

Difficulties in Kinship Analysis in Armed Conflicts

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Regarding human identification in armed conflicts, various complications can be observed. Usually, such difficulties can be social-related, which can include the lack of access to the relative's genetic material, or the unwillingness of administrative and judicial authorities to participate in the process of identification. In the case of genetics, the analysis allows identifying the individual from a blood sample, a part of an organ, or from skeletal remains, which is why it is considered a much more extensive and effective method when compared with fingerprint techniques or odontology. However, several factors can prevent this identification, such as considerably degraded genetic material. For successful identification, it is mandatory to have access to antemortem biological samples unequivocally attributed to the individual in question, using recombinant nuclear markers, as well as using biological samples from close relatives, whether parents or sons. Nevertheless, the problems associated with armed conflicts make this type of study very difficult.

Keywords: DNA ; kinship analysis ; victims' identification ; armed conflicts

1. Introduction

Armed conflicts and terrorist acts, characterized by hostility, aggression, and (extreme) violence ([Singh et al. 2022](#)), usually bring with them the disappearance or the profound difficulty to identify numerous persons. The situation of these individuals can be quite variable, from their disappearance in formal displacements to escape or participate in the conflict ([Le and Nguyen 2020](#)), or due to a possible arrest and/or execution, with what this implies. Other persons may have been victims of various events of the conflict itself and have perished, for example, victims of bombings, explosions, attacks with grenades, and missiles, among others.

Regardless of the reason for the individual's disappearance, the lack of news about his well-being or activity leads to a deep feeling of insecurity in the society in question, mainly among the affected relatives. The adequate recovery and identification of human remains is a necessary process during and after an armed conflict, for the reparation not only of the relatives of disappeared persons but also for the re-establishment of the community identity itself.

2. Civil and Family Involvement in the Identification Process

Taking as an example the Spanish Civil War (1936–1939), considered the military preparation for the Second World War, several graves are, gradually, being studied ([Baeta et al. 2019a, 2019b](#); [C. Gomes et al. 2019a, 2019b](#); [Palomo-Díez et al. 2019](#); [Etxeberria et al. 2021](#); [Herrasti et al. 2021](#); [Palomo-Díez et al. 2021](#)), mostly due to the concerns of the affected family members. It is estimated that the number of victims could exceed 300,000 individuals ([Thomas 1977](#); [Simkin 2012](#); [Alonso-Milan 2015](#); [Clodfelter 2017](#)). The action model for the identification of human remains is based on annual governmental calls for family or historical associations so that they take the necessary steps for the identification process to begin properly ([Ríos 2012](#); [Etxeberria et al. 2021](#); [Herrasti et al. 2021](#)). The financial support initially provided by families and/or associations is what often allows for the beginning of the investigation process and the victims' identification ([Etxeberria et al. 2021](#); [Herrasti et al. 2021](#)).

3. The International Commission for Missing Persons—ICMP

The International Commission for Missing Persons, ICMP, physically situated in The Hague, Netherlands, works with different civil society organizations and governments to investigate “people who have gone missing as a result of armed conflict, human rights abuses, disasters, organized crime, irregular migration and other causes” ([ICMP 2022](#)). ICMP aims to promote legislation in affected countries and provide scientific and specialized knowledge to locate and identify victims. On the other hand, ICMP supports the process of justice, guaranteeing that governments adhere to a rule-of-law-based approach to investigating disappearances and presenting, whenever possible, evidence in criminal trials. Since its

creation in 1996, the ICMP has been implicated in the excavation of more than “3000 mass and clandestine gravesites” ([ICMP 2022](#)) and has been also involved in the identification of more than 20,000 persons from different conflicts.

ICMP operates at a global level, as can be seen on its official website (<https://www.icmp.int/where-we-work/>, accessed on 16 January 2023), in different regions of Africa, Europe, the Americas, and Asia. However, for this organization to act, it is mandatory to cooperate with the governments in question, so many of the world’s armed conflicts are beyond its reach. Examples include the Spanish Civil War (1936–1939), Afghanistan (from the 1970s of the 20th century), Argentina (from the 1960s to the 1980s of the 20th century), the period of armed terrorist conflict in Peru (1980–2000), Burundi (since 2015), and Nigeria (since from 2015).

