Investigation into X-STR haplotype frequencies for forensic human identification in South Africa

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Abbreviations

AMOVA	Analysis of molecular variance
AS-STRs	Autosomal short tandem repeats
bp	base pair
CA	California
CE	Capillary electrophoresis
ChrX	X chromosome
DNA	Deoxyribonucleic acid
EMPOP	European DNA Profiling Group (EDNAP) mtDNA Population Database
ENSI	European Network of Forensic Science Institute
Fig.	Figure
F_{ST}	Pairwise genetic distance
FTA	Flinders Technology Associates
GD	Gene diversity
GHEP-ISFG	Spanish and Portuguese Speaking Working Group of the International Society for Forensic Genetics
HD	Haplotypic diversity
HREC	Human Research Ethics Committee
HWE	Hardy-Weinberg equilibrium
i.e.	Latin – id est, meaning “namely”
IBD	Identity-by-descent
ISO	International Organisation of Standardisation
LD	Linkage disequilibrium
LG	Linkage group
MEC	Mean exclusion chance
MPS	Massively parallel sequencing
mtDNA	Mitochondrial DNA
NFDD	National Forensic DNA Database of South Africa
NTC	Non-template control
PAR	Pseudo-autosomal regions
PCR	Polymerase chain reaction

PD	Power of discrimination
PIC	Polymorphism information content
PRISMA	Preferred reporting items for systematic reviews and meta-analyses
QS	Quality sensor
r^2	Squared coefficient of correlation
RFU	Relative fluorescent units
RMP	Random match probability
SAPS	South African Police Service
SD	Standard deviation
STR	Short tandem repeat
SWGDAM	Scientific Working Group on DNA Analysis Methods
UCT	University of Cape Town
URL	Uniform resource locators
USA	United States of America
WI	Wisconsin
X-INDELS	X-linked insertion and deletion polymorphisms
X-STRs	X-chromosome short tandem repeats
YHRD	Y-STR Haplotype Reference Database
Y-SNPs	Y chromosome single nucleotide polymorphisms
Y-STRs	Y-chromosome short tandem repeats
µl	Microlitre

Abstract

The utilisation of X-chromosome short tandem repeats (X-STRs) for DNA profiling has been demonstrated to be particularly useful in resolving distant familial relations and deficiency paternity testing. The implementation of X-STRs within a medico-legal context requires baseline frequency data for the general population to allow for appropriate statistical interpretations of results. This study aimed to generate the first X-STR data for the South African population and internally validate the Qiagen Investigator Argus X-12 QS kit. Biological samples from 781 South African individuals (517 males and 264 females) with either African, mixed, European, or Indian/Asian ancestry were processed. Statistical analyses were performed using StatsX and Arlequin. Herein, allele and haplotype frequencies and forensic parameters for the South African population are reported, as well as data related to the reproducibility, sensitivity, limit of detection, and concordance of the Investigator Argus X-12 QS kit. DXS10135 was the most informative locus, while DXS7423 was the least informative locus. The combined power of discrimination for both males and females was greater than 0.999999999. The haplotype diversity of all four linkage groups exceeded 0.993. Linkage group 1 was the most informative, with 421 unique haplotypes. Possible linkage disequilibrium was detected in five loci pairs in male samples and three loci pairs in female samples. However, it is expected that the effects of false linkage disequilibrium were present, and only loci pairs within the same linkage group may be in true linkage disequilibrium. All loci in female samples were in Hardy-Weinberg equilibrium, except DXS10148. Additionally, a total of 59 off-ladder alleles were identified. The discriminatory power of these results suggests X-STRs may be beneficial for forensic casework in South Africa. The availability of this data could allow this method to be used locally to assist with civil inheritance disputes and the identification of unknown individuals.

Keywords: X-STRs; haplotype frequencies; Investigator Argus X-12 QS; South Africa

Chapter 1: Systematic Literature Review

1.1. Introduction

The development and implementation of DNA profiling within the field of forensics has contributed greatly to the successful closure of many medico-legal investigations. This is because DNA profiling has enabled authorities to use DNA evidence to identify unknown missing persons and/or skeletal remains, identify victims and possible suspects of a crime, as well as provide exoneration to those who have previously been wrongfully convicted [1]. DNA profiling has also been utilised in civil disputes of paternity and kinship testing [2].

DNA profiles are typically produced using DNA of an unknown origin, and compared to a known reference profile [3] obtained from an individual's family or the national forensic DNA database. For this, autosomal short tandem repeats (STRs) are routinely targeted using polymerase chain reaction (PCR) and capillary electrophoresis-based methods. However, a match alone does not indicate positive identification. To provide statistical confidence to the match, the random match probability (RMP) must be calculated. This is done using allele frequencies previously generated for a representative subset of the general population [4].

Limitations regarding the discriminatory power and informativeness of autosomal STRs in resolving distant familial relations or cases involving complex pedigrees have been widely reported [2,5,6]. When using autosomal STR analysis, there is always a possibility that a true biological relationship will be excluded due to an insufficient number of shared alleles or certain discrepancies between individuals. These discrepancies may be attributed to several factors, including rare mutations or silenced alleles [7]. This highlights the need to utilise linkage markers, such as those on the sex chromosomes, to improve the efficiency of the identification and familial testing using DNA profiling [8].

The use of Y-chromosome STRs (Y-STRs) are particularly beneficial in sexual offence investigations, as they can be used to discern a male's identity, even in the presence of female DNA [9,10]. Additionally, Y-STRs can be utilised to resolve paternity disputes involving an alleged father and son. Similarly, X-chromosome STRs (X-STRs) can be implemented in complex kinship testing and deficiency paternity testing of female offspring [2], which refers specifically to situations where a DNA sample from the alleged father is unattainable.

This can be attributed to the differences observed in the recombination patterns of sex chromosomes when compared to that of autosomal chromosomes. As autosomal chromosomes occur in pairs, it is true that each chromosome will recombine with its homologous counterpart prior to being passed on to offspring. However, sex chromosomes differ between male (XY) and female (XX) individuals [9]. As such, only maternally inherited X-chromosomes undergo a recombination event prior to inheritance. Contrarily, the paternal sex chromosomes are transmitted to offspring almost entirely unaltered. This is because the X and Y chromosomes are mostly meiotically incompatible apart from small shared pseudo-autosomal regions (PAR1 and PAR2), wherein the occurrence of recombination between these two chromosomes is limited to [11]. Thus, most of the informative value of the X-chromosome lies within paternal sex chromosomes.

Additionally, the X-chromosome harbours unique inheritance patterns which can aid forensic applications. For example, STR markers on the X-chromosome are situated close to each other (*i.e.,* linked) and are therefore inherited as a haplotype. As males only inherit a maternal X-chromosome, their X-chromosome haplotype is easily detected. This X-chromosome haplotype is also passed on directly from father to female offspring, meaning it will be common amongst sisters who share a father [6,12]. It is also true that siblings who have the same mother will have a portion of their maternal X-chromosome haplotype in common [12]. Lastly, although STRs have a higher mutation rate than single nucleotide polymorphisms (SNPs), the X-chromosome has remained relatively stable overtime, making it possible to trace the lineage of X-STR haplotypes across previous familial generations [2,13].

Thus, the use of chromosomes that undergo separate meiotic processes provides a new perspective, which can be useful for certain cases that would otherwise remain inconclusive due to the insufficient discriminatory power possessed by autosomal STRs. However, the integration of X-STRs into forensic casework remains relatively new and as data from the general population is necessary for interpretation, the usefulness of X-STR profiling is dependent on the availability of appropriate haplotype frequency databases for local population groups. This type of data is yet to be collected in many regions of the world, which has led to an inconsistency in the success of identification between different populations. This has prompted researchers across the globe to produce X-STR population data for their relevant countries and population groups [9].

This literature review aims to provide an overview of the advancements of X-STRs in forensic and medico-legal casework. To address this aim appropriately, four objectives have been identified, namely (i) to briefly describe the applications of X-STRs in a medico-legal setting; (ii) to assess the evolution of commercial X-STR multiplex PCR kits; (iii) to evaluate the use of X-STR repositories/databases and (iv) to provide a global exhaustive summary of available X-STR population data, with a specific focus on data generated using the most popular commercial kit, the Investigator® Argus X-12 (QS) kit (Qiagen, Hilden).

1.2. Methods

1.2.1. Literature search strategy

This systematic literature review was performed using the "Preferred Reporting Items for Systematic reviews and Meta-Analyses" (PRISMA) guidelines. A literature search was conducted on major databases, namely Web of Science, Scopus and PubMed. Keywords were chosen to create a search string, separated by Boolean operators, to use across the aforementioned databases (Table 1.1). These keywords were systematically curated to ensure the search returned publications that encompassed the entirety of this literature review's aim as well as the respective objectives.

Table 1.1 *Keywords utilised in the systematic literature review.*

Keywords	
X-STR population data	X-STR database
Investigator Argus X-12 QS	Deficiency paternity testing
Investigator Argus X-12	X-STR typing
X-STR	X-chromosomal STRs

The search was limited to publications released between the years 2000 and 2022, as the introduction of X-STRs became more apparent approximately 20 years ago. An additional search of the available literature on the ChrX-STR.org 2.0 database was conducted.

Publications that were duplicated across databases or published under alternative titles by the same author(s) were removed from the results. The remaining publications were considered against all inclusion and exclusion criteria (Table 1.2) using the title and abstract, followed by the full text, to ascertain their relevance to the scope of this literature review. Hand-searching was performed on the reference lists of all included publications to ensure saturation of relevant literature.

Table 1.2 *Search strategy inclusion and exclusion criteria*

Inclusion criteria	**Exclusion criteria**
Available in English	Non-human populations
X-STR multiplexes of four or more loci	Review articles
Investigation of X-STRs within a forensic genetic context	Investigation of X-STRs within a clinical context
X-STR population data produced using conventional DNA profiling	X-STR population data produced using massively parallel sequencing

1.3. Results

The search produced a total of 1142 publications across all three databases. Additionally, 47 articles were identified on the ChrX-STR.org 2.0 database and a further 32 articles were identified through hand-searching. After the application of the eligibility criteria, a total of 293 unique publications were included (Fig. 1.1.).

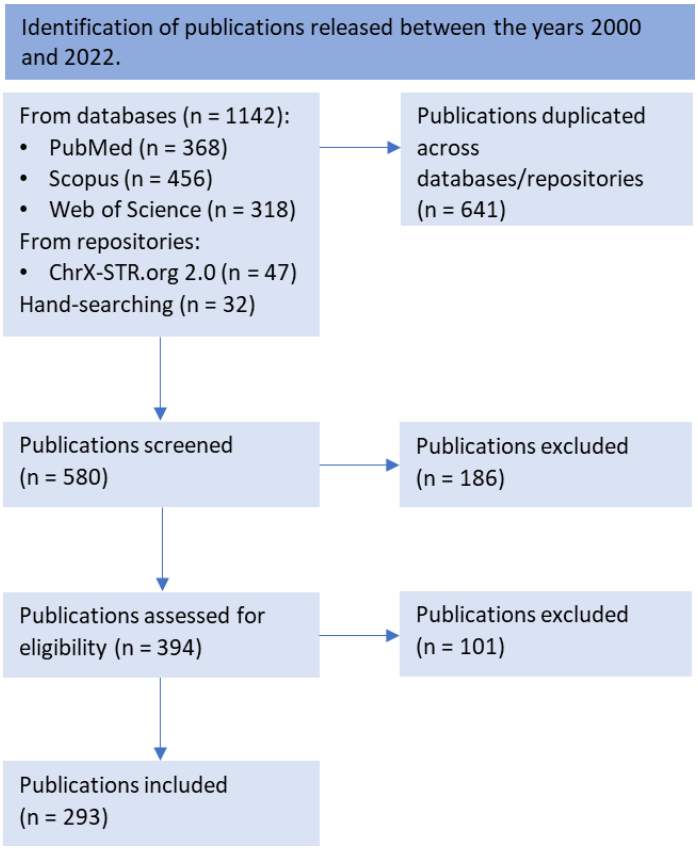

Fig. 1.1*. Adapted PRISMA flow diagram representing the search strategy used and the implementation of the inclusion and exclusion criteria.*

The results consisted of articles that were published across 35 different journals (Appendix A). The most prevalent journals are summarised in Fig. 1.2., with the leading journals in X-STR research being the International Journal of Legal Medicine (*n* = 67), Forensic Science International: Genetics Supplement Series (*n* = 56) and Forensic Science International: Genetics (*n* = 56).

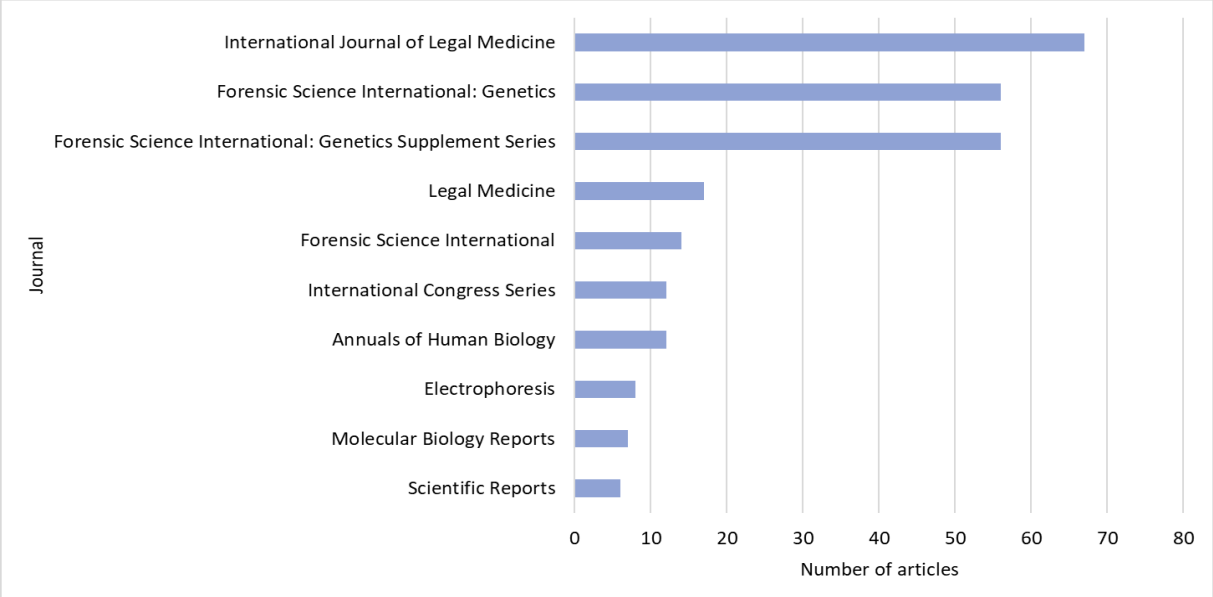

Fig. 1.2. *The most prevalent journals identified during the search and their corresponding published articles.*

The number of publications related to X-STR research per year fluctuated over time, with the year 2011 being the most popular. Since then, a slight decline in publications has been observed. However, the relevance of X-STRs remains, as seen by the surges in publications in recent years (*i.e.,* 2017, 2019, 2021) (Fig. 1.3.).

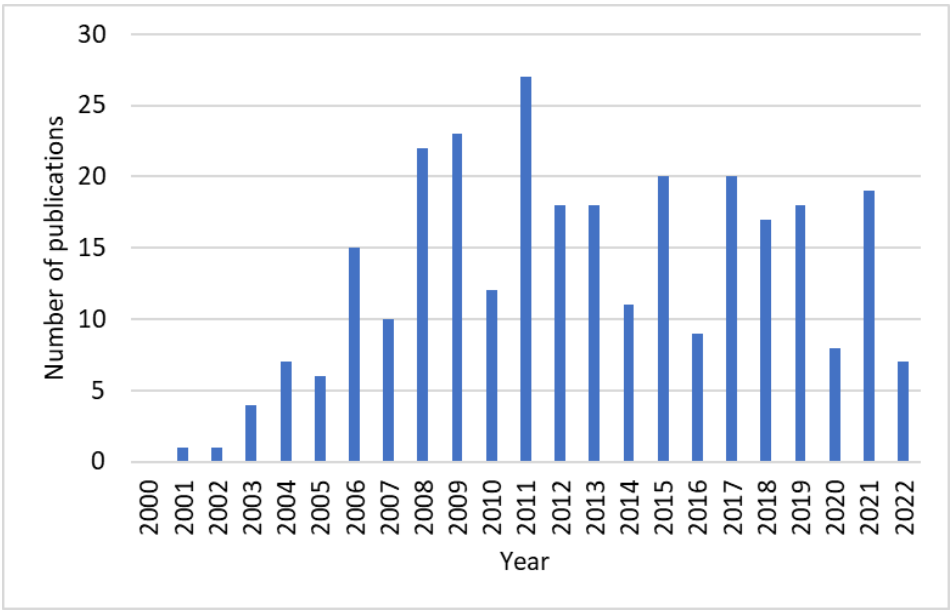

Fig. 1.3*. The number of publications released during a 22-year period (2000 – 2022).*

1.3.1. Applications of X-STRs

A total of 36 included articles focused on the use/applications of X-STRs within a medico-legal context (Appendix A). From these articles, three broad applications of X-STRs were identified. The first and most common is complex kinship testing, which includes deficiency paternity testing (*n* = 29, 80.56 %) [4,7,8,12,14–38], followed by human identification (*n* = 5, 13.89 %) [39–43] and lastly mixture interpretation (*n* = 2, 5.56 %) [44,45].

