Review

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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 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 allow 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. With the new advances in the genetic field, it is expected to allow soon the identification of victims from disasters only with his/her biological postmortem samples, being possible to draw a robot portrait and its 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

Introduction

Different types of catastrophes, from natural causes, armed conflicts or different acts of terrorism, lead not only to movement, and disappearance but as well as 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, like armed conflicts or natural disasters. Specifically, to understand what genetic identification implies, its importance, and its limitations when establishing kinship analysis during data comparison.

The concept of "catastrophe"

There are different concepts important to define, such as the meaning of "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, being resolved with the 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 can only be answered with local resources. Finally, "*catastrophe*" is a word of Greek origin,

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which means disorder or ruin, acquiring nowadays a broader meaning, like chaos or calamity. It is defined by the magnitude of its impact, typically an event or series of severe events that cause an extraordinary magnitude of physical destruction, 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

- *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.
- The *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, like 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 catastrophes: this last group 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 (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).

- "*Open catastrophes*" is 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 said event. An example would be an earthquake or a plane crash in a busy city.
- "*Closed catastrophes*" a closed disaster occurs 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, for example, the geographical extension, the number of victims, the region, the duration of the triggering factor, and beyond others. Although 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 something closed.

The catastrophe response protocol

Intervention in disaster zones is regulated by different international legislation (Pereira 2009), whether in the form of regulations or multilateral or bilateral treaties, from the most 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/). On the other hand, through the International Strategy for Disaster Reduction (UDRR) (https://www.undrr.org/) the United Nations has been extremely active within the framework of global efforts to reduce and mitigate disasters.
2. NATO also has an important capacity to respond to emergencies, which extends to all the countries of the Atlantic-North partnership. The Euro-Atlantic Coordination Center for Disaster Response (EADRCC) was created in 1998, always in close coordination with the OCHA Coordination Office of the Euro–Atlantic Partnership Council, without situations of natural or technological catastrophe, occurring in its geographic space.
3. The International Civil Defense Organization (ICDO) (https://icdo.org/), based in Geneva, is an intergovernmental organization whose objective is to contribute to the development of

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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) has the objectives to encourage technical and scientific cooperation in matters of disaster management, increase and improve the exchange of information and experiences and promote the capacity and development of human resources in the field of Civil Protection.
5. The Central Europe Initiative (CIS) (https://www.cei.int/), 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/) of March 1987 is intended to promote closer cooperation, regarding the prevention and response of 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/) and ICMP (https://www.icmp.int/) have over the years developed protocols for the rapid intervention of professionals at the scene of the disaster to strictly comply with the chain of custody, 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/). Other organizations, such as the International Society for Forensic Genetics (ISFG) (https://www.isfg.org/) and the Spanish and Portuguese Speaking Group of the ISFG (GHEP) (https://ghep-isfg.org/en/) have also developed extremely precise protocols for the collection of evidence, belongings and human remains, for the correct victims' identification in catastrophes. In most cases, all procedures are based on the protocols INTERPOL has been publishing 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 take into account 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 and property and infrastructures; 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 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, explosions, among others; d) assess the scale of the catastrophe; e) establish a security perimeter.

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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; d) research and collection of other material evidence.
   As mentioned, the epicentre of the catastrophe can be the location of a crime, therefore, this possibility should be considered by the teams that work, considering for example the possibility of a kidnapping of people for subsequent human trafficking, so that the assistance to the victims, as the identification of the deceased should be an absolute priority, being able to rule out 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.

1. 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 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 these 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; Cardoso 2013; Lloret 2018; Muñoz et al. 2022 and genetic (Mendonça 2009; Pinheiro 2009, 2013; Gomes et al. 2021; Gomes et al. 2022; Palomo et al. 2022; William Goodwin, Tal Simmons 2023)

Traditionally, anthropology was used as a base 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 colour, height, skin colour, among others) and identifying physical traits (general characteristics of sex, approximate age, tattoos, scars) (Muñoz et al. 2022). Although these techniques were fast, they do not let the identification of an individual, only allowing to guide 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 to *identify* of the victim.

Currently, the identification of individuals is carried out using three methods, in the following order: 1st) fingerprints; 2nd dental record; 3rd 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, both from living individuals and human remains.