4. An Attempt to *Harmonize* Human Identification—Interpol DVI Protocol

In 1984, in an attempt to standardize procedures for carrying out human identification in cases of disasters, Interpol published a guide for the first time—the Interpol Manual for the Identification of Victims. Through time, technological progress and the new experiences acquired by governments after numerous catastrophes led to a necessary revision of this guide. Updating and correcting the manual led to the publication in 1997 of the Disaster Victim Identification Guide. It provides practical guidance on the issue of victim identification, allowing better and faster identification in the event of an actual disaster situation. This guide has inevitably had to go through many scrutiny processes, but it continues as the central document used by Interpol member countries, and an updated version is currently available in 2018 ([INTERPOL 2018](#)). Following Interpol’s recommendations, many countries should have a special national team for the disaster victim identification (DVI) process. This protocol should be activated whenever necessary, and the procedures to follow and the limitations of the centers must be known in advance. In a case of disaster, open communication must be established with local laboratories, private or not, if more resources are needed in an emergency. Additionally, an agreement between teams from different nations must exist as a way to guarantee a plan in the event of an international catastrophe ([Vullo 2019](#)).

According to the Interpol Manual for Victims Identification, the process consists of four stages ([INTERPOL 2018](#)): (1) the examination of the crime scene; (2) recovery of postmortem (PM) data; (3) recovery of antemortem (AM) data, and (4) harmonization. The third stage, in particular, depends largely on the existence of living relatives who can provide useful information on the victim before his death (antemortem data). They do so through personal interviews and provide data such as ([INTERPOL 2018](#); [Vullo 2019](#)):

- Biological samples for genetic identification—DNA sources can be medical samples, personal belongings, or relatives of the victim.
- Surgical data—provision of a detailed medical history.
- Dental data—including the facilitation of contact with the last dentist that the victim visited, to obtain an updated dental profile.
- Affiliation data—including the National Identity Document, driver’s wallet, passport, etc.
- Detailed physical description, including scars, moles, malformations, tattoos, etc.
- A detailed description of the clothing he was wearing at the time of his death and his personal effects (piercings, earrings, glasses, rings, etc.)

5. Types of Identification in Armed Conflicts

5.1. Fingerprint Techniques

Lofoscopy is the science dedicated to human identification that is based on the study of the epidermal crests on the extremities of the fingers (dactyloscopy), palms of the hands (chiroscopy), and soles of the feet (pelmatoscopy) ([Correia and Pinheiro 2013](#)), and cheiloscopy (lip prints). Fingermarks are the impressions—generally “latent” (invisible)—which are left on smooth surfaces that are touched with bare hands. Such impressions will typically be composed of natural secretions plus contaminants derived from the environment. Various optical, physical, and chemical methods are available for the detection and recording of these impressions ([Bleay et al. 2018](#); [Lennard 2019](#)). Fingermarks can be compared to reference fingerprints (e.g., from suspects or convicted offenders) to determine whether they may have been deposited by

a particular individual. Fingerprint classification is based on the overall ridge pattern, while fingerprint identification (individualization) is based on the configuration of individual ridge features, or minutiae ([Bleay et al. 2018](#); [Lennard 2019](#)).

The identification of fatal victims of catastrophes of different etiologies has been successfully carried out using this identification method which, among other advantages, has proven to be effective, fast, and inexpensive ([Correia and Pinheiro 2013](#)). Additionally, the existence of a fingerprints international software analysis is also an advantage, such as the Automated Fingerprint Identification System (AFIS), a computer system that allows the capture, consultation, and automatic comparison of fingerprints. At a European level, it is also worth mentioning the existence of EURODAC, an informatic system, which collects, transmits, and compares fingerprints, assisting, for example, in the examination of an application for international protection lodged in an EU Member State by a third-country national or a stateless person. If two or more very similar individuals are present, with identical personal data, the comparison of their fingerprints allows their individualization. However, the identification of a fingerprint depends on the quantity and quality of dermopapillary traces detected at the crime scene and on the availability of fingerprints that allow unambiguous analysis, comparison, evaluation, and verification ([Correia and Pinheiro 2013](#)).