1.3.2. X-STR multiplex systems/kits

A variety of X-STR multiplex systems have been used for the various applications of X-STRs as well as the generation of X-STR population data. Many researchers have opted to develop laboratory-specific multiplex X-STR marker systems as a means of producing X-STR population data. Alternatively, companies have manufactured commercially available X-STR kits [46,47]. Table 1.3 provides a comprehensive summary of the most prevalent X-STR systems used throughout the literature. This summary shows that a multitude of advancements have been made to X-STR kits over time with a particular focus on the number of X-STR markers included and additional quality features. The most frequently used kit globally was the Investigator Argus X-12 (QS) (Qiagen, Hilden), followed by the GHEP-ISFG X-STR decaplex developed by the Spanish and Portuguese Speaking Working Group of ISFG [48] and the Mentype Argus X-8 (Biotype, Dresden).

Table 1.3 *Evolution of X-STR multiplex kits/systems used in the reviewed literature.*

Kit Name	Number of X-STR loci	Additional features	Occurrence in population data
Investigator Argus X-12 (QS) (Qiagen, Hilden)	12	Amelogenin marker, Quality Sensor, D21S11	66
GHEP-ISFG X-STR decaplex	10	N/A	26
Mentype Argus X-8 (Biotype, Dresden)	8	Amelogenin marker	26
AGCU X19 (AGCU ScienTech, Jiangsu)	19	N/A	23
Goldeneye 17X (Peoplespot Incorporation, Beijing)	16	Amelogenin marker	10

Kit Name	Number of X-STR loci	Additional features	Occurrence in population data
Mentype Argus X-UL (Biotype, Dresden)	4	Amelogenin marker	7
In-house [49]*	17	N/A	5
In-house (mini X-STRs) [50]*	15	N/A	3
ZJGA-X12 STR/AGCU X12 (AGCU ScienTech, Jiangsu)	12	N/A	2
Microreader 19X Direct ID System	19	Amelogenin marker	2
TYPER X19	18	Amelogenin marker	1

**Reference provided for in-house kits for better understanding.*

1.3.3. X-STR databases/websites

The search returned three articles which described the creation of online X-STR databases (Table 1.4). This included two active databases which focus on the storage of X-STR population data and related calculations, namely the ChrX database and FamLinkX. Additionally, the Brazilian Genetic Database of X Chromosome was identified but the URL was unavailable.

Table 1.4 *A list of available X-STR databases or websites from the reviewed literature.*

Database/Website	URL (date accessed)	Reference
ChrX database	https://www.chrx-str.org/xdb/ (Date Accessed: 27/12/2022)	[51]
Brazilian Genetic Database of X Chromosome	http://www.bgbx.com.br/ (Unavailable)	[52]
FamLinkX	https://www.famlink.se/fx_index.html (Date Accessed: 27/12/2022)	[53]

1.3.4. Global X-STR population data

A multitude of publications pertaining to X-STR population data were identified (Appendix B). A comprehensive summary of the number of X-STR population studies that have been conducted on a global scale using any available X-STR multiplex system (Fig. 1.4.), revealed substantial variation between the X-STR population data available for each continent. Most

X-STR data was available for populations within Asia and Europe, while X-STR population data were limited for Africa and the Americas.

This variation is also present when focusing on X-STR population data that has been produced per country, with X-STR population data only available for a total of 72 countries worldwide, and most of these countries were only represented by the availability of limited X-STR data. A comparison of the number of population studies showed that China was the leading country in X-STR population data generation and thereafter, only five other countries, namely Japan, Germany, Italy, Spain and Brazil, have produced 10 or more publications related to X-STR population data (Fig. 1.4.).

The combined sample size of each country showed that within China, at least 47 different subpopulations and approximately 36 500 individuals, excluding families, were investigated. Other large countries, namely India (*n* = 1132), the United States of America (*n* = 2525), Brazil (*n* = 6221), Nigeria (*n* = 218) and Russia (*n* = 803), included much smaller sample sizes (Appendix B). In smaller countries such as Poland, Portugal and Croatia, the combined sample size for each country was greater than 1000 individuals. However, for many countries, only a single population study was available and often the sample sizes used were below 300 individuals (Appendix B). Some of these countries included East Timor (*n* = 149), Tunisia (*n* = 139), Bangladesh (*n* = 209), Saudi Arabia (*n* = 200), Greenland (*n* = 198) and Denmark (*n* = 210).

The X-STR population data generated with the most widely utilised commercial kit, the Investigator Argus X-12 (QS) kit (Qiagen, Hilden), is presented in Fig. 1.5. This figure illustrates that this kit has been utilised the most by researchers in China, which is consistent with China having produced the most X-STR population data publications. Following China, the use of this kit has also been frequently reported in smaller countries, namely Croatia and Portugal.

From Fig. 1.5., it is also clear that there is a paucity of the use of this kit in other largely populated countries such as India, the Russian Federation and the United States of America, with each of these countries only having one or two X-STR population data publications using this kit. Additionally, the use of this kit remains particularly scarce across countries on the African continent.

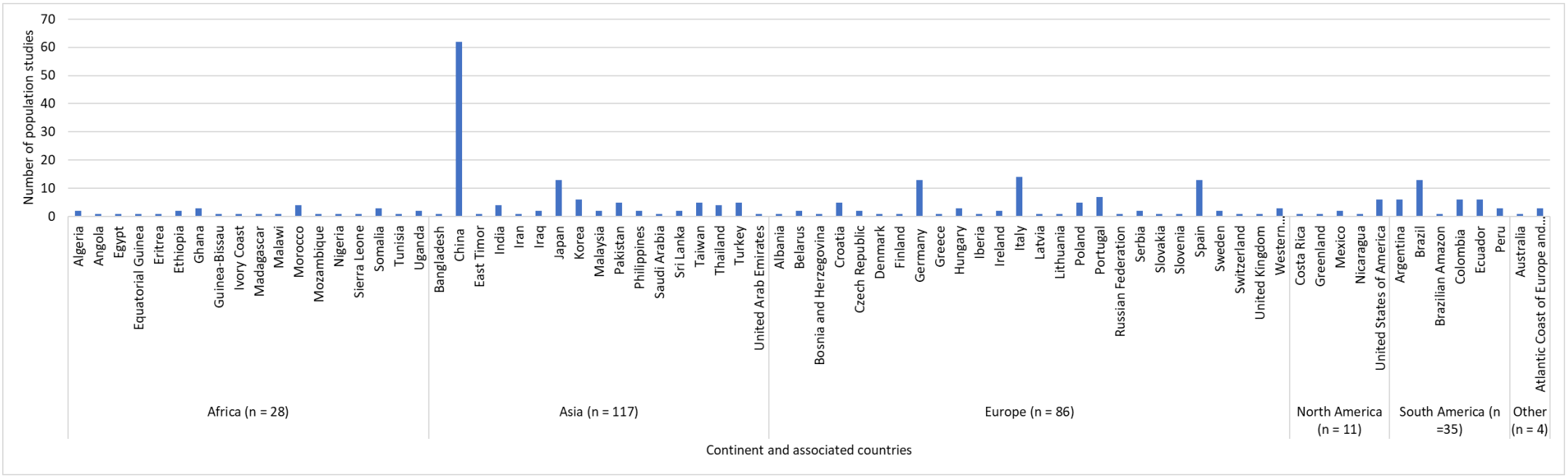

***Fig. 1.4**. A graphical illustration of the globally available X-STR population data based on the reviewed literature.*

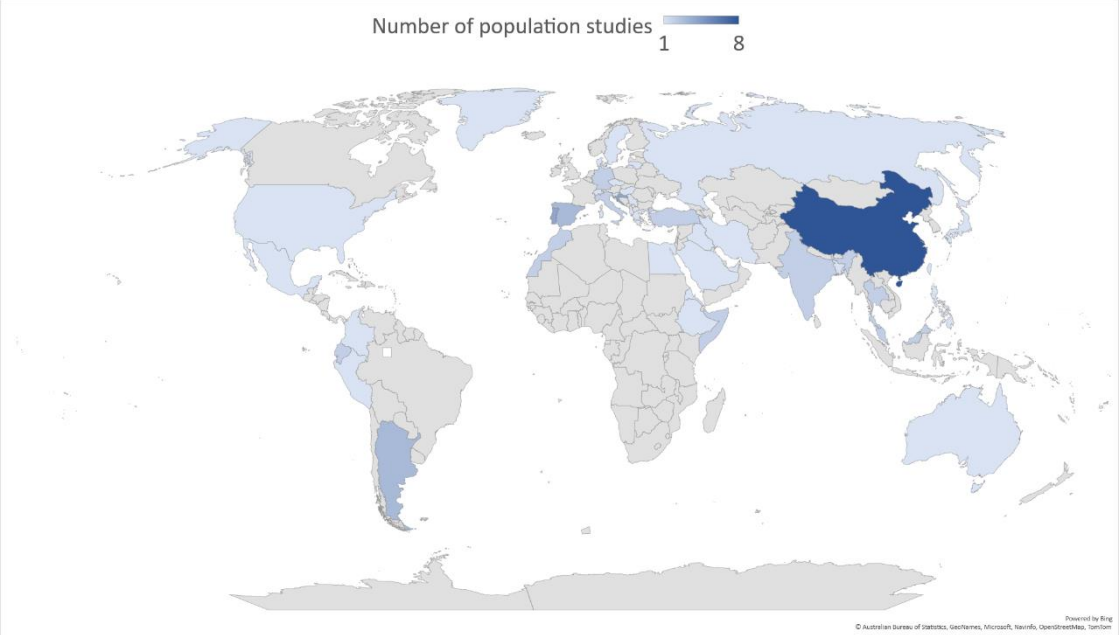

Fig. 1.5. *A map illustrating the global use of the Investigator Argus X-12 (QS) kit (Qiagen, Hilden) across the reviewed literature.*

1.4. Discussion

1.4.1. Applications of X-STRs

The incorporation of X-STRs within forensic laboratories, unlike autosomal STRs and Y-STRs, is not as well-established. This is because investigations into situations where X-STRs provide greater discriminatory value compared to other more extensively studied markers are more recent [2,6]. As explained in the introduction, the informativeness of autosomal STRs comes into question when there is a need to differentiate between related individuals or establish biological relationships while using an incomplete pedigree.

The most common application of X-STRs was identified as complex kinship testing and deficiency paternity testing. An example of complex kinship testing in which X-STRs would be useful is the analysis of possible incest cases involving a father, daughter and female offspring, as both the mother and female offspring would share the same paternal X-chromosome haplotype through identity-by-descent (IBD) [6].

For deficiency paternity testing, X-STR profiles obtained from paternal relatives or other female paternal offspring can be analysed in the alleged father's absence [27]. This may be necessary to resolve civil disputes, especially those regarding inheritance. A case example of

deficiency paternity testing was demonstrated by Serra *et al.,* (2008), whereby X-STRs were used to assist in a case involving a mother, a female child and alleged paternal grandparents. Initially, autosomal STRs were implemented, but the paternity results were inconclusive due to the presence of multiple mismatches between the DNA profiles. Thereafter, X-STR profiles were produced for the child and the alleged paternal grandmother. A comparison of these profiles, together with the data produced using autosomal STRs, provided sufficient evidence to exclude the alleged biological father from paternity [34]. This example especially illustrated that X-STRs can accompany routinely used autosomal-STRs to support findings and strengthen conclusions.

This same principle has been translated to forensic casework concerning the identification of missing individuals or human remains. Barbaro *et al.,* (2006) demonstrated the use of X-STRs to link a strand of hair found in a suspect's house, to a never-found missing female. An X-STR profile was generated for the hair, as well as the missing female's biological mother and sister. The sister's profile represented the paternal X-chromosome haplotype of the biological father in his absence. From this, a successful match was concluded [40].

Furthermore, the scope of X-STRs could be expanded into mortuary settings. Due to the low mutation rates of X-STRs, the use of X-STR profiling could also be utilised in an attempt to alleviate the burden of unidentified bodies. Many countries across the world face the harsh reality of an accumulation of unidentified bodies at their mortuaries year after year. Although an ongoing problem, this topic remains poorly documented, with minimal publications available [54–57]. It is possible that in some of these cases, the immediate family is unavailable for familial matching using autosomal STRs. If X-STRs were to be implemented as part of routine identification practice, alongside autosomal STRs, the analysis could be broadened to include distant familial members.

Although infrequently utilised, another application identified in the results was the use of X-STRs to support autosomal STRs and/or Y-STRs in mixture interpretation and criminal investigations, particularly those involving related suspects. An interesting case example by Lancia *et al.,* (2011) demonstrated the use of X-STRs in a rape and murder investigation involving a female victim and multiple male suspects, namely her husband and his brother. A mixed DNA sample was tested and X-STRs were able to differentiate between the victim's and

the suspect's DNA profiles, as well as used to discern the identity of the perpetrator by discriminating between the husband and his brother [41].

Therefore, the results show that the implementation of X-STRs may be useful in a variety of applications in both civil and forensic instances. However, the gap in which the use of X-STR markers fill lies particularly in deficiency paternity testing and complex kinship analyses involving at least one female (*i.e.,* mother/son, mother/daughter, father/daughter) [6].

1.4.2. Evolution of X-STR multiplex systems

There is a multitude of X-STRs spanning the X-chromosome. Over time, these STRs and the linkage properties thereof have been well-studied by many researchers [58–60]. STR loci that are inherited together as clusters are known as linkage groups. Four main linkage groups have been described at particular locations on the X-chromosome, namely Xq28, Xq26, Xq12 and Xp22 [2,61]. In addition to this, and similarly to the Y-chromosome, the X-chromosome houses the Amelogenin marker within its intronic region. This marker is traditionally used for biological sex determination, due to its 6 bp deletion on the X-chromosome, which allows for efficient differentiation between the sex chromosomes [62,63].

Many researchers have developed laboratory-specific multiplex X-STR systems as a means of simultaneously amplifying multiple X-STR loci for the generation of population data. For example, Sun *et al.* (2013) described the use of an internally developed 16 X-STR loci system (DXS9902, DXS6803, DXS10134, DXS6789, HPRTB, DXS6810, GATA31E08, DXS6795, DXS8378, GATA165B12, DXS6800, DXS10159, DXS7132, GATA172D05, DXS7424, and DXS6807) to perform X-STR typing on a Chinese Shanghai Han population [64]. However, the use of the PCR multiplex was limited to this publication.

The Spanish and Portuguese-speaking Working Group of the International Society for Forensic Genetics (GHEP-ISFG) have developed an X-STR decaplex, which includes 10 X-STR loci, namely GATA172D05, DXS6809, DXS9902, DXS7133, DXS8378, DXS6789, DXS9898, DXS7132, GATA31E08 and DXS7423 [48]. Although not commercially manufactured, this multiplex system has been widely used by many researchers across the globe and had the second highest prevalence in X-STR population studies (Table 1.3).

However, the increase in popularity in X-STR population research and the emergence of X-STRs in forensic and civil casework has prompted the need for the development of appropriate X-STR kits. X-STR loci located within the linkage groups, along with the Amelogenin marker have formed the basis for most of these commercially developed kits.

The Mentype® Argus X-UL kit (Biotype, Dresden) was the first commercially developed kit and amplified four X-STR loci (HPRTB, DXS7132, DXS7423 and DXS8378), along with the Amelogenin marker [46]. However, due to the limited number of loci included, this kit would have provided minimal discriminatory power within a forensic context. This prompted the development of the Mentype® Argus X-8 kit (Biotype, Dresden), which targeted a further four X-STR loci for amplification (DXS10135, DXS10101, DXS10134 and DXS10074) [65,66]. Thereafter, the Investigator® Argus X-12 kit (Qiagen, Hilden) was developed, which amplifies the Amelogenin marker and a total of twelve X-STR loci, consisting of the eight aforementioned loci, as well as four additional loci (DXS10148, DXS10079, DXS10103, DXS10146) [9]. Since then, advancements to this kit have been made and developmentally validated to create the current commercially available X-STR kit, known as the Investigator Argus X-12 QS kit (Qiagen, Hilden). A quality sensor (QS) was added to allow researchers to monitor PCR success, as well as an autosomal STR marker (D21S11) to facilitate an evaluation of concordance between X-STR and autosomal STR typing kits [47,67]. Furthermore, the Investigator Argus X-12 QS kit (Qiagen, Hilden) is ISO18385 certified, meaning that the appropriate measures were taken to reduce the risk of contaminating DNA during the manufacturing process.

The Investigator Argus X-12 (QS) kit (Qiagen, Hilden) was the most commonly used kit globally (Table 1.3, Fig. 1.5.), suggesting that this kit is widely accessible to many countries and may account for this kit becoming the most widely utilised for X-STR typing. However, it is also important to consider that the frequent use of this kit may be due to the limited number of manufacturers of commercial X-STR kits and none of these current competitors are as globally established within the field of forensics as Qiagen is.