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2. 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 is 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 it 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 to determine substantially important data such as the victim`s autosomal profile, biological sex, biogeographical origin, or external phenotype, or perform kinship analysis.

However, the individuals' 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 have access to 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 we believe those remains are associated or through biological relatives (William Goodwin, Tal 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.

2.1. 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, 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; William Goodwin, Tal Simmons 2023). Despite the complications that may arise at the time of sample collection, all human remains and corpses found must be analysed. The collection must be done during the autopsy and 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 traced by the characteristics of the catastrophe and the state of the human remains. According to the GHEP protocol (2000), the most frequent samples are skeletal muscle, organ fragments, blood from myocardial cavities, and bone and dental samples. Human hairs are not the best sample for the identification process, since there is a high probability that it does 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. 2021, 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. It should also be considered siblings of the deceased, or other relatives in the event that the previous relative's samples could not be carried out. Usually, the biological sample taken from the biological relative is saliva, since it brings DNA from the cells of the buccal mucosa, being 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.

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2.2. 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 since even though mitochondria have their genome, it follows that most of its coding activity is carried out in strict collaboration with the nucleus progressively through a process of evolution (Cooper et al. 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).

2.2.1. Informative markers in forensic genetic identification

Considering forensic genetics, the most informative data is 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; William Goodwin, Tal 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, like SNPs or InDel polymorphisms.
- SNPs (Single Nucleotide Polymorphism) are the most abundant genetic markers within the human genome since they are based on single-base variations. Used in multiplexes, it is 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 is needed a much higher number than with STRs, due to the lower discrimination power of the SNPs (they only present six possible allelic forms) against the 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 (Sapan 2022).

2.2.1. 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. On the one hand, 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).

2.2.2. X-chromosomal markers

Usually, 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. 201, 2011, 2012; Gomes I 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,

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as situations can arise where it is not possible to distinguish whether individuals are avuncular-nephew or niece or grandparent-grandparents.

2.2.3. Y-chromosome markers

As it 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, associating with other family data, lead to a positive identification.

2.3. 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.

2.4. 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.

2.4.1. DNA fragmentation

The structural damage presented by a DNA chain is known as DNA fragmentation (Gomes 2020, Amber 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, or, 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, Amber 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, often not being 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 its length and probable allelic dropout, 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).

2.4.2. 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.

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2.4.3. Allelic dropout as a consequence of degradation

As mentioned before, 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 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, faeces), or because they have undergone a degradation process that has caused a loss of its concentration. For this reason, forensic genetics tries 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. 2019; Gomes 2020; Soniya E. V. and Kumar U. Suresh 2022).

3. Kinship analysis

After analyzing the available DNA samples and obtaining the genetic profile of the remains to be identified, it is essential to compare this genetic profile obtained with others in order to complete the identification process (Pinheiro 2009; Pinheiro 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.

3.1. 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 test 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; Pinheiro 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 (William Goodwin, Tal Simmons 2023). Therefore, they must be complemented with the analysis of other markers such as SNPs or InDels.

3.2. 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 knowing if an individual is related to the alleged father, employing an indirect test through the closest relatives such as grandparents, paternal uncles, nephews and even with a brother who is known for certain to be the biological son of the alleged father (half-brother).

The advantages of lineage markers rely on 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

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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, different in men and women, allows the distinction of this type of genealogies (Gomes C et al. 2012, 2019; Pinto et al. 2012; Gomes C 2020; Gomes I et al. 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 only 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 discard 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 study 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) (are) affected by the disaster. Over the years, it is possible that distant relatives can donate a biological sample and identify victims, or at least place the victim in a certain family through maternal or paternal lines.

4. 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 massively parallel sequencing (MPS, Massive Parallel Sequencing), for example, to determine some phenotypic characteristics (skin, eye and hair colour) (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 colour, hair colour, eye colour, male pattern baldness, type/shape of head hair, age, facial morphology, height, earlobe folding, and hair greying, among others (Ortega- Llobet et a. 2023; Kataria et al., 2023; Kayser et a. 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, like tattoos and scars. Als, with MPS other informative information could be reached, like 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 and identification of more or less accurate statistical character, depending on whether nuclear or lineage markers are used.

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