5.2. Forensic Odontology

The aim of forensic odontology is the personal identification, of not only those mutilated, burnt, and decomposed, but also victims of bioterrorism and mass disasters ([Forrest 2019](#); [Jayakrishnan et al. 2021](#); [Mohammed et al. 2022](#)), using odontostomatological methods ([Labajo and Perea 2022](#); [Mohammed et al. 2022](#)).

The tooth is a fundamental piece of an anthropological record and necro-identification since it has a series of characteristics that make it suitable for forensic studies, such as resistance to physical, chemical, biological, and taphonomic agents. At the site of removal of the corpse, the dentist can determine antemortem, perimortem, and postmortem odontostomatological injuries, determine postmortem dental losses (which would indicate the need to look for them in the place of discovery), classify, and individualize the located pieces, and determine bite injuries, among others ([Labajo and Perea 2022](#)).

In the laboratory, the dentist studies the jaws and/or isolated dental pieces, to subsequently perform a postmortem odontogram. With the comparison of the postmortem and antemortem odontograms, as well as the dental radiological comparison, the dentist is often able to determine the identity of the individual ([Forrest 2019](#); [Jayakrishnan et al. 2021](#); [Labajo and Perea 2022](#); [Mohammed et al. 2022](#)).

5.3. Genetic Identification in Armed Conflicts

One of the advantages of genetic identification is the possibility to be applied to most human samples. However, to identify an individual, or to attribute a sample to a specific individual, two procedures can be done. On the one hand, antemortem biological samples from the victim can be analyzed and compared with genetic profiles from the human remains. On the other hand, the profile from the human remains can be compared with biological samples from biological family members ([Vullo 2019](#)).

The different topics that involve the forensic genetics laboratory in the identification process, and the considerations in each step, can be summarized as:

- Evaluation of postmortem samples;
- Evaluation and analysis of antemortem samples;
- Family member's sample(s) selection;
- DNA extraction, quantification, and genotyping;
- Statistical evaluation.

Normally, the manipulation of biological samples for the identification of individuals from armed conflicts (and also from other major catastrophes) is carried out in laboratories specialized in the analysis of degraded DNA. These laboratories usually have separate areas, to avoid not only external contamination but also contamination between biological samples. The areas dedicated to samples from postmortem victims are normally physically isolated, with UV sterilization mechanisms both in the work equipment and in the walls and ceiling, together with restricted access. All material used in these rooms is for single use and disposable, and all personnel working in these areas are completely protected with

clothing that prevents the transfer of genetic material from the outside. Concerning the areas used for the analysis of antemortem samples of the victims, along with the next of kin, these are analyzed in areas that are also restricted, but with different characteristics, similar to those used in the forensic casuistry of samples with a high concentration of genetic material. In the case of family members, the sample normally used is saliva, due to its universal character (it exists in men and women) and painless collection through the buccal mucosa. Concerning the victim's antemortem samples, they can range from biopsies to other types of samples that can irrefutably be associated with the victim.

The evolution of forensic science and, in particular, forensic genetics through DNA (deoxyribonucleic acid) analysis, has allowed many families of disappeared persons to resolve the uncertainty about the unknown whereabouts of their relatives (Palomo-Díez et al. 2019). Before the use of current genetic tools in forensic investigation, one of the elements used in human identification programs was forensic homogenetic, a technique that was applied particularly in Argentina during the 1980s and was based on the transmission of the ABO system inherited (Toscanini 2019), applied widely as Ouchterlony's test. The first DNA profile was produced for forensic purposes in 1984, and since then, forensic DNA analysis has evolved enormously, being more sensitive, accurate, cheaper, and faster. The pioneering studies were complex, costly, and lacked the scope and facilities that forensic genetics offers today. In recent years, the ability to recover and analyze low concentrations of DNA from biological material has improved forensic genetics sensibility (Toscanini 2019), both in terms of new techniques for extracting degraded DNA, and amplification, detection, and sequencing, which have become increasingly more sensitive.