Alternative X-STR multiplex kits that have been frequently described in the literature include the AGCU X19 X-STR amplification kit (AGCU ScienTech Inc., Wuxi, Jiangsu), which refers to a multiplex PCR system consisting of 19 X-STR loci (DXS10162, DXS6809, DXS10174, DXS10159, DXS10079, DXS8378, DXS101, DXS7132, DXS10103, DXS7424, DXS10135, DXS10148,

DXS10101, DXS10075, DXS10164, DXS6789, DXS7423, DXS10134, and HPRTB) [68] and the Goldeneye™ DNA identification system 17X kit (Peoplespot Inc., R&D, Beijing), which utilises the Amelogenin marker and 16 X-STR loci (DXS8378, DXS7424, DXS6789, GATA31E08, DXS6807, DXS10159, DXS9902, DXS7132, DXS6800, DXS6795, GATA165B12, DXS10134, HPRTB, DXS6810, DXS6803 and GATA172D05) [69]. However, the implementation of these two kits has been greatly limited to Chinese populations only (Appendix B). A reason for this may be that these kits are manufactured in China, thus providing ease of access to researchers in China, while remaining unavailable on a global scale.

1.4.3. X-STR databases/websites

A few researchers have attempted to develop a global X-STR database, which would allow for the storage of X-STR population data generated for different populations around the world (Table 1.4). However, these attempts have not yet been effective.

The Forensic ChrX Research database was created to serve as a repository for researchers to submit their published X-STR haplotype frequency data, provided the necessary quality requirements are met [51,70]. In theory, this would allow researchers to readily access this type of data for any population across the globe. Unfortunately, this database is currently underutilised and only provides frequency data for a few populations, namely Chinese Han, Ghanesen, German, and Japanese. This may be due to many articles not meeting the requirements stipulated on the database to qualify for publication to the database [70]. Albeit underutilised, the Forensic ChrX Research database provides researchers with information regarding the X-chromosome, as well as a mathematical model to calculate various forensic parameters related to X-STR population data. The latter aspect of the database has shown to be widely efficient and is often described by researchers as part of their data analysis in various publications [71–73].

Another database that stores X-STR population data and provides computational X-STR marker software for download is known as FamLinkX [53]. While FamLinkX provides a larger compilation of global X-STR population data, the last modification to the list of available population data occurred in 2019. This database is newer and lacks the quality standards

implemented by the Forensic ChrX Research database, possibly making it less well-known. Together, these reasons may explain its scarcity in the literature.

Lastly, a third database exists, known as the Brazilian Genetic Database of Chromosome X, which acted as a repository for Brazilian X-STR population data [52]. The authors of this database intended on expanding it to include various calculations related to X-STR markers which could be utilised by other researchers, as well as X-linked insertions and deletion polymorphisms (X-INDELS). However, it currently remains unavailable for use.

The underutilisation of these X-STR databases may also be due to the lack of consent from participants for their data to be stored on an openly accessible platform. Unlike other well-established databases, such as the Y-STR Haplotype Reference Database (YHRD) [74,75] and European DNA Profiling Group (EDNAP) mtDNA Population Database (EMPOP) [76], these X-STR databases do not have a privacy policy in place regarding the storage of the X-STR data. Furthermore, the data available on the YHDR and EMPOP databases are collated for each country and access to this population reference data must be requested, while population data available on the X-STR databases represent individual publications, which are readily downloadable. Although this is useful for population studies and comparisons, it could bring about ethical concerns around privacy. Additionally, the frequent contributions to the YHRD and EMPOP databases by researchers may be due to publication requirements. For example, the Forensic Science International: Genetics journal stipulates that all mtDNA and Y-STRs/Y-SNPs data must be submitted to the relevant database for quality assessment prior to submission for publication [77], while submissions of X-STR data do not hold this same requirement.

Therefore, the establishment of a single designated X-STR reference database with appropriate quality standards and management may increase the utilisation of such a database by researchers.

1.4.4. Global X-STR population data

There were a multitude of articles pertaining to X-STR population data (Fig. 1.4., Appendix B). As previously mentioned, the majority of the X-STR population data was within Asian and European populations, while African and American populations remained under-represented.

This may be because most STR multiplex kits are manufactured within these regions and are more readily accessible. However, this is highly disproportionate considering Africa has the second-largest continental population, after Asia. Furthermore, the African continent holds some of the world's most diverse populations [78], thus preventing the translation of X-STR datasets from one African population to another. This motivates for the generation of localised indigenous knowledge.

Fig. 1.4 also showed that as an individual country, China has the most extensive X-STR dataset. This is due to the availability of a large amount of X-STR data, which includes a large amount of separate Chinese populations from different regions across the country as well as a considerable sample size. However, evaluation of the sample size used and the number of different subpopulations/regions investigated for each country can provide a deeper understanding of how well a country is represented by the X-STR population data produced. An overview of the combined sample size utilised in each X-STR population study compared to the general population size of each country revealed that Croatia was the most well-represented country, as X-STR data is available for all major regions of the country and the density of Croatia's population is considerably smaller than China's. In contrast to this, the majority of the countries listed in Fig. 1.4 only have a limited number of X-STR population data publications available and these publications often lack the use of a sample size that appropriately mimics the relevant population. For example, publications for populations within East Timor [79], Tunisia [80], Bangladesh [81], Saudi Arabia [82], Greenland and Denmark [83] include less than 300 samples. In 2013, the Forensic Science International: Genetics journal released guidelines for the publication of X-STR population data, whereby a minimum of 500 individuals need to be included when performing X-STR typing [77]. Many publications fall short of adhering to these guidelines (Appendix B) and although the aforementioned studies were not published in this journal, researchers should consider this guideline when investigating X-STRs within different populations to ensure that the data they produce are informative.

When focusing on X-STR population data generated using the Investigator Argus X-12 (QS) kit as seen in Fig. 1.5., it showed that although this kit is the most popularly utilised globally, it has only been utilised for a maximum of eight publications within any particular country. Once again, China has produced the highest number of population studies, while other densely

populated countries such as India [84,85], the Russian Federation [86], the United States of America [87], have limited X-STR population data available. Therefore, although X-STR data is available for some populations, it is clear that unless these populations are homogenous throughout all regions, they will remain under-represented until additional X-STR data is collected. This further highlights the need for more extensive X-STR research within each population/region of a country. Fig. 1.5 also illustrates that Africa continues to have the least amount of available X-STR population data produced using the Investigator Argus X-12 QS kit (Qiagen, Hilden), as many countries, including South Africa, are not represented at all. This is unfortunate as African countries are considered to hold some of the most diverse populations globally [78], thus warranting exploration. However, the absence of this data may be due to the limited availability of resources for this type of research within Africa.

1.5. Conclusion

Sex-linked STRs (Y-STRs and X-STRs) have been shown to be critical in scenarios where autosomal STRs are not informative enough. This literature review focussed specifically on the use of X-STRs and the applications thereof. Published literature regarding X-STRs continuously highlights the importance of X-STRs in deficiency paternity testing and other kinship scenarios as a solution to dealing with incomplete and/or complex pedigrees. Although this supports the inclusion of X-STRs, it is clear that the scope thereof is limited to a certain niche. This may account for the lack of X-STR popularity in many countries.

There is a movement towards the incorporation of X-STRs as a supplementary analysis to support autosomal STRs. However, the literature suggests that there is a lack of uniformity within the kits that are used in forensic casework, as well as for population data generation. The Investigator® Argus X-12 (QS) kit (Qiagen, Hilden) is currently the most common commercially available multiplex PCR kit. Its wide availability and quality standards are currently unmatched. However, this is not to say that improvements are not necessary. In time, manufacturers may draw on literature to include a larger multiplex of X-STR markers to further increase the informativeness of the kit.

Furthermore, many researchers have undertaken the task of generating X-STR data for different populations. However, many countries remain underrepresented, limiting the use

of X-STRs in a forensic context, as the necessary statistical analyses cannot be adequately performed. X-STRs repositories are underutilised, meaning there is a lack of proper sorting and storing of population data for it to be made accessible to the rest of the world. Therefore, while the advancements of X-STRs in a medico-legal context over the years are appreciated, it is integral to acknowledge the gap in the field and the work that still lies ahead to ensure the inclusion of X-STRs during casework and research.

Chapter 2: Manuscript

2.1. Introduction

Human identification is primarily achieved through the use of DNA profiling [1]. During medico-legal investigations, DNA profiles are generated using autosomal short tandem repeats (AS-STRs) [8] and compared to a reference DNA profile of known origin. Random match probabilities (RMP) must be determined for each match, which requires allele frequency data from the general population [3]. However, limitations in the use of AS-STRs for resolving distant familial relationships have previously been identified [4,35]. This has led to research into the use of STR markers located on the sex chromosomes, which can be used to complement the results obtained from AS-STRs [8].

X-STRs have shown to be particularly useful in deficiency paternity testing involving daughters as well as complex kinship testing [6]. This is due to the unique way in which sex chromosomes recombine and are passed on, with only the mother's X-chromosomes undergoing recombination before being inherited by offspring, while the father's X-chromosome is passed on to female offspring virtually unchanged due to its hemizygous nature [2,9]. Consequently, females who share the same father have the same paternal X-chromosome haplotype. Additionally, X-STRs are located within linkage groups and inherited as a haplotype [12].

Many researchers have developed in-house laboratory X-STR multiplex polymerase chain reaction (PCR) systems which can be utilised to generate X-STR population data [88–91]. However, the use of developmentally validated and commercially available X-STR multiplex kits is often preferred within the framework of a forensic laboratory setting. The most popularly used commercially available kit for the investigation of X-STRs is the Investigator Argus X-12 QS (Qiagen, Hilden) [9]. This kit was developmentally validated according to the European Network of Forensic Science Institute (ENFSI) and the Scientific Working Group on DNA Analysis Methods (SWGDAM) and allows for simultaneous amplification of 12 X-STR loci located within linkage groups 1 – 4 (LG1 – LG4) on the X-chromosome. Also included within this kit is a quality sensor (QS), the Amelogenin locus and an autosomal locus (D21S11) [92].

Currently, most X-STR data available has been generated for populations within Europe and Asia, while populations of African origin remain underrepresented. As such, the value of X-

STRs is often overlooked within many African countries, including South Africa, due to the lack of an appropriate reference database.

South Africa consists of nine provinces, namely Eastern Cape, Free State, Gauteng, KwaZulu-Natal, Limpopo, Mpumalanga, Northern Cape, North West and Western Cape, and has an overall national population exceeding 60 million individuals. These individuals have been classified into four major population groups according to the South African national census, namely Black African (81 %), Coloured (8.8 %), Indian/Asian (2.6 %) and White (7.7 %) [93]. The National Forensic DNA Database of South Africa (NFDD) utilised by the South African Police Service (SAPS) also makes use of these population groups. However, for this population study, population groups were rather reported as ancestry, whereby African ancestry, European ancestry, Mixed ancestry and Indian/Asian ancestry refers to the Black African, White, Coloured and Indian/Asian population groups, respectively. This was to ensure both the global and local applicability of this data.

The aim of this study is, therefore, to provide a 'starting point' and platform for expanding the application of forensic genetics in South Africa by generating X-STR data for the overall South African population.

2.2. Methods and materials

This population study was quantitative and prospective, with the purpose of generating X-STR frequency data for the South African population. Before this could be achieved, the workflow needed to be optimised and internally validated.

2.2.1. Sample selection and experimentation

This study was sub-linked to an umbrella population study (HREC 342/2016) and obtained ethical approval from the Faculty of Health Science Human Research Ethics Committee (HREC) at the University of Cape Town (UCT) (HREC 136/2022) (Appendix C).

The samples utilised in this study were collected from both living and deceased individuals. Participation in this study was voluntary and informed consent was provided by the participant themself or if deceased, their next-of-kin, for their sample to be utilised in any

future research conducted within the Division of Forensic Medicine and Toxicology. Adult participants were at least 18 years of age at the time of sample collection. Any individual who had received a bone marrow transplant or blood transfusion was excluded from this study.

2.2.1.1. Internal validation

The DNA profiling workflow for the Investigator Argus X-12 QS kit (Qiagen, Hilden) was internally validated for lysate samples. These samples were created by processing buccal swabs with Qiagen STR GO! Lysis Buffer (Qiagen, Hilden) or Promega SwabSolution™ (Promega Corporation, WI, USA), according to the respective manufacturer's handbook [94,95]. Internal validation experimentation included the establishment of the analytical threshold, stochastic threshold and stutter peak threshold as well as an evaluation of sensitivity, limit of detection, reproducibility and concordance.

For the analytical threshold, lysate blanks representing each lysate preparation methods were used (n = 6 (3x2)). These samples were subjected to the DNA profiling workflow in triplicate.

The stochastic threshold, stutter peak threshold, sensitivity and limit of detection were established using three female lysate samples, for which informed consent was obtained. These samples were serially diluted according to the manufacturer's developmental validation guidelines [96], and processed in triplicate.

To evaluate reproducibility using repeated measurements, control DNA 9947A and 2800M, as well as a subset of 20 lysate samples were subjected to the DNA profiling workflow on separate days.

For concordance testing, a subset of 483 samples was used to compare the genotype of each sample at the autosomal marker, D21S11, between the Investigator Argus X-12 QS kit (Qiagen, Hilden) and the Investigator 24plex GO! kit (Qiagen, Hilden) [96]. Additionally, a subset of 340 samples was used to evaluate the concordance of 7 X-STR markers (DXS10135, DXS8378, DXS7132, DXS10074, DXS10103, HPRTB and DXS7423), which are common to both the Investigator Argus X-12 QS kit (Qiagen, Hilden) and the massively parallel sequencing (MPS) ForenSeq™ DNA Signature Prep kit (Illumina, CA, USA).

2.2.1.2. Population study

For the population study, a total of 781 biological samples belonging to unrelated South African individuals (male = 517, female = 264) were utilised. These individuals were located across the nine provinces and fell within one of the four major population groups of South Africa, *i.e.,* African ancestry (*n* = 178; male = 131, female = 47), European ancestry (*n* = 223; male = 129, female = 94), mixed ancestry (*n* = 240; male = 161, female = 79) and Indian/Asian ancestry (*n* = 140; male = 96, female = 44). These samples included lysates (*n* = 686), which were previously collected under the umbrella study as buccal swabs and processed as described in section 2.2.1.1., as well as the DNA profiles of previously genotyped extracted DNA samples (*n* = 95).

For all experimentation, control DNA 9947A and a non-template control (NTC) were included in each batch as a quality control measure.

2.2.2. Workflow optimisation

The workflow was optimised for each lysate type, which resulted in certain adjustments to the manufacturer's protocol (Table 2.1) [67,94].

Table 2.1 *Optimised DNA profiling workflow conditions for lysate samples.*

Optimised conditions	**Qiagen STR GO! Lysis Buffer**	**Promega SwabSolution**
Final reaction volume (µl)	6.25	6.25
Volume of 5X AmpSolution (µl)	-	0.3
Volume of lysate (µl)	1	1
Number of PCR cycles	24	23
CE injection time (seconds)	15	20
CE run time (seconds)	1800	1800

2.2.3. X-chromosome STR typing

DNA amplification was performed using the Investigator Argus X-12 QS kit (Qiagen, Hilden) on the T100 thermal cycler (Bio-Rad, California). The resultant PCR products were separated using capillary electrophoresis (CE) on the Applied Biosystems 3500*xl* Genetic Analyser (Thermo Fisher Scientific, Massachusetts) with POP4 polymer and a 36 cm capillary array.

2.2.4. Data analysis

2.2.4.1. Internal validation

The data were analysed using GeneMapper® *ID-X* Software Version 1.5 (Thermo Fisher Scientific, Massachusetts) and subsequent calculations were performed using Microsoft® Excel 365. For the analytical threshold, the peak amplitude thresholds were set to 1 relative fluorescent unit (RFU) to identify the highest peak. The RFU of that peak was doubled and considered as the analytical threshold. For the stochastic threshold, the point at which allelic drop-out occurred for a known heterozygote was identified. The RFU of all false homozygotes were recorded to calculate the mean and standard deviation. The stochastic threshold was calculated using Equation 2.1.

$$Stochastic\ threshold = mean + 3\ x\ (standard\ deviation)$$

Equation 2.1 *Stochastic threshold calculation*

For the stutter peak threshold, peak amplitude thresholds were set to 25 RFU, to allow for the adequate calling of the stutter peaks. A stutter peak ratio for each marker was calculated using Equation 2.2 and an average was determined. The stutter peak threshold for each marker and overall was calculated using Equation 2.3.

$$Stutter\ peak\ ratio\ = \frac{Height\ of\ stutter\ peak\ (RFU)}{Height\ of\ true\ allelic\ peak\ (RFU)}$$

Equation 2.2 *Stutter peak ratio calculation*

$$Stutter\ peak\ threshold = Mean\ stutter\ peak\ ratio + 3\ x\ (standard\ deviation)$$

Equation 2.3 *Stutter peak threshold calculation*

The sensitivity of the kit was determined as the lowest amount of DNA at which a full, accurate and reliable DNA profile was obtained, whereas the limit of detection was considered to be the lowest amount of DNA that was able to be detected, even if the thresholds were not met or a full profile was not obtained. To determine reproducibility between samples, as well as concordance between workflows, the number of concordant alleles was summed and divided by the total number of alleles (Equation 2.4).

$$Concordance = \frac{Number\ of\ concordant\ alleles}{Total\ number\ of\ alleles}$$

Equation 2.4 *Frequency of concordance calculation*

2.2.4.2. Population study

The resultant DNA profiles were analysed using GeneMapper® *ID-X* Software Version 1.5 (Thermo Fisher Scientific, Massachusetts), with the internally validated thresholds applied. Off-ladder alleles were manually characterised according to allele size and verified using MPS data, where available.

StatsX v2.0 [97] was used to calculate allele and haplotype frequencies as well as relevant forensic parameters, namely gene diversity (GD)/haplotypic diversity (HD), polymorphism information content (PIC), power of discrimination (PD) for males and females and mean exclusion chance (MEC).

