the probable fate of relatives or even the fact that someone is trying to identify the victims, the lack of evident services where to ask for information or seek for the missing, and again the worldwide scattering of relatives". According to this, authorities and organizations (such as the International Organization for Migration, Italian Red Cross, Amnesty International, Fondazione Migrantes, Comitato 3 Ottobre, Borderline-Europe and the embassies) were involved in order to inform the living relatives, mainly in Europe, that antemortem data collection was being performed, and different migrant communities were encouraged to report the disappearance of possible relatives.

Nine individuals were identified only through DNA; eight were identified through non-genetic methods, and in fourteen cases it was possible to identify the individuals through anthropological and genetic methods. In total, it was possible to identify 31 persons.

In their study, Olivieri et al. (2018) also demonstrate that families continue to seek their relatives, despite important difficulties such as distance or lack of data or lack of information about the route taken by the migrants.

8. Future Perspectives

The new technological revolution in the field of forensic genetics is allowing the implementation in laboratories (both public and private) of the methodology of massive parallel sequencing (MPS), for example, to determine some phenotypic characteristics (skin, eye and hair color) (Butler 2023). The use of this new technology constitutes a tool of undoubted utility in criminal investigation, as well as in the identification of victims from disasters and catastrophes. Several studies have already evaluated the existence of polymorphisms associated with skin color, hair color, eye color, male pattern baldness, type/shape of head hair, age, facial morphology, height, earlobe folding and hair graying,

among others (Llobet et al. 2023; Kataria et al. 2023; Kayser et al. 2023; Phillips 2023). Predicting other externally visible features, such as facial features for a robot portrait, will be even more difficult and, at present, still impossible because while all features of a person have a genetic basis, facial features are determined by genetics but also by the environment, such as tattoos and scars. Als, with MPS other informative information could be reached, such as autosomal and Y chromosome informative identity SNPs (Claerhout et al. 2021).

Despite the different difficulties encountered in identifying victims resulting from a catastrophe, genetics is the only modern tool with universal character, which can be used in essentially all biological samples, giving an identification of more or less accurate statistical character, depending on whether nuclear or lineage markers are used.

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