The same technology that enables samples recovered from a crime scene to be compared with those from a suspect can be used to match human remains with biological relatives of missing persons (Vullo 2019). Nevertheless, studying human remains from armed conflicts or other catastrophes has associated problems that are less frequent at crime scenes. For example, the possible exposure to heavy metals and in the case of being exposed to external weather conditions, other complications can be observed, such as the acceleration of the cadaveric decomposition and skeletonization, due to extreme temperatures, excess soil humidity, acidity or basicity, among others. In general, these are factors that lead to the degradation and/or destruction of genetic material (Emmons 2015).

5.3.1. Direct Identification

Direct identification takes place when there is a biological sample or genetic profile attributed to the victim in question. In this case, the analysis focuses on the comparison of recombinant markers, usually by routine autosomal markers, verifying that there is no difference between both profiles: antemortem and postmortem.

However, depending on the conditions of conservation of the corpse, the postmortem genetic profile may be degraded and/or partial, and may even translate into an inconclusive result. Thus, the genetic profile may be so partial that the genetic information could belong, by frequency, to any of the individuals in that population. It is in these cases that traditionally resort to the use of lineage markers to guide the investigation, since, although they do not allow identification, they allow the inclusion or exclusion of the individual from a family lineage in question.

5.3.2. Indirect Identification

Autosomal markers

Autosomal markers are genetic noncoding polymorphisms, located on autosomal chromosomes (from chromosome 1 to chromosome 22). In each cell, there are always two copies of each polymorphism, one on the chromosome inherited via the paternal path and the other on the maternally inherited chromosome. Since it is inherited both paternally and maternally, it is considered essential information for cadaveric identification, since the probability that two unrelated individuals share exactly the same set of autosomal polymorphisms, both maternally and paternally inherited, is highly unlikely. At present, the set of polymorphisms that are analyzed allows a probability of identity of 6.58×10^{-29} for the genetic kit PowerPlex® Fusion (Promega, Madison, WI, USA), referring to the probability of two persons sharing the same genotype by chance and not by descent.

X-chromosomal markers

Due to its transmission properties, X-chromosome markers have emerged as an advantage in certain genealogical situations, not only completing autosomal marker information but also resolving certain kinship investigations unviable with autosomal markers (C. Gomes et al. 2020; I. Gomes et al. 2020; Gomes and Arroyo-Pardo 2022). The transmission depends on the sex of the individuals. In women's cells, there is a pair of X-chromosomes that recombine with each other, just like autosomes. As for male cells, the X-chromosome has no homologue, only recombining with the Y-chromosome at

the level of the homologous PAR1 and PAR2 regions ([Gomes and Arroyo-Pardo 2022](#)). In this way, a father transmits to all his daughters a full copy of his X-chromosome, while a mother arbitrarily transmits a copy of one of her two X-chromosomes to daughters and sons, after recombination, as for autosomes.

Lineage markers

mtDNA

When the nuclear information is not informative, depending on the case in question and when individuals are related by maternal side, mtDNA is traditionally used ([Baeta et al. 2019b](#); [Marshall et al. 2019](#); [Mienkerd et al. 2019](#); [C. Gomes et al. 2019a](#); [I. Gomes et al. 2020](#); [Palomo-Díez and López-Parra 2022](#)). Transmitted by the maternal side, without recombination, between mothers and all their offspring, whether male or female, the SNPs from the mtDNA allow, in the event of a match, to associate the victim with a particular family. It does not allow the identification in its strict sense, it has a null power of discrimination, since any member of this family through the mother's side shares this genetic information. Still, associated with other information (anthropological and historical, among others) it allows for determining a unique profile of the individual, leading to a later identification ([C. Gomes et al. 2019a, 2019b](#); [Palomo-Díez et al. 2019](#); [Palomo-Díez and López-Parra 2022](#)).

Y-Chromosome

In the case of kinship by the paternal side, the most employed lineage marker is the Y-chromosome. In this case, this information is transmitted from father to son. As observed for mtDNA, the Y-chromosome does not allow for individualization, allowing each male to be associated with a specific family (paternal lineage) ([Palomo-Díez and López-Parra 2022](#)).