Arlequin software v3.5.2.2 was used to evaluate population differentiation for each locus between males and females, Hardy-Weinberg equilibrium (HWE) per locus using female samples, linkage disequilibrium (LD) between loci by exact test using a Markov chain for males and likelihood ratios test for females, a locus by locus analysis of molecular variance (AMOVA) using conventional F-statistics (only haplotype frequencies) and pairwise F_{ST} genetic distance matrix between the different population groups for male haplotypic data.

2.3. Results

2.3.1. Internal validation

2.3.1.1. Interpretation thresholds

Qiagen STR GO! Lysis Buffer (Qiagen, Hilden) and Promega SwabSolution (Promega Corporation, WI, USA) lysate blanks were processed in triplicate, and the analytical threshold was calculated to be 60 RFU and 100 RFU, respectively.

Using three serially diluted female lysate samples, the stochastic threshold for Qiagen STR GO! Lysis Buffer (Qiagen, Hilden) and Promega SwabSolution (Promega Corporation, WI, USA) lysate samples were established as 201 RFU and 264 RFU, respectively.

Similarly, the marker-specific and overall stutter peak thresholds were determined (Table 2.2). The overall stutter peak threshold for the Qiagen STR Go! Lysis Buffer (Qiagen. Hilden) and the Promega SwabSolution (Promega Corporation, WI, USA) lysates was 14 %.

Table 2.2 *Marker-specific and overall stutter peak thresholds.*

	Qiagen STR Go! Lysis Buffer			**Promega SwabSolution**		
Locus	**Mean stutter ratio (%)**	**SD (%)**	**Marker-specific stutter threshold (%)**	**Mean stutter ratio (%)**	**SD (%)**	**Marker-specific stutter threshold (%)**
DXS10103	6.80	1.93	12.59	6.96	2.15	13.41
DXS8378	7.28	1.28	11.12	7.29	1.63	12.18
DXS10101	7.48	2.96	16.36	6.74	1.50	11.24
DXS10134	7.94	1.71	13.07	7.93	1.51	12.46
DXS10074	5.13	1.18	8.67	5.26	1.33	9.25
DXS7132	9.14	2.69	17.21	8.62	2.61	16.45
DXS10135	11.09	1.80	16.49	11.01	1.69	16.08
DXS7423	7.27	1.20	10.87	7.14	1.34	11.16
DXS10146	7.70	1.77	13.01	7.86	1.71	12.99
DXS10079	7.67	2.26	14.45	7.86	3.63	18.75
HPRTB	11.16	2.82	19.62	11.42	2.10	17.72
DXS10148	7.83	2.85	16.38	8.56	3.31	18.49
D21S11	8.93	2.20	15.53	9.06	2.80	17.46
Average (%)	8.11	2.05	-	8.13	2.10	-
Overall stutter threshold (%)			**14**			**14**

Abbreviation - SD: standard deviation.

2.3.1.2. Sensitivity and limit of detection

It was determined that the sensitivity was 1:32 for Qiagen STR GO! Lysis Buffer (Qiagen, Hilden) lysates and 1:16 for Promega SwabSolution (Promega Corporation, WI, USA) lysates, while the limit of detection was determined to be 1:128 for Qiagen STR GO! Lysis Buffer (Qiagen, Hilden) and Promega SwabSolution (Promega Corporation, WI, USA) lysates.

2.3.1.3. Reproducibility

A comparison between the DNA profiles produced for each of the 20 lysate samples, as well as the two control DNA samples (9947A and 2800M), revealed 100 % concordance between allele calls, indicating successful reproducibility.

2.3.1.4. Concordance

A comparison between the genotypes obtained at the D21S11 locus from the Investigator Argus X-12 QS kit (Qiagen, Hilden) and the Investigator 24plex GO! kit (Qiagen, Hilden) revealed 99.59 % concordance. Two samples were found to be non-concordant, whereby the Investigator Argus X-12 QS kit (Qiagen, Hilden) produced the genotypes: 29, 32.2 and 28.3, 31.2 rather than 29, 29 and 29, 31.2 as seen with the Investigator 24plex GO! kit (Qiagen, Hilden), respectively. The first instance of non-concordance is likely due to allele drop-out in the Investigator 24plex GO! kit (Qiagen, Hilden), while the second instance may be due to variation in the migration of DNA fragments through the capillary.

An assessment of concordance was also conducted between the Investigator Argus X-12 QS kit (Qiagen, Hilden) and the ForenSeq™ DNA Signature Prep kit (Illumina, CA, USA). Where MPS data were available and allele drop-out had not occurred, allelic calls were fully concordant between workflows across all eight loci, with six exceptions (Appendix D). Locus DXS10135 had the highest number of non-concordant alleles (n = 3), followed by locus DXS10074 (n = 2) and locus DXS8378 (n = 1).

2.3.2. Population study

2.3.2.1. Statistical analyses

Biological samples belonging to 264 female and 517 male South African individuals were processed using the Investigator Argus X-12 QS kit (Qiagen, Hilden). From these samples, full DNA profiles were obtained and a total of 120 unique alleles were identified. The Exact test performed per locus revealed no significant differentiation between males and females was present ($p > 0.05$) (Appendix E). This allowed for the allele frequencies of male and female individuals to be pooled (Appendix F) and subsequently used to calculate forensic parameters for the 12 loci (Table 2.3). Forensic parameters for the overall South African population were evaluated to determine each locus's usefulness in discerning the identity of different individuals. Locus DXS10135 was the most informative (PIC = 0.952), with 53 unique alleles, while locus DXS7423 was the least informative (PIC = 0.623), with only seven unique alleles. GD for all loci was greater than 0.6. DXS10135 had the highest GD (0.955) and DXS7423 had the lowest (0.681). The combined PD of males and females for the 12 loci were 0.999999999919563 and 1, respectively.

Table 2.3 *Forensic parameters for the 781 South African individuals.*

Linkage group	Locus	Number of unique alleles	GD	PIC	PD_{Male}	PD_{Female}
1 (Xp22)	DXS8378	7	0.699	0.643	0.698	0.853
	DXS10135	53	0.955	0.952	0.954	0.996
	DXS10148	56	0.937	0.933	0.936	0.993
2 (Xp11)	DXS7132	9	0.751	0.709	0.750	0.896
	DXS10074	21	0.874	0.860	0.873	0.971
	DXS10079	14	0.832	0.810	0.831	0.950
3 (Xp26)	HPRTB	10	0.744	0.702	0.743	0.893
	DXS10101	27	0.917	0.910	0.916	0.987
	DXS10103	8	0.754	0.718	0.753	0.904
4 (Xp28)	DXS7423	7	0.681	0.623	0.681	0.841
	DXS10134	38	0.882	0.870	0.881	0.975
	DXS10146	41	0.917	0.910	0.916	0.987
Combined		-	-	-	0.9999	1

Abbreviations - GD: gene diversity, PIC: polymorphism information content, PD: power of discrimination.

HWE was assessed in female samples, and after the application of a Bonferroni correction for multiple comparisons, all loci were found to be in HWE, except DXS10148 ($p < 0.0042$) (Appendix G).

Haplotype frequencies and haplotype forensic parameters for the 517 male individuals were determined (Appendix H). No shared haplotypes were observed for the full 12-loci haplotype definition: DXS8378-DXS10135-DXS10148-DXS7132-DXS10074-DXS10079-HPRTB-DXS10101-DXS10103-DXS7423-DXS10134-DXS10146. A total of 421, 228, 218 and 302 unique three loci haplotypes were observed in LG1, LG2, LG3 and LG4, respectively. LG1 was the most informative (PIC = 0.997), while LG2 and LG3 were the least informative (PIC = 0.992). Additionally, the HD values for all LGs were greater than 0.99. The most common haplotype in each LG was as follows, LG1: 11-24-18 (n = 5), LG2: 14-15-19 and 14-16-19 (n = 13), LG3: 12-30.2-19 (n = 12) and LG4: 14-35-28 (n = 12).

LD tests were performed separately for male and female samples to evaluate the presence of non-random associations between loci (Appendix I). After a Bonferroni correction was applied, significant LD ($p < 0.0008$) was detected in five loci pairs in males (DXS10148-DXS10101, HPRTB-DXS10101, DXS10101-DXS10103, DXS10101-DXS10134 and DXS10134-DXS10146) and three loci pairs in females (DXS10148-DXS10074, DXS10101-DXS10103 and DXS10134-DXS10146). The maximum squared coefficient of correlation (r^2) value for each unlinked loci-pair in LD for males, *i.e.,* DXS10148-DXS10101, HPRTB-DXS10101 and DXS10101-DXS10134, was 0.2485, 0.0574 and 0.1651, respectively.

Pairwise F_{ST} and an AMOVA were calculated using haplotype frequencies to assess the intra-population genetic structure within the South African population. Using pairwise F_{ST} values, significant differences were observed between the African population group and all three other population groups, namely European, Mixed ancestry and Indian/Asian, after a Bonferroni correction was applied ($p < 0.0083$) (Fig. 2.1). Additionally, the highest population differentiation was observed between the African and European groups (F_{ST} value = 0.02301). The AMOVA showed that molecular variation among the population groups was only 1.04 %, while molecular variation within the population groups was 98.96 % (F_{ST} = 0.01042; p = 0.00000).

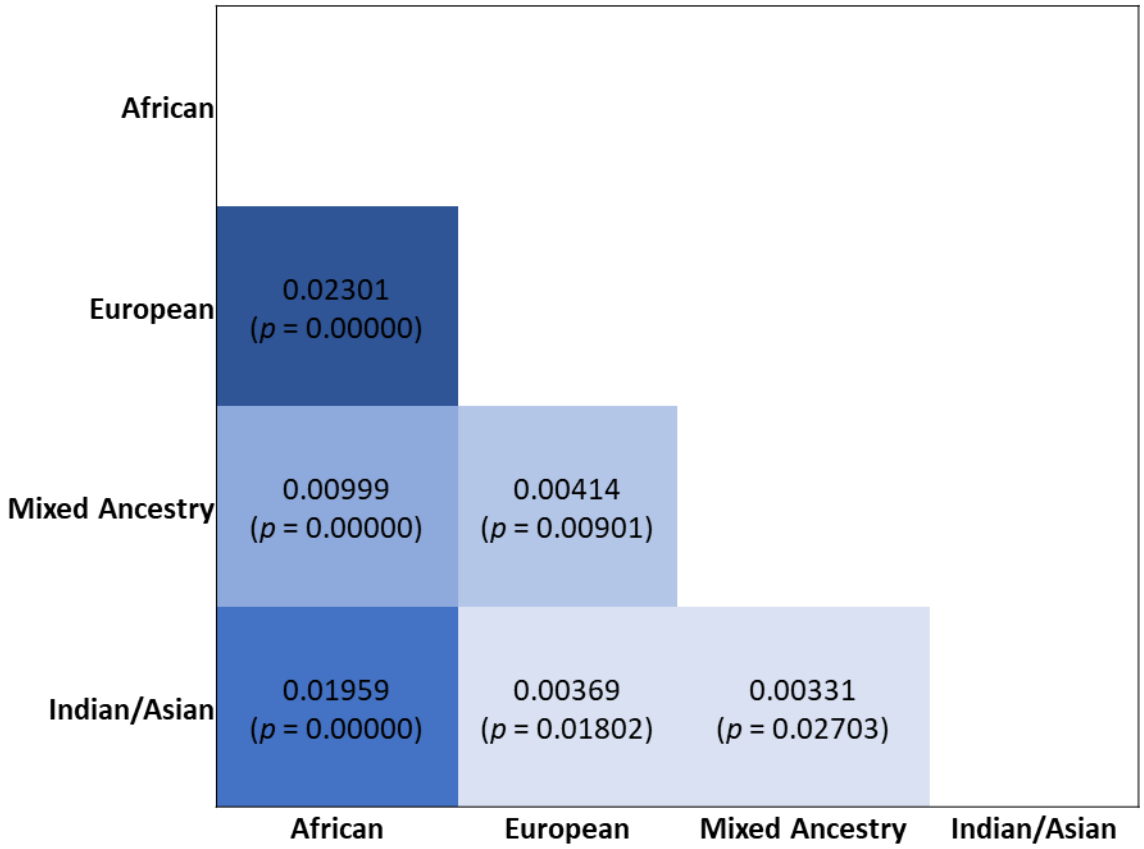

Fig. 2.1. *Distance matrix of pairwise F_{ST} values (as indicated by the different shades of blue) for the four major South African population groups.*

2.3.2.2. Off-ladder and null alleles

A total of 59 unique off-ladder peaks were identified across seven different loci included in the Investigator Argus X-12 QS kit (Qiagen, Hilden) (Appendix J). These peaks fell within regions of the loci where allelic representation is currently absent within the allelic ladder. These off-ladder alleles were detected in approximately 19 % (n = 149) of the total cohort utilised in this study, and a total of 166 off-ladder allele observations were made. From this, it was determined that 134 individuals had one off-ladder allele, 13 individuals had two off-ladder alleles and two individuals had three off-ladder alleles. Furthermore, the majority of the off-ladder alleles were observed within the African (n = 96) and Mixed ancestry (n = 53) population groups. Locus DXS10148 had the highest number of unique off-ladder alleles (n = 23), followed by locus DXS10134 (n = 10). However, the most prevalent off-ladder allele was 36.2 at locus DXS10146, with a total of 20 observations within the cohort (allele frequency = 0.0191). MPS data were able to verify alleles 26.3, 27.1, 28.3, 29.3, 30.1, 33.1 and 37.1 at

locus DXS10135, as well as alleles 13.2 and 16.3 at locus DXS10074. Null alleles were observed at locus DXS10146 in four male individuals and the Amelogenin locus in three male individuals.

2.4. Discussion

2.4.1. X-STR profiling in South Africa

The primary utilisation of X-STRs has been outlined within complex kinship testing, including deficiency paternity testing and testing distant familial relations [6]. These applications are relevant to the South African population and highlight the gap in which X-STRs can be implemented within medico-legal investigations. For example, South Africa is a country which legally permits polygynous marriages within indigenous communities [98]. Due to this, deficiency paternity inheritance disputes may arise. X-STRs can be used to resolve these complex family structures, particularly when involving daughters. Additionally, like many other countries [56,57], South Africa continues to be challenged by the large number of unidentified bodies remaining within the country's mortuary system [54,99]. These are individuals who were not able to be identified through routine processes [54] and lack a reference profile on the NFDD. Familial searching can be initiated in these instances, but this too is limited if only distant blood relatives are available as a reference. This is because DNA profiling in South Africa is routinely performed using AS-STRs, which lack sufficient discriminatory power to resolve these distant relationships. To overcome this, an alternative DNA profiling target, such as X-STRs, may be used.

However, the utilisation of X-STRs to assist in medico-legal investigations has not yet been implemented in South Africa. This is likely due to the absence of an appropriate X-STR population reference database, which is necessary to provide statistical confidence to X-STR profiling results [3]. Therefore, this study represents the first X-STR data generated for the South African population.

Previously, it was determined that allele frequency databases should contain at least 100 – 150 individuals per population group included [3,100]. As this study included 781 individuals from the four major population groups within South Africa, namely African ancestry (n = 178),

European ancestry (*n* = 223), Mixed ancestry (*n* = 240) and Indian/Asian ancestry (*n* =140), it is believed that this data provides a reliable insight into the distribution of X-STRs within the South African population as a whole. Additionally, an overall sample size of greater than 500 individuals was utilised, which exceeds the Forensic Science International: Genetics journal guidelines [77].

2.4.2. The use of lysate samples

The conventional DNA profiling workflow requires a DNA extraction and quantification stage. Studies related to DNA profiling using the Investigator Argus X-12 QS kit (Qiagen, Hilden) typically include the use of extracted DNA from blood, buccal swabs or FTA cards [72,82,101–104]. Although effective, DNA extraction and quantification increase the processing time per sample and can result in sample loss. To address this, the direct PCR amplification approach has been introduced, whereby these stages within the DNA profiling workflow are eliminated. Shrivastava and Kumawat (2021) investigated the impact of direct PCR using FTA cards on the quality of DNA profiles produced for the Investigator Argus X-12 QS kit (Qiagen, Hilden) and concluded that this approach was indeed appropriate. This aligned with the developmental validation of the Investigator Argus X-12 QS kit (Qiagen, Hilden), which found the kit to be stable during direct amplification of FTA cards and lysates [105].

In this study, direct PCR amplification was performed on lysate samples prepared with two different lysis buffers, namely Qiagen STR GO! Lysis Buffer (Qiagen, Hilden) and Promega SwabSolution (Promega Corporation, WI, USA). Following optimisation and internal validation, full DNA profiles were obtained for all included samples. This illustrates that lysate samples are compatible with the Investigator Argus X-12 QS kit (Qiagen, Hilden) and motivates the implementation of this workflow within medico-legal settings where a rapid turnaround time for identification is required.

2.4.3. Internal validation

This study presents the first internal validation data available on the Investigator Argus X-12 QS kit (Qiagen, Hilden) for direct amplification. As the developmental validation of the

Investigator Argus X-12 kit (Qiagen, Hilden) utilised extracted DNA samples, the Investigator validation guide [96] was implemented in this study instead.

Full DNA profiles were obtained for 98.24 % of individuals (*n* = 781/795). This indicates that the optimisation and the establishment of interpretation thresholds during the internal validation component of this study were successful. The analytical and stochastic thresholds were greater for Promega SwabSolution lysates compared to Qiagen STR GO! Lysis Buffer lysates. This was expected due to the difference in chemistry between the Promega SwabSolution lysates and the Investigator Argus X-12 QS kit (Qiagen, Hilden), thus requiring the addition of 5X AmpSolution (Promega Corporation, WI, USA). Subsequently, these DNA profiles often contained peaks of much higher RFU than the Qiagen STR GO! Lysis Buffer lysates.

The limit of detection for both lysate types was 1:128, while the sensitivity for the Qiagen STR GO! Lysis Buffer (Qiagen, Hilden) and the Promega SwabSolution (Promega Corporation, WI, USA) lysates were 1:32 and 1:16, respectively. The difference observed in sensitivity may be due to the use of different PCR and CE conditions for each lysate type (Table 2.1) and/or the differences in kit chemistry.

An evaluation of the reproducibility using repeated measurements for 20 lysate samples and two control DNA samples (9947A and 2800M) revealed 100 % concordance. This suggests that the DNA profiles obtained using the Investigator Argus X-12 QS kit (Qiagen, Hilden) are reliable.

Concordance testing between the autosomal locus, D21S11, included in the Investigator Argus X-12 QS kit (Qiagen, Hilden) and the Investigator 24plex GO! kit (Qiagen, Hilden) showed 99.59 % concordance. This illustrates that the inclusion of this locus within the Investigator Argus X-12 QS kit (Qiagen, Hilden) to avoid sample mix-up, as suggested by the manufacturers [67], is valid. Furthermore, the Investigator Argus X-12 QS kit (Qiagen, Hilden) and the ForenSeq™ DNA Signature Prep kit (Illumina, CA, USA) were fully concordant, except for six alleles (Appendix D). Similarly, Salvador *et al.* (2018) found 100 % concordance between these two workflows [106]. This indicates that the DNA profiles produced using the Investigator Argus X-12 QS kit (Qiagen, Hilden) are comparable to MPS workflows.

Overall, the internal validation of this study demonstrated that the Investigator Argus X-12 QS (Qiagen, Hilden) is sensitive and produces reliable results, making it appropriate for forensic use.

2.4.4. Population study

2.4.4.1. Shared haplotypes

The haplotypes of 517 males were evaluated. No shared haplotypes were observed when the full 12-loci haplotype definition was considered. This is interesting as the expectation of shared haplotypes increases when a large number of individuals are evaluated. Additionally, shared haplotypes have been observed in studies which utilised smaller sample sizes. For example, Curtis *et al.* (2022) investigated 298 Australian Aboriginal male individuals and found haplotype sharing between eight individuals [107].

Contrarily, the evaluation of three-loci haplotypes located at each linkage group showed haplotype sharing within the South African population (Appendix H). LG1 was identified as the most polymorphic (HD = 0.999, PIC = 0.997), while LG2 and LG3 were the least polymorphic (HD = 0.994, PIC = 0.992). A comparison to data generated for other African countries, namely Guinea-Bissau [108], Eritrea [109], Ethiopia [110] and Egypt [111], revealed that LG1 is consistently reported as the most diverse, while LG2 and LG3 were considered the least diverse in Eritrea and Ethiopia and Egypt, respectively. These trends were also observed in data generated globally for other populations [73,97,112,113]. Furthermore, 81.43 % (*n* = 421/517) of haplotypes identified at LG1 were unique for this South African cohort. This was the highest when compared to other reviewed literature [82,97,107,109,112]. Therefore, this indicates that LG1 is highly informative and of particular forensic interest, both locally and globally.

Together, these results illustrate the highly diverse nature of the South African population and suggest that X-STRs hold great discriminatory power within the population.

2.4.4.2. Forensic and population parameters

The individual population groups, namely African ancestry, European ancestry, Mixed ancestry and Indian/Asian ancestry were combined (*n* = 781) to evaluate the forensic

parameters of the 12 loci included in the Investigator Argus X-12 QS kit (Qiagen, Hilden) within a South African context. The results showed that locus DXS10135 was the most informative, while locus DXS7423 was the least informative (Table 2.3). These loci were also commonly reported as the most and least informative in many other population studies [97,101,106,107]. However, the number of unique alleles observed at locus DXS10135 (*n* = 53) was considerably higher in the South African population as opposed to the other populations. Loci DXS10148 and DXS10146 were also particularly informative within the South African population, with PIC values equivalent to 0.933 and 0.910, respectively. This may be due to the high number of novel alleles observed at these loci specifically. Lastly, the PIC value for all 12 loci was greater than 0.6, indicating a high level of polymorphism within this South African cohort.

Genetic comparisons between population groups revealed that all pairwise F_{ST} values were relatively low (Fig. 2.1). The greatest F_{ST} value (0.02301) was observed between the African ancestry and European ancestry population groups. According to Hartl and Clark (1997), an F_{ST} value between the range of 0.05 – 0.15 is considered to be "moderate" population differentiation [114]. Therefore, although there may be slight genetic variability between the population groups, the results suggest that sufficient gene flow between population groups has occurred to minimise the presence of any obvious intrapopulation substructure. This was supported by the AMOVA results, which showed that 98.96 % of the variability was within the population groups, while variability between population groups was only 1.04 % (F_{ST} = 0.01042; *p* = 0.00000). However, the significance indicated by the *p*-values should not be disregarded, suggesting these results should be interpreted with caution.

HWE was tested for the 12 loci using the genotypic data obtained from female individuals (*n* = 264). Deviations from HWE were identified at locus DXS10148, even after applying a Bonferroni correction (Appendix G). Deviations from HWE were also detected in other population studies. For example, Messaoudi *et al*., (2021) reported HWE deviations at loci DXS10135, DXS10074, DXS10148 and DXS10101 in the Saudi population and Tomas *et al*. (2012) reported a deviation from HWE at locus DXS10148 in the Somali population [82,83]. These deviations from HWE could be due to the use of insufficient sample size within this study, resulting in sampling error [82,114]. Alternatively, null alleles have previously been reported at locus DXS10148 in African other populations [83,111]. Therefore, the significantly

low observed heterozygosity may be due to the presence of null alleles at locus DXS10148 [83] within the South African population. This would cause genotyping errors and ultimately lead to the false assignment of homozygosity to a female individual. As such, sequencing of alleles at this locus in female individuals may be more informative for HWE testing.

2.4.4.3. Linkage disequilibrium

Significant LD was found between several loci pairs after Bonferroni correction (Appendix I). In both male and female individuals, LD was detected between loci pairs DXS10101-DXS10103 and DXS10134-DXS10146, which belong to LG3 and LG4, respectively. This was expected as these markers are physically linked due to their proximity to each other, reducing the occurrence of recombination. Additionally, LD between these two loci pairs was also reported in other population studies [97,107,115]. LD was also detected between loci pairs DXS10148-DXS10101, HPRTB-DXS10101 and DXS10101-DXS10134 in males and DXS10148-DXS10074 in females. However, these loci pairs are not located within the same linkage groups. LD between unlinked loci (*i.e.,* from different linkage groups) has also previously been reported in the aforementioned studies [97,107,115]. The maximum r^2 value of these loci pairs was evaluated in males and showed that all values were relatively low ($r^2 < 0.25$). This may suggest that an unintentional association between these loci pairs may be present, rather than true LD.

2.4.4.4. Off-ladder and null alleles

A total of 59 unique off-ladder alleles were identified across seven loci, namely DXS10148, DXS10134, DXS10135, DXS10146, DXS10101, DXS10074, DXS10079 and HPRTB (Appendix J). The majority of these alleles were identified at locus DXS10148 (n = 23), of which 11 had previously been reported in other populations, particularly those of African origin. For example, Gomes *et al.* (2017) detected alleles 35.1, 37.1, 39.1, 40.1, 41.1, 42.1, 43.1 and 44.1 in the Guinea-Bissau population [116], while Elakkary *et al.* (2014) detected alleles 36.1, 37.1, 39.1, 42.1 and 43.1 in the Egyptian population [111]. Samejima *et al.* (2012) and Bottinelli *et al.* (2022) detected allele 40.1 at relatively low frequencies in the Malay (f = 0.002) and Swiss (f = 0.0006) populations, respectively [117,118]. Additionally, Samejima *et al.* (2012) reported

this as the largest allele to be detected within an eastern Asian population at that time. This may suggest that alleles with larger repeat core motifs (*i.e.,* > 35), at locus DXS10148, are more frequently observed within African populations compared to the rest of the world.

Further investigation into the off-ladder alleles revealed that allele 36.2, located at locus DXS10146, was the most prevalent within the South African cohort, with a total of 20 observations. A review of the literature revealed that this allele was also reported in a few other populations, namely Switzerland [118], Eritrea [109] and a Cabo Verde immigrant population residing in Lisbon [113]. Additionally, null alleles at locus DXS10146 were detected in four male individuals included in this study. However, this was not unexpected as null alleles at loci DXS10146 and DXS10148 have previously been described [110,111].

In this study, 134 individuals had one off-ladder allele, 13 individuals had two off-ladder alleles and two individuals had three off-ladder alleles identified from their DNA profile. This high frequency of off-ladder alleles is yet another demonstration of the diversity within the South African population. Most of these observations were in individuals with African ancestry, followed by individuals with Mixed ancestry, while only a few observations were in individuals with European and Indian/Asian ancestry (Appendix J). This suggests that there is an underrepresentation of alleles observed in African populations for approximately half of the loci included in the Investigator Argus X-12 QS kit (Qiagen, Hilden), and highlights the need for the development of an allelic ladder with improved allele coverage, to provide accurate allele calling in populations with different genetic compositions.

A total of 31 off-ladder alleles detected in this study had not previously been reported, which suggests that these alleles are likely to be novel. As such, these alleles must be verified, especially those which were only detected in a single individual (Appendix J). The use of MPS can be implemented for this purpose. For example, at locus DXS10135, only four of the nine off-ladder alleles identified in this study were reported in previous studies [108,109,113,118], while the use of available MPS data was able to verify the presence of seven of these alleles within the South African population. However, this approach is only appropriate for novel alleles located at loci included within the currently available MPS kits. Therefore, Sanger sequencing can be performed as an alternative method of novel allele verification.

Lastly, null alleles were also observed at the Amelogenin locus in two males from the Indian/Asian ancestry population group and one male from the Mixed Ancestry population group, whereby the Y-chromosome was absent from the DNA profile. This aligns with the literature, which suggests that this anomaly occurs more frequently in Indian populations compared to African and European populations [3]. Due to the hemizygous nature of the X-chromosome in male individuals, it was still possible to discern the sex of the individual using their DNA profile. However, this may become challenging when investigating mixed profiles or unknown individuals with X-chromosomal aberrations *e.g.,* Turner's syndrome (X0). Therefore, it may be beneficial for manufacturers of the Investigator Argus X-12 QS kit (Qiagen, Hilden) to include an additional locus for sex determination [63].

2.4.5. Limitations and future expansion

Although the cohort utilised in this study was appropriate [3,77], future studies could investigate a larger sample size due to the diversity within South Africa. Additionally, as this study served as a baseline for X-STRs within the South African population, it would be beneficial for future studies to investigate the composition of X-STRs within each of the four major population groups. This is because South Africa harbours multiple distinct population groups and is an admixed population [119]. As such, authorities have previously opted to generate autosomal STR allele frequency data per population group. Therefore, the separation of X-STR frequencies and other statistical calculations per population group would be necessary to ensure the casework applicability of this data within South Africa. Furthermore, as there are multiple cultural subgroups within the African ancestry population group itself [120], further investigation of X-STRs within and between each of these subgroups may be forensically informative. Lastly, verification of novel and null alleles using sequencing is required and a larger internal validation study should be performed for the Investigator Argus X-12 QS kit (Qiagen, Hilden), in which specificity, mixture, inhibition and degradation studies are included and tested.

2.5. Conclusion

In this study, X-STR data were successfully produced for lysate samples belonging to 781 South African individuals, using the Investigator Argus X-12 QS kit (Qiagen, Hilden). To this end, the data generated are highly polymorphic and informative. Internal validation of the Investigator Argus X-12 QS kit (Qiagen, Hilden) showed the kit to be reliable and comparable to other workflows, such as MPS. Multiple novel and null alleles were identified, which require confirmation in future studies. Comparisons to X-STR literature available for both other African and global populations illustrated the diverse nature of the South African population, as well as the paucity of African continental representation within the Investigator Argus X-12 QS kit (Qiagen, Hilden). Overall, the use of this kit for forensic purposes in the South African population is appropriate and motivates the generation of a national X-STR database for the South African population groups.

References

[1] M.A. Jobling, P. Gill, Encoded evidence: DNA in forensic analysis, Nat. Rev. Genet. 5 (2004) 739–751. https://doi.org/doi:10.1038/nrg1455.

[2] R. Szibor, X-chromosomal markers: Past, present and future, Forensic Sci. Int. Genet. 1 (2007) 93–99. https://doi.org/doi:10.1016/j.fsigen.2007.03.003.

[3] J.M. Butler, Fundamentals of Forensic DNA Typing, Academic Press, USA, 2009.

[4] D. Hatsch, C. Keyser, R. Hienne, L. Bertrand, Resolving paternity relationships using X-chromosome STRs and Bayesian networks, J. Forensic Sci. 52 (2007) 895–897. https://doi.org/doi: 10.1111/j.1556-4029.2007.00483.x.

[5] N. Pinto, P. V. Silva, A. Amorim, A general method to assess the utility of the X-chromosomal markers in kinship testing, Forensic Sci. Int. Genet. 6 (2012) 198–207. https://doi.org/10.1016/j.fsigen.2011.04.014.

[6] R. Szibor, M. Krawczak, S. Hering, J. Edelmann, E. Kuhlisch, D. Krause, Use of X-linked markers for forensic purposes, Int. J. Legal Med. 117 (2003) 67–74. https://doi.org/10.1007/s00414-002-0352-5.

[7] C. Gomes, M. Magalhaes, C. Alves, A. Amorim, N. Pinto, L. Gusmao, Comparative evaluation of alternative batteries of genetic markers to complement autosomal STRs in kinship investigations: Autosomal indels vs. X-chromosome STRs, Int. J. Legal Med. 126 (2012) 917–921. https://doi.org/10.1007/s00414-012-0768-5.

[8] U. Toscanini, G. Berardi, A. Gómez, E. Raimondi, X-STRs analysis in paternity testing when the alleged father is related to the biological father, Forensic Sci. Int. Genet. Suppl. Ser. 2 (2009) 234–235. https://doi.org/doi:10.1016/j.fsigss.2009.08.150.

[9] T.M. Diegoli, Forensic typing of short tandem repeat markers on the X and Y chromosomes, Forensic Sci. Int. Genet. 18 (2015) 140–151. https://doi.org/https://doi.org/10.1016/j.fsigen.2015.03.013.

[10] L. Roewer, Y chromosome STR typing in crime casework, Forensic Sci. Med. Pathol. 5 (2009) 77–84. https://doi.org/10.1007/s12024-009-9089-5.

[11] B. Trombetta, E. D'Atanasio, F. Cruciani, Patterns of inter-chromosomal gene conversion on the male-specific region of the human Y chromosome, Front. Genet. 8 (2017) 1–7. https://doi.org/10.3389/fgene.2017.00054.

[12] R. Szibor, I. Plate, J. Edelmann, S. Hering, E. Kuhlisch, M. Michael, D. Krause, Chromosome X haplotyping in deficiency paternity testing principles and case report, Int. Congr. Ser. 1239 (2003) 815–820.

[13] I. Gomes, N. Pinto, S. Antão-Sousa, V. Gomes, L. Gusmão, A. Amorim, Twenty Years Later: A Comprehensive Review of the X Chromosome Use in Forensic Genetics, Front. Genet. 11 (2020) 1–17. https://doi.org/10.3389/fgene.2020.00926.

[14] C. Gomes, M. Magalhães, A. Amorim, C. Alves, N. Pinto, L. Gusmão, How useful is your X in discerning pedigrees?, Forensic Sci. Int. Genet. Suppl. Ser. 3 (2011) 161–162. https://doi.org/10.1016/j.fsigss.2011.08.081.

[15] N. Pinto, L. Gusmão, T. Egeland, A. Amorim, Paternity exclusion power: Comparative behaviour of autosomal and X-chromosomal markers in standard and deficient cases with inbreeding, Forensic Sci. Int. Genet. 7 (2013) 290–295. https://doi.org/10.1016/j.fsigen.2012.12.002.

[16] A. Trindade-Filho, S. Ferreira, S.F. Oliveira, Impact of a chromosome X STR Decaplex in deficiency paternity cases, Genet. Mol. Biol. 36 (2013) 507–510. https://doi.org/10.1590/S1415-47572013000400008.

[17] C. Tavares, S. Loiola, I. Pontes, D.A. Silva, E.F. Carvalho, A multiplex typing system composed of autosomal and X-chromosomal STR markers, Forensic Sci. Int. Genet. Suppl. Ser. 4 (2013) e288–e289. https://doi.org/10.1016/j.fsigss.2013.10.147.

[18] A. Shyla, S.R. Borovko, A.O. Tillmar, N.N. Kuzub, S.A. Kotova, I.S. Tsybovsky, K. Rębała, Belarusian experience of the use of FamLinkX for solving complex kinship cases involving X-STR markers, Forensic Sci. Int. Genet. Suppl. Ser. 5 (2015) e539–e541. https://doi.org/10.1016/j.fsigss.2015.09.213.