5.3.3. New Trends in Forensic Genetics

In recent years, the number of laboratories in the field of forensic genetics that are investigating and beginning to use massively parallel sequencing (MPS) technologies has increased considerably, for the analysis of markers classically used in this field (control region of mtDNA and STRs), and in the study of other markers of potential application for the determination of identity, ancestry, and/or phenotype (such as SNPs, InDel markers, or complete mtDNA sequencing) ([Alonso et al. 2018](#)). One of the advantages of this type of platform is the ability to incorporate into a single workflow the simultaneous analysis of hundreds or thousands of different DNA markers, and the determination of variations at the sequence level. An example of the application of MPS in the field of armed conflicts is the research published by [Pajnič et al. \(2020\)](#), where they analyze 10 people by massive sequencing, which they consider to have been the "largest Second World War family massacre in Slovenia".

6. Difficulties in Victims' Genetic Identification in Armed Conflicts

In some cases of victims' identification after armed conflicts, the judicial and administrative authorities are not in charge of the organization, control, or provision of human resources. Instead, it transfers these tasks to civil organizations ([Etxeberria et al. 2021](#); [Herrasti et al. 2021](#)), commonly known as the "Association of Victims and Relatives of X conflict", and/or families. This conduct adds difficulties to the process, owing to the associations' and/or families' total lack of knowledge about the steps to be taken to start. As previously mentioned, an example of this situation is the extensive number of victims unidentified in different civil wars of the 20th century.

Another problem present in many armed conflicts is the movement of individuals, both during and after the conflict. In the case of the deceased, displacement may have occurred during the war, either as a means of escape or as part of the conflict. In these cases, families completely lose track of the family member, not knowing where to start the search. If in that specific territory, there is no national database with data from victims and possibly family members, the identification of human remains may be impossible. If the conflict has spread to more than one country, it is practically impossible to carry out the identification of the human remains, since there is no way to attribute them to a specific family.

The identification process could be very extensive, involving a large number of professionals from the criminalistic field but also professionals related to documentary research, topographers, photographers, historians, and archaeologists ([Fernández-Álvarez et al. 2016](#); [Vullo 2019](#); [Etxeberria et al. 2021](#)). On the other hand, scarce funding leads to some parts of the work, such as the osteological study and archival research, being carried out by volunteers, who are usually professionals who are not dedicated full-time to this investigation. On the other hand, the reports generated can be dissimilar in terms of the quantity and quality of the data obtained, since they are created by independent teams, and are not organized under a centralized system. All this has given rise to unreliable files and enormous complexity in

maintaining a complete chain of custody of the remains, from their appearance to their return to relatives, passing through distinct laboratories. It also creates the problem of who will be in charge of contact with the victim's family in case of identification ([Vullo 2019](#)).

In this way, it is common for the funding granted to end, exhausted before an identification case is completed, or for the results to be communicated to the relatives up to three years after the request, sometimes after the death of the relatives who have requested the identification ([Ríos 2012](#); [Palomo-Díez et al. 2019](#)).

In the case of the European civil wars of the 20th century, one of the difficulties is that, with time, there are fewer and fewer relatives of the first degree to carry out the identifications. For this reason, it is very important to analyze all possible markers, including lineage markers, allowing a possible future identification.

DNA Degradation

As a consequence of the degradation process, two biological samples, even if they are of the same type (two teeth, two blood or saliva samples, etc.) and/or from the same individual, must be analyzed according to their state of conservation. The factors that most affect DNA are pH, temperature, humidity, and certain components in the soil ([C. Gomes et al. 2017](#); [I. Gomes et al. 2020](#)). Humidity favors hydrolytic and oxidative degradation reactions. In such environments, the proliferation of fungi and bacteria is favored. Microbial contamination brings two problems: nucleases that degrade the genetic material of interest and the exogenous DNA of the microorganisms ([Pääbo et al. 2004](#)). High temperatures, although, provide dryness and the absence of microorganisms, usually lead to the denaturation of DNA chains, and can promote their degradation. Slightly basic pH helps to preserve DNA, but acidic pH causes the degradation of hydroxyapatite from bone samples ([Figueru et al. 2007](#)). A very acidic or basic pH, very different from the physiological one, causes changes in the nitrogenous bases of the nucleotides and decreases and weakens the hydrogen bonds between complementary bases. On the other hand, samples deposited on the soil usually have another problem that prevents an effective genetic analysis, the presence of inhibitors ([Baeta 2012](#); [C. Gomes et al. 2017](#)).