[19] S. Hering, J. Edelmann, S. Haas, N. Grasern, Paternity testing of two female siblings with Investigator Argus X-12 kit: A case with several rare mutation and recombination events, Forensic Sci. Int. Genet. Suppl. Ser. 5 (2015) e341–e343. https://doi.org/10.1016/j.fsigss.2015.09.135.

[20] E. Auler-Bittencourt, E.S.M. Iwamura, M.J.M. Lima, I.D.C.G. da Silva, S.E.B. dos Santos, Exploring the applicability of analysing X chromosome STRs in Brazilian admixed population, Sci. Justice. 55 (2015) 323–328. https://doi.org/10.1016/j.scijus.2015.03.004.

[21] Q.L. Liu, L. Xue, H. Zhao, D.J. Lu, A Case of Maternal Half-sisters Sharing Alleles at 18 X-chromosomal Short Tandem Repeat Loci, J. Forensic Sci. Med. 2 (2016) 115–118. https://doi.org/10.4103/2349-5014.184194.

[22] A.O. Tillmar, D. Kling, J.M. Butler, W. Parson, M. Prinz, P.M. Schneider, T. Egeland, L. Gusmão, DNA Commission of the International Society for Forensic Genetics (ISFG): Guidelines on the use of X-STRs in kinship analysis, Forensic Sci. Int. Genet. 29 (2017) 269–275. https://doi.org/10.1016/j.fsigen.2017.05.005.

[23] S. Palomo-Díez, Á. Esparza Arroyo, M. Tirado-Vizcaíno, J. Velasco Vázquez, A.M. López-Parra, C. Gomes, C. Baeza-Richer, E. Arroyo-Pardo, Kinship analysis and allelic dropout: a forensic approach on an archaeological case, Ann. Hum. Biol. 45 (2018) 365–368. https://doi.org/10.1080/03014460.2018.1484159.

[24] D. Kling, Curiosities of X chromosomal markers and haplotypes, Int. J. Legal Med. 132 (2018) 361–371. https://doi.org/10.1007/s00414-017-1612-8.

[25] M. Puiu, R. Parvanescu, A.F. Rogobete, A. Enache, R. Dumache, Advantages of chromosome X-STRS markers in solving a father-daughter paternity case with one mismatch on SE33 locus, Clin. Lab. 65 (2019) 1661–1667. https://doi.org/10.7754/Clin.Lab.2019.190207.

[26] J. Zhang, S. Hao, Y. Liu, L. Yuan, Identification of half-sisters from different mothers by autosomal and X chromosomal short tandem repeats: A case study, J. Forensic Sci.

Med. 7 (2021) 66–69. https://doi.org/10.4103/jfsm.jfsm_30_21.

[27] J. Edelmann, R. Lessig, M. Klintschar, R. Szibor, Advantages of X-chromosomal microsatellites in deficiency paternity testing: Presentation of cases, Int. Congr. Ser. 1261 (2004) 257–259. https://doi.org/10.1016/S0531-5131(03)01722-9.

[28] R. Szibor, S. Hering, E. Kuhlisch, I. Plate, S. Demberger, M. Krawczak, J. Edelmann, Haplotyping of STR cluster DXS6801-DXS6809-DXS6789 on Xq21 provides a powerful tool for kinship testing, Int. J. Legal Med. 119 (2005) 363–369. https://doi.org/10.1007/s00414-005-0550-z.

[29] C. Toni, S. Presciuttini, I. Spinetti, A. Rocchi, R. Domenici, Usefulness of X-chromosome markers in resolving relationships: Report of a court case involving presumed half sisters, Int. Congr. Ser. 1288 (2006) 301–303. https://doi.org/doi:10.1016/j.ics.2005.09.044.

[30] D. Silveira, F.F. Silva, P.R. Jesus, M.R. Whittle, Use of X-linked short tandem repeat loci in routine parentage casework, Transfusion. 47 (2007) 1050–1053. https://doi.org/10.1111/j.1537-2995.2007.01238.x.

[31] M. Krawczak, Kinship testing with X-chromosomal markers: Mathematical and statistical issues, Forensic Sci. Int. Genet. 1 (2007) 111–114. https://doi.org/10.1016/j.fsigen.2007.01.014.

[32] C. Bobillo, M. Marino, A. Sala, L. Gusmão, D. Corach, X-STRs: Relevance in complex kinship cases, Forensic Sci. Int. Genet. Suppl. Ser. 1 (2008) 496–498. https://doi.org/10.1016/j.fsigss.2007.10.080.

[33] W. Branicki, P. Wolańska-Nowak, A. Parys-Proszek, T. Kupiec, Application of the mentype ARGUS X-8 kit to forensic casework, Z Zagadnien Nauk Sadowych. 73 (2008) 53–64.

[34] A. Serra, A.M. Bento, M. Carvalho, L. Andrade, L. Batista, M.C. Oliveira, V. Lopes, F. Balsa, F. Corte-Real, M.J. Anjos, X-chromosome STR typing in deficiency paternity cases, Forensic Sci. Int. Genet. Suppl. Ser. 1 (2008) 162–163.

[35] J.J. Builes, A. Manrique, D. Aguirre, Y. Puerto, M.L. Bravo, L. Gusmão, Utility of Y- and X-STRs in the research of complex biological relationship, Forensic Sci. Int. Genet. Suppl. Ser. 2 (2009) 236–237. https://doi.org/10.1016/j.fsigss.2009.08.142.

[36] J. Aquino, C. Peixe, D. Silva, C. Tavares, E.F. de Carvalho, A X-chromosome STR hexaplex as a powerful tool in deficiency paternity cases, Forensic Sci. Int. Genet. Suppl. Ser. 2 (2009) 45–46. https://doi.org/10.1016/j.fsigss.2009.08.183.

[37] D.A. Silva, F.S.N. Manta, M. Desidério, C. Tavares, E.F. de Carvalho, Paternity testing involving human remains identification and putative half sister: Usefulness of an X-hexaplex STR markers, Forensic Sci. Int. Genet. Suppl. Ser. 2 (2009) 230–231. https://doi.org/10.1016/j.fsigss.2009.08.179.

[38] N. Pinto, L. Gusmão, A. Amorim, X-chromosome markers in kinship testing: A generalisation of the IBD approach identifying situations where their contribution is crucial, Forensic Sci. Int. Genet. 5 (2011) 27–32. https://doi.org/10.1016/j.fsigen.2010.01.011.

[39] H. Asamura, H. Sakai, K. Kobayashi, M. Ota, H. Fukushima, MiniX-STR multiplex system population study in Japan and application to degraded DNA analysis, Int. J. Legal Med. 120 (2006) 174–181. https://doi.org/10.1007/s00414-005-0074-6.

[40] A. Barbaro, P. Cormaci, A. Barbaro, X-STR typing for an identification casework, Int. Congr. Ser. 1288 (2006) 513–515. https://doi.org/doi:10.1016/j.ics.2005.09.035.

[41] M. Lancia, S. Severini, A. Coletti, G. Margiotta, M. Dobosz, E. Carnevali, Using X-chromosomal markers in rape investigation, Forensic Sci. Int. Genet. Suppl. Ser. 3 (2011) e55–e56. https://doi.org/10.1016/j.fsigss.2011.08.027.

[42] D. Schmidt, S. Hummel, B. Herrmann, Brief communication: Multiplex X/Y-PCR improves sex identification in aDNA analysis, Am. J. Phys. Anthropol. 121 (2003) 337–341. https://doi.org/10.1002/ajpa.10172.

[43] J. Votrubova, L. Saskova, J. Frolik, D. Vanek, DNA identification of a 10th century female skeleton from the Prague Castle belonging to a member of the Przemyslids Dynasty, Forensic Sci. Int. Genet. Suppl. Ser. 6 (2017) e135–e136. https://doi.org/10.1016/j.fsigss.2017.09.029.

[44] T.M. Diegoli, A. Linacre, M.D. Coble, A gonosomal marker multiplex to aid in mixture interpretation, Forensic Sci. Int. Genet. Suppl. Ser. 4 (2013) e184–e185. https://doi.org/10.1016/j.fsigss.2013.10.095.

[45] A. Spitzer, L. Elkayam Sapir, M. Amiel, What is she doing here? Klinefelter syndrome in forensic casework, Sci. Justice. 61 (2021) 443–448. https://doi.org/10.1016/j.scijus.2021.03.003.

[46] C. Gehrig, A. Teyssier, Validation of the Mentype® Argus X-UL kit, Int. Congr. Ser. 1288 (2006) 325–327. https://doi.org/10.1016/j.ics.2005.12.060.

[47] M. Scherer, M. König, M. Bussmann, A. Prochnow, R. Peist, Development and validation of the new Investigator® Argus X-12 QS Kit, Forensic Sci. Int. Genet. Suppl. Ser. 5 (2015) e256–e257. https://doi.org/10.1016/j.fsigss.2015.09.102.

[48] L. Gusmão, C. Alves, P. Sánchez-Diz, M.T. Zarrabeitia, M.A. Abovich, I. Aragón, B. Arce, G. Arrieta, E. Arroyo, I. Atmetlla, C. Baeza, M.C. Bobillo, L. Cainé, R. Campos, L. Caraballo, E. Carvalho, M. Carvalho, R.M.B. Cicarelli, D. Comas, D. Corach, M. Espinoza, M.R. Espinheira, F. Rendo, O. García, I. Gomes, A. González, A. Hernández, M. Hidalgo, P. Lozano, M. Malaghini, D. Manzanares, B. Martínez, J.A. Martins, K. Maxzud, I. Miguel, N. Modesti, M. Montesino, R. Ortiz, J.J. Pestano, M.F. Pinheiro, L. Prieto, E. Raimondi, J.A. Riancho, M.B. Rodríguez, I. Salgado, N. Salgueiro, J.J. Sánchez, S. Silva, U. Toscanini, C. Vidales, C. V. Silva, M.C. Villalobos, C. Vullo, I. Yurrebaso, A.I. Zubillaga, A. Carracedo, A. Amorim, Results of the GEP-ISFG collaborative study on an X-STR Decaplex, Forensic Sci. Int. Genet. Suppl. Ser. 1 (2008) 677–679. https://doi.org/10.1016/j.fsigss.2007.10.012.

[49] E. Prieto-Fernández, M. Baeta, C. Núñez, S. Jiménez-Moreno, M.M. de Pancorbo, A new 17 X-STR multiplex for forensic purposes, Forensic Sci. Int. Genet. Suppl. Ser. 5 (2015) e283–e285. https://doi.org/10.1016/j.fsigss.2015.09.112.

[50] T.M. Diegoli, M.D. Coble, Development and characterization of two mini-X

chromosomal short tandem repeat multiplexes, Forensic Sci. Int. Genet. 5 (2011) 415–421. https://doi.org/10.1016/j.fsigen.2010.08.019.

[51] R. Szibor, S. Hering, J. Edelmann, A new Web site compiling forensic chromosome X research is now online, Int. J. Legal Med. 120 (2006) 252–254. https://doi.org/10.1007/s00414-005-0029-y.

[52] J.A. Martins, B. Kawamura, A.E. Cardoso, M.R.B. Cicarelli, Brazilian genetic database of chromosome X, Mol. Biol. Rep. 41 (2014) 4077–4080. https://doi.org/10.1007/s11033-014-3277-4.

[53] D. Kling, B. Dell'Amico, A.O. Tillmar, FamLinkX - Implementation of a general model for likelihood computations for X-chromosomal marker data, Forensic Sci. Int. Genet. 17 (2015) 1–7. https://doi.org/10.1016/j.fsigen.2015.02.007.

[54] K.M. Reid, L.J. Martin, L.J. Heathfield, Bodies without names: A retrospective review of unidentified decedents at Salt River Mortuary, Cape Town, South Africa, 2010 - 2017, S. Afr. Med. J. 110 (2020) 223–228. https://doi.org/10.7196/SAMJ.2020.v110i3.14192.

[55] C. Cattaneo, D. Porta, D. De Angelis, D. Gibelli, P. Poppa, M. Grandi, Unidentified bodies and human remains: An Italian glimpse through a European problem, Forensic Sci. Int. 195 (2010) 167.e1-167.e6. https://doi.org/10.1016/j.forsciint.2009.11.008.

[56] C. Behera, P. Singh, P. Shukla, D.R. Bharti, R. Kaushik, N. Sharma, B.K. Mahapatra, K. Chauhan, S.K. Meher, A. Yadav, M. Tabin, S.K. Gupta, H. Singh, Development of the first DNA database and identification portal for identification of Unidentified bodies in India – UMID, Sci. Justice. 62 (2022) 110–116. https://doi.org/10.1016/j.scijus.2021.12.002.

[57] D. Mazzarelli, L. Milotta, L. Franceschetti, L. Maggioni, V.G. Merelli, P. Poppa, D. Porta, D. De Angelis, C. Cattaneo, Twenty-five years of unidentified bodies: an account from Milano, Italy, Int. J. Legal Med. 135 (2021) 1983–1991. https://doi.org/10.1007/s00414-021-02560-9.

[58] S. Hering, C. Augustin, J. Edelmann, M. Heidel, J. Dressler, H. Rodig, E. Kuhlisch, R. Szibor, DXS10079, DXS10074 and DXS10075 are STRs located within a 280-kb region of Xq12 and provide stable haplotypes useful for complex kinship cases, Int. J. Legal Med. 120 (2006) 337–345. https://doi.org/10.1007/s00414-005-0061-y.

[59] T. Hundertmark, S. Hering, J. Edelmann, C. Augustin, I. Plate, R. Szibor, The STR cluster DXS10148-DXS8378-DXS10135 provides a powerful tool for X-chromosomal haplotyping at Xp22, Int. J. Legal Med. 122 (2008) 489–492. https://doi.org/10.1007/s00414-008-0277-8.

[60] M. Nothnagel, R. Szibor, O. Vollrath, C. Augustin, J. Edelmann, M. Geppert, C. Alves, L. Gusmão, M. Vennemann, Y. Hou, U.D. Immel, S. Inturri, H. Luo, S. Lutz-Bonengel, C. Robino, L. Roewer, B. Rolf, J. Sanft, K.J. Shin, J.E. Sim, P. Wiegand, C. Winkler, M. Krawczak, S. Hering, Collaborative genetic mapping of 12 forensic short tandem repeat (STR) loci on the human X chromosome, Forensic Sci. Int. Genet. 6 (2012) 778–784. https://doi.org/10.1016/j.fsigen.2012.02.015.

[61] M. Nothnagel, R. Szibor, O. Vollrath, C. Augustin, J. Edelmann, L. Gusma, M. Vennemann, Y. Hou, M. Geppert, U. Immel, S. Inturri, H. Luo, S. Lutz-bonengel, C. Robino, L. Roewer, B. Rolf, J. Sanft, K. Shin, J. Eun, P. Wiegand, C. Winkler, M. Krawczak, S. Hering, Collaborative genetic mapping of 12 forensic short tandem repeat (STR) loci on the human X chromosome, Forensic Sci. Int. Genet. 6 (2012) 778–784. https://doi.org/10.1016/j.fsigen.2012.02.015.

[62] E. Acar, O. Bulbul, G. Rayimoglu, M.S. Shahzad, D. Argac, H. Altuncul, G. Filoglu, Optimization and validation studies of the Mentype® Argus X-8 kit for paternity cases, Forensic Sci. Int. Genet. Suppl. Ser. 2 (2009) 47–48. https://doi.org/10.1016/j.fsigss.2009.08.189.

[63] N. Siddique, A.A. Shahid, K. Sughra, Diversification of Pakistani amelogenin-Y-null male haplotypes, Scientifica (Cairo). 2021 (2021). https://doi.org/10.1155/2021/5521411.

[64] K. Sun, S. Zhao, H. Tian, S. Zhang, C. Li, Development of the 16 X-STR loci typing system and genetic analysis in a Shanghai Han population from China, Electrophoresis. 34 (2013) 3008–3015. https://doi.org/10.1002/elps.201300234.

[65] D. Becker, H. Rodig, C. Augustin, J. Edelmann, F. Götz, S. Hering, R. Szibor, W. Brabetz, Population genetic evaluation of eight X-chromosomal short tandem repeat loci using Mentype Argus X-8 PCR amplification kit, Forensic Sci. Int. Genet. 2 (2008) 69–74. https://doi.org/10.1016/j.fsigen.2007.08.013.

[66] Biotype, Mentype® Argus X-8 PCR Amplification Kit, (2009). http://www.biotype.de/fileadmin/user/MANUALS/Mentype_Argus_X-8_eng.pdf (accessed May 24, 2020).

[67] QIAGEN, Investigator Argus X-12 QS Handbook, Hilden, Germany, 2015. https://www.qiagen.com/us/resources/resourcedetail?id=d3ab4ec3-33ec-4be3-8a88-6b66ebebdcf0&lang=en.

[68] Y. Li, J. Zeng, Y. Fan, G. He, M. Xie, T. Gao, S. Wang, J. Wu, Genetic portrait and phylogenetic analysis of an Aksu Uyghur population based on the 19 X-STR system, Int. J. Legal Med. 133 (2019) 91–93. https://doi.org/https://doi.org/10.1007/s00414-018-1861-1.

[69] Z. Yang, C. Chen, J. Zhang, R. Tao, R. Xia, X. Zhang, J. Zhang, L. Yu, S. Zhang, C. Li, Genetic polymorphisms in 16 X-STR loci analyzed in the She population from Zhejiang Province, China, Leg. Med. 39 (2019) 25–28. https://doi.org/10.1016/j.legalmed.2019.06.002.

[70] S.H. R. Szibor, J. Edelmann, ChrX-STR.org 2.0, (2018). http://www.chrx-str.org/ (accessed February 27, 2022).

[71] S. Elakkary, S. Hoffmeister-Ullerich, C. Schulze, E. Seif, A. Sheta, S. Hering, J. Edelmann, C. Augustin, Genetic polymorphisms of twelve X-STRs of the investigator Argus X-12 kit and additional six X-STR centromere region loci in an Egyptian population sample, Forensic Sci. Int. Genet. 11 (2014) 26–30. https://doi.org/10.1016/j.fsigen.2014.02.007.

[72] S. Uchigasaki, J. Tie, D. Takahashi, Genetic analysis of twelve X-chromosomal STRs in Japanese and Chinese populations, Mol. Biol. Rep. 40 (2013) 3193–3196. https://doi.org/10.1007/s11033-012-2394-1.

[73] C. Bini, L.N. Riccardi, S. Ceccardi, F. Carano, S. Sarno, D. Luiselli, S. Pelotti, Expanding X-chromosomal forensic haplotype frequencies database: Italian population data of four linkage groups, Forensic Sci. Int. Genet. 15 (2015) 127–130. https://doi.org/10.1016/j.fsigen.2014.11.008.

[74] S. Willuweit, L. Roewer, Y chromosome haplotype reference database (YHRD): Update, Forensic Sci. Int. Genet. 1 (2007) 83–87. https://doi.org/10.1016/j.fsigen.2007.01.017.

[75] S. Willuweit, L. Roewer, The new y chromosome haplotype reference database, Forensic Sci. Int. Genet. 15 (2015) 43–48. https://doi.org/10.1016/j.fsigen.2014.11.024.

[76] W. Parson, A. Brandstätter, M. Pircher, M. Steinlechner, R. Scheithauer, EMPOP—the EDNAP mtDNA population database concept for a new generation, high-quality mtDNA database, Int. Congr. Ser. 1261 (2004) 106–108. https://doi.org/10.1016/S0531-5131(03)01629-7.

[77] Á. Carracedo, J.M. Butler, L. Gusmão, A. Linacre, W. Parson, L. Roewer, P.M. Schneider, New guidelines for the publication of genetic population data, Forensic Sci. Int. Genet. 7 (2013) 217–220. https://doi.org/http://dx.doi.org/10.1016/j.fsigen.2013.01.001.

[78] S. Tucci, J.M. Akey, The long walk to African genomics, Genome Biol. 20 (2019) 19–21. https://doi.org/10.1186/s13059-019-1740-1.

[79] H. Moreira, H. Costa, F. Tavares, L. Souto, Genetic variation of 12 X-chromosomal STR loci in an East Timor sample, Int. J. Legal Med. 129 (2015) 257–258. https://doi.org/10.1038/nrg1247.

[80] M. Messoussi, E. Prieto-Fernández, M. Baeta, C. Núñez, A.B.A. El Gaaied, M.M. de Pancorbo, K. Fadhlaoui-Zid, Genetic variation of 17 X-chromosome STR loci in Tunisian population of Nabeul, Int. J. Legal Med. 133 (2019) 85–88. https://doi.org/10.1007/s00414-018-1827-3.

[81] A. Sufian, M.I. Hosen, K. Fatema, T. Hossain, M.M. Hasan, A.K. Mazumder, S. Akhteruzzaman, Genetic diversity study on 12 X-STR loci of investigator® Argus X STR kit in Bangladeshi population, Int. J. Legal Med. 131 (2017) 963–965. https://doi.org/10.1007/s00414-016-1513-2.

[82] S.A. Messaoudi, S.R. Babu, A.B. Alsaleh, M. Albujja, N.R. Al-Snan, A.R. Chaudhary, A.C. Kassab, M. Assidi, Population genetic data for 12 X-STR loci in the Central Saudi region using investigator Argus X-12 amplification kit, Ann. Hum. Biol. 48 (2021) 321–326. https://doi.org/10.1080/03014460.2021.1957147.

[83] C. Tomas, V. Pereira, N. Morling, Analysis of 12 X-STRs in greenlanders, danes and somalis using argus X-12, Int. J. Legal Med. 126 (2012) 121–128. https://doi.org/10.1007/s00414-011-0609-y.

[84] P. Shrivastava, T. Jain, U. Gupta, V. Ben Trivedi, Genetic polymorphism study on 12 X STR loci of investigator Argus X STR kit in Bhil tribal population of Madhya Pradesh, India, Leg. Med. 17 (2015) 214–217. https://doi.org/10.1016/j.legalmed.2014.11.004.

[85] S. Kakkar, P. Shrivastava, V. Sahajpal, A. Sharma, N. Devi, S.P. Mandal, R.K. Kumawat, Genetic diversity of X-STR markers in Jat Sikh population of Punjab, India and its comparison with other 39 global populations, Ann. Hum. Biol. 47 (2020) 490–497. https://doi.org/10.1080/03014460.2020.1772876.

[86] A. Semikhodskii, Y. Krassotkin, T. Makarova, V. Zavarin, V. Ilina, D. Sutyagina, Genetic diversity and forensic parameters of 12 X-STR included in Argus X-12® marker panel in the population of the Russian Federation, Ann. Hum. Biol. 48 (2021) 430–436. https://doi.org/10.1080/03014460.2021.1980104.

[87] T.M. Diegoli, A. Linacre, P.M. Vallone, J.M. Butler, M.D. Coble, Allele frequency distribution of twelve X-chromosomal short tandem repeat markers in four U.S. population groups, Forensic Sci. Int. Genet. Suppl. Ser. 3 (2011) e481–e483. https://doi.org/10.1016/j.fsigss.2011.09.102.

[88] I. Gomes, C. Alves, K. Maxzud, R. Pereira, M.J. Prata, P. Sánchez-Diz, A. Carracedo, A. Amorim, L. Gusmão, Analysis of 10 X-STRs in three African populations, Forensic Sci. Int. Genet. 1 (2007) 208–211. https://doi.org/10.1016/j.fsigen.2007.01.001.

[89] I. Gomes, M. Prinz, R. Pereira, C. Meyers, R.S. Mikulasovich, A. Amorim, A. Carracedo, L. Gusmão, Genetic analysis of three US population groups using an X-chromosomal STR decaplex, Int. J. Legal Med. 121 (2007) 198–203. https://doi.org/10.1007/s00414-006-0146-2.

[90] S.H. Shin, J.S. Yu, S.W. Park, G.S. Min, K.W. Chung, Genetic analysis of 18 X-linked short tandem repeat markers in Korean population, Forensic Sci. Int. 147 (2005) 35–41. https://doi.org/10.1016/j.forsciint.2004.04.012.

[91] J. Edelmann, R. Lessig, A. Willenberg, R. Wildgrube, S. Hering, R. Szibor, Forensic validation of the X-chromosomal STR-markers GATA165B12, GATA164A09, DXS9908 and DXS7127 in German population, Int. Congr. Ser. 1288 (2006) 298–300. https://doi.org/10.1016/j.ics.2005.09.022.

[92] Qiagen, Investigator® Argus X-12 Handbook, 2015. https://www.qiagen.com/us/resources/download.aspx?id=d3ab4ec3-33ec-4be3-8a88-6b66ebebdcf0&lang=en.

[93] Statistics South Africa, Statisitcal Release P0302: Mid-year population estimates, 2022.

[94] QIAGEN, Direct amplification of FTA® and swab samples using the Investigator® Argus X-12 QS Kit, Hilden, Germany, 2016. https://www.qiagen.com/cn/resources/download.aspx?id=02c9a610-b412-44b2-9faa-1d85df7343e5&lang=en.

[95] Promega Corporation, SwabSolution™ Kit Technical Manual, Wisconsin, USA, 2016. https://worldwide.promega.com/resources/protocols/technical-manuals/101/swabsolution-kit-protocol/.

[96] QIAGEN, Investigator® Validation Guide, Hilden, Germany, 2015. https://www.qiagen.com/it/resources/resourcedetail?id=7b01fb65-b93a-4272-9a95-78a33430e899&lang=en.

[97] F. Guo, Population genetic data for 12 X-STR loci in the Northern Han Chinese and StatsX package as tools for population statistics on X-STR, Forensic Sci. Int. Genet. 26 (2017) e1–e8. https://doi.org/10.1016/j.fsigen.2016.10.012.

[98] Republic of South Africa, Recognition of Customary Marriages Act 120 of 1998, 1998. https://www.gov.za/documents/recognition-customary-marriages-act.

[99] K.M. Reid, L.J. Heathfield, Evaluation of direct PCR for routine DNA profiling of non-decomposed deceased individuals, Sci. Justice. 60 (2020) 567–572. https://doi.org/https://doi.org/10.1016/j.scijus.2020.08.004.

[100] R. Chakraborty, Sample Size Requirements for Addressing the Population Genetic Issues of Forensic Use of DNA Typing, Hum. Biol. 64 (1992) 141–159.

[101] J. Xing, A. Adnan, A. Rakha, K. Kasim, A. Noor, J. Xuan, X. Zhang, J. Yao, D. McNevin, B. Wang, Genetic analysis of 12 X-STRs for forensic purposes in Liaoning Manchu population from China, Gene. 683 (2019) 153–158. https://doi.org/10.1016/j.gene.2018.10.020.

[102] G. Mršić, P. Ozretić, J. Crnjac, S. Merkaš, V. Sukser, I. Račić, S. Rožić, L. Barbarić, M. Popović, M. Korolija, Expanded Croatian 12 X-STR loci database with an overview of anomalous profiles, Forensic Sci. Int. Genet. 34 (2018) 249–256. https://doi.org/10.1016/j.fsigen.2018.03.004.

[103] J. Crnjac, P. Ozretić, S. Merkaš, M. Ratko, M. Lozančić, M. Korolija, M. Popović, G. Mršić, Investigator argus X-12 study on the population of northern Croatia, Genet. Mol. Biol. 40 (2017) 80–83. https://doi.org/10.1590/1678-4685-GMB-2015-0261.

[104] G. Mršić, P. Ozretić, J. Crnjac, S. Merkaš, I. Račić, S. Rožić, V. Sukser, M. Popović, M. Korolija, Analysis of 12 X-STR loci in the population of south Croatia, Mol. Biol. Rep. 44 (2017) 183–189. https://doi.org/10.1007/s11033-017-4096-1.

[105] QIAGEN, Developmental validation of the Investigator® Argus X-12 QS Kit, Hilden, Germany, 2016. https://www.qiagen.com/us/resources/resourcedetail?id=0b830262-79c4-4746-925c-4f08328eb154&lang=en.

[106] J.M. Salvador, D.L.T. Apaga, F.C. Delfin, G.C. Calacal, S.E. Dennis, M.C.A. De Ungria, Filipino DNA variation at 12 X-chromosome short tandem repeat markers, Forensic Sci. Int. Genet. 36 (2018) e8–e12. https://doi.org/10.1016/j.fsigen.2018.06.008.

[107] R. Curtis, D. Ward, D. Taylor, J. Henry, Investigation of X-STR haplotype diversity in the Australian Aboriginal population, Aust. J. Forensic Sci. 00 (2022) 1–13. https://doi.org/10.1080/00450618.2022.2048690.

[108] I. Gomes, P.J.P. Pereira, S. Harms, A.M. Oliveira, P.M. Schneider, A. Brehm, Genetic characterization of Guinea-Bissau using a 12 X-chromosomal STR system: Inferences from a multiethnic population, Forensic Sci. Int. Genet. 31 (2017) 89–94. https://doi.org/10.1016/j.fsigen.2017.08.016.

[109] C. Bini, S. Sarno, E. Tangorra, A. Iuvaro, Y.G. Tseghereda, S. Pelotti, D. Luiselli, Haplotype data and forensic evaluation of 23 Y-STR and 12 X-STR loci in eight ethnic groups from Eritrea, Int. J. Legal Med. 135 (2021) 449–453.

[110] K. Haddish, E. Chierto, G. Di Vella, D. Lacerenza, S. Raddi, S. Aneli, A.L. Bogale, E. Kidane, A. Yizengaw, Y. Getaneh, G. Tewelemedhin, H.R.S. Kumar, C. Robino, A reference database of forensic autosomal and gonosomal STR markers in the Tigray population of Ethiopia, Forensic Sci. Int. Genet. 56 (2022) 102618. https://doi.org/10.1016/j.fsigen.2021.102618.

[111] S. Elakkary, S. Hoffmeister-Ullerich, C. Schulze, E. Seif, A. Sheta, S. Hering, J. Edelmann, C. Augustin, Genetic polymorphisms of twelve X-STRs of the investigator Argus X-12 kit and additional six X-STR centromere region loci in an Egyptian population sample, Forensic Sci. Int. Genet. 11 (2014) 26–30. https://doi.org/10.1016/j.fsigen.2014.02.007.

[112] A.O. Tillmar, Population genetic analysis of 12 X-STRs in Swedish population, Forensic Sci. Int. Genet. 6 (2012) e80–e81. https://doi.org/10.1016/j.fsigen.2011.07.008.

[113] H. Afonso Costa, P. Morais, C. Vieira Da Silva, S. Matos, R. Marques Santos, R. Espinheira, J. Costa Santos, A. Amorim, X-Chromosome STR markers data in a Cabo Verde immigrant population of Lisboa, Mol. Biol. Rep. 41 (2014) 2559–2569.

[114] D. Hartl, A. Clark, Principles of Population Genetics, 3rd ed., Sinauer Associates, Inc., Sunderland Massachusetts, 1997.

[115] A. Zidkova, P. Capek, A. Horinek, P. Coufalova, Investigator® Argus X-12 study on the population of Czech Republic: Comparison of linked and unlinked X-STRs for kinship analysis, Electrophoresis. 35 (2014) 1989–1992. https://doi.org/10.1002/elps.201400046.

[116] I. Gomes, P.J.P. Pereira, S. Harms, A.M. Oliveira, P.M. Schneider, A. Brehm, Genetic characterization of Guinea-Bissau using a 12 X-chromosomal STR system : Inferences from a multiethnic population, Forensic Sci. Int. Genet. 31 (2017) 89–94. https://doi.org/10.1016/j.fsigen.2017.08.016.

[117] M. Samejima, Y. Nakamura, P. Nambiar, K. Minaguchi, Genetic study of 12 X-STRs in Malay population living in and around Kuala Lumpur using Investigator Argus X-12 kit, Int. J. Legal Med. 126 (2012) 677–683.

[118] M. Bottinelli, A. Gouy, S. Utz, M. Zieger, Population genetic analysis of 12 X - chromosomal STRs in a Swiss sample, Int. J. Legal Med. 136 (2022) 561–563. https://doi.org/10.1007/s00414-021-02684-y.

[119] M. Lin, D.S. Park, N.A. Zaitlen, B.M. Henn, C.R. Gignoux, Admixed Populations Improve Power for Variant Discovery and Portability in Genome-Wide Association Studies, Front. Genet. 12 (2021) 1–11. https://doi.org/10.3389/fgene.2021.673167.

[120] B.G. Adams, F.J.R. Van de Vijver, G.P. De Bruin, Identity in South Africa: Examining self-descriptions across ethnic groups, Int. J. Intercult. Relations. 36 (2012) 377–388. https://doi.org/10.1016/j.ijintrel.2011.11.008.

[121] K.A. Tabbada, M.C.A. De Ungria, L.P. Faustino, D. Athanasiadou, B. Stradmann-

Bellinghausen, P.M. Schneider, Development of a pentaplex X-chromosomal short tandem repeat typing system and population genetic studies, Forensic Sci. Int. 154 (2005) 173–180. https://doi.org/10.1016/j.forsciint.2004.10.005.

[122] H. Li, H. Tang, Q. Zhang, Z. Jiao, J. Bai, S. Chang, A multiplex PCR for 4 X chromosome STR markers and population data from Beijing Han ethnic group, Leg. Med. 11 (2009) 248–250. https://doi.org/10.1016/j.legalmed.2009.03.013.

[123] M. Chen, H. Ren, Z. Liu, J. Zhao, C. Chen, Y. Shi, L. Jia, F. Cheng, T. Chen, Q. Fan, Y. Yang, Y. Liu, G. Zhang, J. Yan, Genetic polymorphisms and mutation rates of 16 X-STRs in a Han Chinese population of Beijing and application examples in second-degree kinship cases, Int. J. Legal Med. 134 (2020) 163–168. https://doi.org/10.1007/s00414-019-02047-8.

[124] J. Jia, X. Liu, Q. Fan, C. Fang, M. Wang, J. Zhang, W. Li, L. Shi, X. Zhang, C. Chen, Z. Yu, C. Li, K. Yun, J. Yan, Development and validation of a multiplex 19 X-chromosomal short tandem repeats typing system for forensic purposes, Sci. Rep. 11 (2021) 1–12. https://doi.org/10.1038/s41598-020-80414-x.

[125] Q.L. Liu, D.J. Lv, X.L. Wu, H.Y. Sun, X.Y. Wu, H.L. Lu, Development of a five ChX STRs loci typing system, Int. J. Legal Med. 122 (2008) 261–265. https://doi.org/10.1007/s00414-008-0223-9.

[126] H.B. Luo, Y. Ye, Y.Y. Wang, W.B. Liang, L.B. Yun, M. Liao, J. Yan, J. Wu, Y.B. Li, Y.P. Hou, Characteristics of eight X-STR loci for forensic purposes in the Chinese population, Int. J. Legal Med. 125 (2011) 127–131. https://doi.org/10.1007/s00414-009-0386-z.