7. Conclusions

Owing to the efforts carried out, to a large extent, by family members and/or associations for the recovery of victims of armed conflicts, identifications are increasingly a reality. It is usually seen that the accomplishment of these identifications depends not only on scientific-technical mechanisms, such as identification by fingerprints, dentistry, or genetic analysis but also on the budget and predisposition of each government to carry out this work rigorously. It is also crucial that the entire identification process is carried out by independent scientific teams, allowing intercountry collaboration, since many victims of armed conflicts are from other territories. These international collaborations can be decisive for successful identification. As time goes by, it is more complex to find close biological relatives to carry out the identification of victims. A possible answer to this problem would be the existence of national databases that contain the genetic information for each person and/or family who is searching for a specific relative. Additionally, it would be important to include information about each victim, not only historical records but possible genetic profiles based on the analysis of antemortem data, in cases where it is possible.

References

1. Singh, Risha, Srinivas Goli, and Abhra Singh. 2022. Armed conflicts and girl child marriages: A global evidence. *Children and Youth Services Review* 137: 106458.
2. Le, Kien, and My Nguyen. 2020. Armed conflict and birth weight. *Economics & Human Biology* 39: 100921.
3. Baeta, Miriam, Carolina Nuñez, Caterina Raffone, Eva Granizo, Leire Palencia-Madrid, Sergio Cardoso, Francisco Etxeberria, Lourdes Herrasti, and Marian M. de Pancorbo. 2019a. Updating data on the genetic identification of bone remains of victims of the Spanish Civil War. *Forensic Science International: Genetics Supplement Series* 7: 582–84.
4. Baeta, Miriam, Sandra García-Rey, Leire Palencia-Madrid, Caterina Raffone, and Marian M. de Pancorbo. 2019b. Forensic application of a mtDNA minisequencing 52plex: Tracing maternal lineages in Spanish Civil War remains. *Forensic Science International: Genetics Supplement Series* 7: 457–58.
5. Gomes, Cláudia, María Fondevila, Concepción Magaña-Loarte, Juan Fernández-Jiménez, José Fernández-Serrano, Sara Palomo-Díez, C. Baeza-Richer, A. M. López-Parra, and E. Arroyo-Pardo. 2019a. An unusual kinship case from the Spanish Civil War (1936–1939): Ancient versus degraded sample's investigation. *Forensic Science International: Genetics Supplement Series* 7: 690–91.

6. Gomes, Cláudia, Sara Palomo-Díez, Carlos Baeza-Richer, Ana María López-Parra, Ivon Cuscó, Elena García-Arumí, Eduardo Tizzano, Andrea Fernández-Vilela, Diego López-Onaíndia, Ares Vidal Aixalà, and et al. 2019b. X-InDels efficacy evaluation in a critical samples paternity case: A Spanish Civil War case from the memorial of the camposines (Tarragona, Spain). *Forensic Science International: Genetics Supplement Series* 7: 494–95.
7. Palomo-Díez, Sara, Cláudia Gomes, Ana María López-Parra, Carlos Baeza-Richer, Ivón Cuscó, C. Raffone, E. García-Arumí, Núria Montes, Diego López Onaíndia, Assumpció Malgosa Morera, and et al. 2019. Genetic identification of Spanish civil war victims. The state of the art in Catalonia (Northeastern Spain). *Forensic Science International: Genetics Supplement Series* 7: 419–21.
8. Etxeberria, Francisco, Alfredo González-Ruibal, Lourdes Herrasti, Nicholas Márquez-Grant, Laura Muñoz-Encinar, and Jordi Ramos. 2021. Twenty years of forensic archaeology and anthropology of the Spanish Civil War (1936–1939) and Francoist Regime. *Forensic Science International: Synergy* 3: 100159.
9. Herrasti, Lourdes, Nicholas Márquez-Grant, and Francisco Etxeberria. 2021. Spanish Civil War: The recovery and identification of combatants. *Forensic Science International* 320: 110706.
10. Palomo-Díez, Sara, Cláudia Gomes, Ana María López-Parra, Ivon Cuscó, Eduardo Tizzano, María Eulalia Subirá, Andrea Fernández Vilela, Núria Montes, Diego López Onaíndia, Assumpció Malgosa Morera, and et al. 2021. Estado actual de la identificación de víctimas de la Guerra Civil Española y de la posguerra en Cataluña. *Revista d'Arqueologia de Ponent* 31: 273–86.
11. Thomas, Hugh. 1977. *The Spanish Civil War*. London: Penguin Books.
12. Simkin, John. 2012. *Spanish Civil War. The Spanish Civil War Encyclopedia* (Ser. Spanish Civil War). Brighton and Hove: University of Sussex, Spartacus Educational E-Books.
13. Alonso-Milan, Jesús. 2015. *La guerra total en España (1936–1939)*. Scotts Valley: CreateSpace Independent Publishing Platform (Amazon).
14. Clodfelter, Micheal. 2017. *Warfare and Armed Conflicts: A Statistical Encyclopedia of Casualty and Other Figures, 1492–2015*, 4th ed. Jefferson: McFarland. ISBN 978-0786474707.
15. Ríos, Luis. 2012. Identificación en fosas comunes de la guerra civil: Limitaciones y posibilidades a partir del caso de Burgos. *Boletín Gallego de Medicina Legal e Forense* 12: 125–42.
16. ICMP—International Commission on Missing Persons. 2022. About Us, What We Do, Where We Work. Available online: <https://www.icmp.int/> (accessed on 12 June 2022).
17. INTERPOL. 2018. *Identificación de Víctimas de Catástrofes (IVC)*. Lyon: Interpol.
18. Vullo, Carlos María. 2019. Identificación de desaparecidos en gran escala: Grandes catástrofes (DVI) y desapariciones en contextos de crisis Humanitarias (MPI). In *Genética Forense- Del laboratorio a los Tribunales*. Edited by Manuel C. Crespillo Márquez and Pedro Barrio Caballero. Madrid: Díaz de Santos, pp. 405–24.
19. Correia, Pedro, and Maria de Fátima Pinheiro. 2013. Perspectivas actuais da Lofoscopia: Aplicação Criminal e civil do Estudo de impressões epidermicas. In *Ciencias Forenses ao Serviço da Justiça*. Edited by Maria de Fátima Pinheiro. Lisboa: Pactor, pp. 119–22.
20. Bleay, Stephen M., Ruth S. Croxton, and Marcel De Put. 2018. *Fingerprint Development Techniques: Theory and Application*, in *Developments in Forensic Science*. Hoboken: John Wiley & Sons.
21. Lennard, Chris. 2019. *Fingerprint Techniques*. In *Encyclopedia of Analytical Science*, 3rd ed. Edited by Paul Worsfold, Alan Townshend, Colin F. Poole and Manuel Miró. New York: Academic Press, pp. 38–47.
22. Forrest, Alex. 2019. Forensic odontology in DVI: Current practice and recent advances. *Forensic Sciences Research* 4: 316–30.
23. Jayakrishnan, Jijin Mekkadath, Jagat Reddy, and R. B. Vinod Kumar. 2021. Role of forensic odontology and anthropology in the identification of human remains. *Journal of Oral and Maxillofacial Pathology* 25: 543–47.
24. Mohammed, Faraz, Arishiya T. Fairozekhan, Subraya Bhat, and Ritesh G. Menezes. 2022. *Forensic Odontology*. In *StatPearls*. Tampa: StatPearls Publishing.
25. Labajo, Elena, and Bernardo Perea. 2022. *Odontología Forense: El papel del odontólogo en la investigación criminal*. In *Manual para el estudio de las Ciencias Forenses*. Madrid: Tébar Flores Editorial, pp. 51–75.
26. Toscanini, Ulises. 2019. Historia y evolución de la genética forense. Grupos de Trabajo de estandarización científica. In *Genética Forense- Del laboratorio a los Tribunales*. Edited by Manuel C. Crespillo Márquez and Pedro Barrio Caballero. Madrid: Díaz de Santos, pp. 1–21.
27. Emmons, Alexandra. 2015. *The Preservation and Persistence of Human DNA in Soil during Cadaver Decomposition*. Master's thesis, University of Tennessee, Knoxville, TN, USA.

28. Gomes, Cláudia, José David Quintero-Brito, Jesús Martínez-Gómez, Rui Pereira, Carlos Baeza-Richer, Mercedes Aler Gay, Laura Díez-Juárez, Sara Palomo-Díez, Ana María López-Parra, Elena Labajo-González, and et al. 2020. Spanish allele and haplotype database for 32 X-chromosome Insertion-Deletion polymorphisms. *Forensic Science International: Genetics* 46: 102262.
29. Gomes, Iva, Nádia Pinto, Sofia Antão-Sousa, Verónica Gomes, Leonor Gusmão, and António Amorim. 2020. Twenty Years Later: A Comprehensive Review of the X Chromosome Use in Forensic Genetics. *Frontiers in Genetics* 11: 926.
30. Gomes, Cláudia, and Eduardo Arroyo-Pardo. 2022. Usefulness of the X-Chromosome on Forensic Science. In *Handbook of DNA Profiling*. Edited by Hira Ranjan Dash, Pankaj Shrivastava and José Antonio Lorente. Singapore: Springer Nature Singapore, pp. 455–77.
31. Marshall, Charla, Kimberly Sturk-Andreaggi, Joseph D. Ring, Cassandra R. Taylor, Suzanne Barritt-Ross, Walther Parson, and Timothy P. McMahon. 2019. Advancing mitochondrial genome data interpretation in missing persons casework. *Forensic Science International: Genetics Supplement Series* 7: 721–23.
32. Mienkerd, Sirirat, Anillada Nettakul, and Worawee Waiyawuth. 2019. The using of massively parallel sequencing of mitochondrial DNA to assist the missing person identification: Human remains in the wild. *Forensic Science International: Genetics Supplement Series* 7: 716–17.
33. Palomo-Díez, Sara, and Ana María López-Parra. 2022. Utility and Applications of Lineage Markers: Mitochondrial DNA and Y Chromosome. In *Handbook of DNA Profiling*. Edited by Hira Ranjan Dash, Pankaj Shrivastava and José Antonio Lorente. Singapore: Springer Nature Singapore, pp. 423–54.
34. Alonso, Antonio, Pedro Alberto Barrio, Petra Müller, Steffi Köcher, Burkhard Berger, Pablo Martin, Martin Bodner, Sascha Willuweit, Walther Parson, Lutz Roewer, and et al. 2018. Current state-of-art of STR sequencing in forensic genetics. *Electrophoresis* 39: 2655–68.
35. Pajnič, Irena Zupanič, Marcel Obal, and Tomaž Zupanc. 2020. Identifying victims of the largest Second World War family massacre in Slovenia. *Forensic Science International* 306: 110056.
36. Fernández-Álvarez, José-Paulino, David Rubio-Melendi, Antxoka Martínez-Velasco, Jamie K. Pringle, and Hector-David Aguilera. 2016. Discovery of a mass grave from the Spanish Civil War using Ground Penetrating Radar and forensic archaeology. *Forensic Science International* 267: e10–e17.
37. Gomes, Cláudia, Alejandro Alonso, Domingo Marquina, Marc Guardiola, César López-Matayoshi, Sara Palomo-Díez, Bernardo Perea-Peréz, Juan F. Gibaja, and Eduardo Arroyo-Pardo. 2017. “Inhibiting inhibitors”: Preliminary results of a new “DNA extraction-amplification” disinhibition technique in critical human samples. *Forensic Science International: Genetics Supplement Series* 6: e197–9.
38. Pääbo, Svante, Hendrik Poinar, David Serre, Viviane Jaenicke-Després, Juliane Hebler, Nadin Rohland, Melanie Kuch, Johannes Krause, Linda Vigilant, and Michael Hofreiter. 2004. Genetic analyses from ancient DNA. *Annual Review of Genetics* 38: 645–79.
39. Figuero, María Jesús, Peral Diego, and Sánchez José Antonio. 2007. ¿Por qué no se pueden hacer estudios de ADN de restos óseos antiguos en Badajoz? *Revista de estudios extremeños* 63: 215–31.
40. Baeta, Miriam. 2012. New miniSTRs typing methods help in the identification of ancient skeletal remains from the Spanish civil war. *Quaternary International* 33: 279–80.

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