[127] Y. Liu, Y. Ye, X.Q. Yi, J.H. Zhang, G.Y. Fan, D.Y. Hao, Phylogenetic analyses of the 19 STR loci in X chromosome revealed discriminant forensic characteristics for Chinese Daur and Oroqen minorities, Int. J. Legal Med. 136 (2022) 551–553. https://doi.org/10.1007/s00414-021-02697-7.

[128] P. Chen, G. He, X. Zou, M. Wang, H. Luo, L. Yu, X. Hu, M. Xia, H. Gao, J. Yu, Y. Hou, Y. Han, Genetic structure and polymorphisms of Gelao ethnicity residing in southwest china revealed by X-chromosomal genetic markers, Sci. Rep. 8 (2018) 1–13. https://doi.org/10.1038/s41598-018-32945-7.

[129] Q.L. Liu, D.J. Lu, X.G. Li, H. Zhao, J.M. Zhang, Y.K. Lai, Y.F. Chen, Development of the nine X-STR loci typing system and genetic analysis in three nationality populations from China, Int. J. Legal Med. 125 (2011) 51–58. https://doi.org/10.1007/s00414-010-0520-y.

[130] X.P. Zeng, Z. Ren, J.D. Chen, D.J. Lv, D.Y. Tong, H. Chen, H.Y. Sun, Genetic polymorphisms of twelve X-chromosomal STR loci in Chinese Han population from Guangdong Province, Forensic Sci. Int. Genet. 5 (2011) 114–116. https://doi.org/10.1016/j.fsigen.2011.03.005.

[131] X.P. Zeng, Z. Ren, X.J. Wu, X.L. Ou, D.Y. Tong, W.J. Chen, Y.M. Zhang, S.J. Liu, Y. Chen, H.Y. Sun, Development of a 12-plex X chromosomal STR loci typing system, Forensic Sci. Int. Genet. Suppl. Ser. 3 (2011) 365–366. https://doi.org/10.1016/j.fsigss.2011.09.044.

[132] C. Xiao, X. Yang, H. Liu, C. Liu, Z. Yu, L. Chen, C. Liu, Validation and forensic application of a new 19 X-STR loci multiplex system, Leg. Med. 53 (2021) 101957. https://doi.org/10.1016/j.legalmed.2021.101957.

[133] Q. Liu, H. Zhao, J. Chen, X.-G. Wang, D.-J. Lu, L. Quan, Development and population study of the 12 X-STR loci multiplexes PCR systems, Int. J. Legal Med. 126 (2012) 665–670. https://doi.org/10.1007/s00414-012-0676-8.

[134] Q.L. Liu, D.J. Lu, L. Quan, Y.F. Chen, M. Shen, H. Zhao, Development of multiplex PCR system with 15 X-STR loci and genetic analysis in three nationality populations from China, Electrophoresis. 33 (2012) 1299–1305. https://doi.org/10.1002/elps.201100558.

[135] Q.L. Liu, J.Z. Wang, L. Quan, H. Zhao, Y. Da Wu, X.L. Huang, D.J. Lu, Allele and Haplotype Diversity of 26 X-STR Loci in Four Nationality Populations from China, PLoS One. 8 (2013). https://doi.org/10.1371/journal.pone.0065570.

[136] Z. Ren, X.P. Zeng, L. Hong, S. Peng, Y. Chen, H.Y. Sun, The polymorphisms of 12 X-STR loci in six ethnic populations in China, Forensic Sci. Int. Genet. Suppl. Ser. 4 (2013) e49–e50. https://doi.org/10.1016/j.fsigss.2013.10.025.

[137] X. Yang, X. Zhang, J. Zhu, L. Chen, C. Liu, X. Feng, L. Chen, H. Wang, C. Liu, Genetic analysis of 19 X chromosome STR loci for forensic purposes in four Chinese ethnic groups, Sci. Rep. 7 (2017) 1–11. https://doi.org/10.1038/srep42782.

[138] Y.D. Zhang, C.M. Shen, H.T. Meng, Y.X. Guo, Q. Dong, G. Yang, J.W. Yan, Y.S. Liu, T. Mei, R.Z. Huang, B.F. Zhu, Allele and haplotype diversity of new multiplex of 19 ChrX-STR loci in Han population from Guanzhong region (China), Electrophoresis. 37 (2016) 1669–1675. https://doi.org/10.1002/elps.201500425.

[139] Z. Ren, J. Guo, G. He, H. Zhang, X. Zou, H. Zhang, Q. Wang, J. Ji, M. Yang, J. Zhang, Z. Zhang, Y. Nabijiang, J. Huang, C.C. Wang, Forensic genetic polymorphisms and population structure of the Guizhou Bouyei people based on 19 X-STR loci, Ann. Hum. Biol. 46 (2019) 574–580. https://doi.org/10.1080/03014460.2019.1697362.

[140] M. Yang, R. Zhang, X. Jin, Z. Ren, Q. Wang, W. Luo, Z. Ren, J. Xiong, X. Ma, Y. Wei, H. Zhang, J. Huang, Forensic characteristic of 19 X-STRs in Chuanqing, Tujia and Yi groups from Guizhou province and their genetic relationships with other reference populations, Gene Reports. 27 (2022) 101553. https://doi.org/10.1016/j.genrep.2022.101553.

[141] M. Yang, X. Jin, Z. Ren, Q. Wang, H. Zhang, H. Zhang, J. Chen, J. Ji, Y. Liu, J. Huang, X-chromosomal STRs for genetic composition analysis of Guizhou Dong group and its phylogenetic relationships with other reference populations, Ann. Hum. Biol. 48 (2021) 621–626. https://doi.org/10.1080/03014460.2021.2008001.

[142] P. Chen, G. He, X. Zou, M. Wang, F. Jia, H. Bai, J. Li, J. Yu, Y. Han, Forensic characterization and genetic polymorphisms of 19 X-chromosomal STRs in 1344 Han Chinese individuals and comprehensive population relationship analyses among 20 Chinese groups, PLoS One. 13 (2018). https://doi.org/10.1371/journal.pone.0204286.

[143] Y. Han, G. He, S. Gong, J. Chen, Z. Jiang, P. Chen, Genetic diversity and haplotype

analysis of Guizhou Miao identified with 19 X-chromosomal short tandem repeats, Int. J. Legal Med. 133 (2019) 99–101. https://doi.org/10.1007/s00414-018-1871-z.

[144] J. Guo, J. Ji, G. He, Z. Ren, H. Zhang, Q. Wang, M. Yang, Y. Nabijiang, Z. Zhang, J. Zhang, J. Huang, C.C. Wang, Genetic structure and forensic characterisation of 19 X-chromosomal STR loci in Guizhou Sui population, Ann. Hum. Biol. 46 (2019) 246–253. https://doi.org/10.1080/03014460.2019.1623911.

[145] L. Luo, H. Gao, L. Zhang, Y. Liu, L. Yao, F. Long, H. Zhang, Genetic diversity, forensic feature, and phylogenetic analysis of Guizhou Tujia population via 19 X-STRs, Mol. Genet. Genomic Med. (2020) 1–10. https://doi.org/10.1002/mgg3.1473.

[146] G. He, X. Zou, M. Wang, J. Liu, F. Wang, Y. Hou, Z. Wang, Population genetics, diversity, forensic characteristics of four Chinese populations inferred from X-chromosomal short tandem repeats, Leg. Med. 43 (2020) 101677. https://doi.org/10.1016/j.legalmed.2020.101677.

[147] S. Sun, Z. Yang, D. Wen, L. Lan, P. Xie, J. Xiao, G. Li, W. Zhu, L. Zha, Genetic polymorphism investigation of 16 X-STR loci in a Han population in Central South China, Forensic Sci. Int. Genet. 39 (2019) e21–e23. https://doi.org/10.1016/j.fsigen.2018.11.017.

[148] S. Zhang, Y. Bian, L. Li, K. Sun, Z. Wang, Q. Zhao, L. Zha, J. Cai, Y. Gao, C. Ji, C. Li, Population genetic study of 34 X-Chromosome markers in 5 main ethnic groups of China, Sci. Rep. 5 (2015) 1–8. https://doi.org/10.1038/srep17711.

[149] L. Liu, J. Yao, Y. Huang, L. Gao, J. Dai, X. Yuan, X. Zhang, S. Nie, L. Hu, Genetic polymorphisms of 16 X-STR loci in the Hani population from Southwest China, Forensic Sci. Res. 0 (2021) 1–6. https://doi.org/10.1080/20961790.2021.1877389.

[150] W.M. Tang, K.Y. To, Four X-chromosomal STRs and their allele frequencies in a Chinese population, Forensic Sci. Int. 162 (2006) 64–65. https://doi.org/10.1016/j.forsciint.2006.06.018.

[151] Y.S. Liu, H.T. Meng, T. Mei, L.P. Zhang, J.G. Chen, Y.D. Zhang, J. Chen, Y.X. Guo, Q. Dong, J.W. Yan, B.F. Zhu, Genetic diversity and haplotypic structure of Chinese Kazak ethnic group revealed by 19 STRs on the X chromosome, Gene. 600 (2017) 64–69. https://doi.org/10.1016/j.gene.2016.11.018.

[152] I. Gomes, A. Amorim, V. Pereira, A. Carracedo, L. Gusmão, Genetic patterns of 10 X chromosome short tandem repeats in an Asian population from Macau, Forensic Sci. Int. Genet. Suppl. Ser. 2 (2009) 402–404. https://doi.org/10.1016/j.fsigss.2009.09.009.

[153] R. Tao, J. Zhang, Y. Bian, R. Dong, X. Liu, C. Jin, R. Zhu, S. Zhang, C. Li, Investigation of 12 X-STR loci in Mongolian and Eastern Han populations of China with comparison to other populations, Sci. Rep. 8 (2018) 1–7. https://doi.org/10.1038/s41598-018-22665-3.

[154] M. Sun, Y.T. Zhang, X.N. Zhang, S.M. Fu, Y.M. Wu, Genetic polymorphisms of 12 X STR loci in Shaanxi Han population from China, Leg. Med. 26 (2017) 76–78. https://doi.org/10.1016/j.legalmed.2017.01.007.

[155] H.M. Gao, C. Wang, S.Y. Han, S.H. Sun, D.J. Xiao, Y.S. Wang, C.T. Li, M.X. Zhang, Analysis of the 19 Y-STR and 16 X-STR loci system in the Han population of Shandong province, China, Genet. Mol. Res. 16 (2017). https://doi.org/10.4238/gmr16019573.

[156] S.H. Zhang, C.T. Li, S.M. Zhao, L. Li, Genetic polymorphism of eight X-linked STRs of Mentype® Argus X-8 Kit in Chinese population from Shanghai, Forensic Sci. Int. Genet. 5 (2011) 2009–2012. https://doi.org/10.1016/j.fsigen.2009.10.010.

[157] S. Zhang, S. Zhao, R. Zhu, C. Li, Genetic polymorphisms of 12 X-STR for forensic purposes in Shanghai Han population from China, Mol. Biol. Rep. 39 (2012) 5705–5707. https://doi.org/10.1007/s11033-011-1379-9.

[158] Q. Yang, J. Qian, C. Shao, Y. Yao, Z. Zhou, H. Xu, Q. Tang, X. Qian, J. Xie, Identification and Characterization of Nine Novel X-Chromosomal Short Tandem Repeats on Xp21.1, Xq21.31, and Xq23 Regions, Front. Genet. 12 (2021). https://doi.org/10.3389/fgene.2021.784605.

[159] G. He, Y. Li, X. Zou, M. Wang, P. Chen, M. Liao, J. Wu, Genetic polymorphisms for 19 X-STR loci of Sichuan Han ethnicity and its comparison with Chinese populations, Leg. Med. 29 (2017) 6–12. https://doi.org/10.1016/j.legalmed.2017.09.001.

[160] G. He, Y. Li, X. Zou, Y. Zhang, H. Li, M. Wang, J. Wu, X-chromosomal STR-based genetic structure of sichuan tibetan minority ethnicity group and its relationships to various groups, Int. J. Legal Med. 132 (2018) 409–413. https://doi.org/10.1007/s00414-017-1672-9.

[161] Y. Zhang, Z. Yu, X. Mo, X. Zhao, W. Li, H. Liu, C. Liu, R. Wu, H. Sun, Development and validation of a new 18 X-STR typing assay for forensic applications, Electrophoresis. 42 (2021) 766–773. https://doi.org/10.1002/elps.202000168.

[162] C. Li, T. Ma, S. Zhao, S. Zhang, J. Xu, Z. Zhao, L. Jin, S. Li, Development of 11 X-STR loci typing system and genetic analysis in Tibetan and Northern Han populations from China, Int. J. Legal Med. 125 (2011) 753–756. https://doi.org/10.1007/s00414-011-0592-3.

[163] C. Deng, F. Song, J. Li, Y. Ye, L. Zhang, W. Liang, H. Luo, Y. Li, Forensic parameters of 19 X-STR polymorphisms in two Chinese populations, Int. J. Legal Med. 131 (2017) 975–977. https://doi.org/10.1007/s00414-017-1538-1.

[164] R. Tao, J. Zhang, R. Xia, Z. Yang, S. Wang, X. Zhang, Q. Yang, S. Zhang, C. Li, Genetic investigation and phylogenetic analysis of three Chinese ethnic groups using 16 X chromosome STR loci, Ann. Hum. Biol. 47 (2020) 59–64. https://doi.org/10.1080/03014460.2019.1704871.

[165] H.T. Meng, J.T. Han, Y.D. Zhang, W.J. Liu, T.J. Wang, J.W. Yan, J.F. Huang, W.A. Du, J.X. Guo, H.D. Wang, Y.H. Zhang, R.H. Zhou, B.F. Zhu, X. Wei, Diversity study of 12 X-chromosomal STR loci in Hui ethnic from China, Electrophoresis. 35 (2014) 2001–2007. https://doi.org/10.1002/elps.201400045.

[166] C. Li, S. Zhang, Z. Zhao, L. Li, Y. Liu, S. Zhao, Genetic analysis of the 11 X-STR loci in Uigur and Northern Han populations from China, Forensic Sci. Int. Genet. Suppl. Ser. 3 (2011) 423–424. https://doi.org/10.1016/j.fsigss.2011.09.073.

[167] H.T. Meng, C.M. Shen, Y.D. Zhang, Q. Dong, Y.X. Guo, G. Yang, J.W. Yan, Y.S. Liu, T. Mei, J.F. Shi, B.F. Zhu, Chinese Xibe population genetic composition according to linkage groups of X-chromosomal STRs: population genetic variability and interpopulation comparisons, Ann. Hum. Biol. 44 (2017) 546–553. https://doi.org/10.1080/03014460.2017.1318951.

[168] L. Chen, Y. Guo, C. Xiao, W. Wu, Q. Lan, Y. Fang, J. Chen, B. Zhu, Genetic polymorphisms and forensic efficiency of 19 X-chromosomal STR loci for Xinjiang Mongolian population, PeerJ. 6 (2018) 1–14. https://doi.org/10.7717/peerj.5117.

[169] C. Li, J. Xu, S. Zhao, S. Zhang, T. Ma, Z. Zhao, Y. Yang, L. Jin, S. Li, Genetic analysis of the 11 X-STR loci in Uigur population from China, Forensic Sci. Int. Genet. 6 (2012) e139–e140. https://doi.org/10.1016/j.fsigen.2012.02.008.

[170] Y. xin Guo, J. gang Chen, Y. Wang, J. wei Yan, J. Chen, T. hua Yao, L. ping Zhang, G. Yang, H. tian Meng, Y. dang Zhang, T. Mei, Y. shun Liu, Q. Dong, B. feng Zhu, Genetic polymorphism analyses of a novel panel of 19 X-STR loci in the Chinese Uygur ethnic minority, J. Zhejiang Univ. Sci. B. 17 (2016) 367–374. https://doi.org/10.1631/jzus.B1500228.

[171] X.N. Li, J.L. Zheng, J. Yao, M. Ding, H. Pang, B.J. Wang, Population data of 12 X-chromosome STR loci in Yanbian Korean samples from China, Forensic Sci. Int. Genet. 13 (2014) 143–144. https://doi.org/10.1016/j.fsigen.2014.07.012.

[172] G.L. He, Y. Li, X. Zou, P. Li, P.Y. Chen, F. Song, T. Gao, M. Liao, J. Yan, J. Wu, Forensic characteristics and phylogenetic analyses of the Chinese Yi population via 19 X-chromosomal STR loci, Int. J. Legal Med. 131 (2017) 1243–1246. https://doi.org/10.1007/s00414-017-1563-0.

[173] L. Qing, Y. Li, L. Liu, D. Chen, J. Han, Y. Shi, R. Huang, X. Zhang, Genetic polymorphism investigation of 16 X-STR loci in the Bai ethnic minority in Yunnan Province , Southwest China, Int. J. Legal Med. 136 (2022) 543–545.

[174] L. Liu, J. Yuan, L. Miao, R. Huang, X. Zhang, Genetic polymorphisms of 16 X-STR loci analyzed in the Han population of Yunnan Province , Southwest China, Leg. Med. 54 (2022) 101974. https://doi.org/10.1016/j.legalmed.2021.101974.

[175] X. Zhang, X. Yuan, Y. Huang, J. Yao, J. Zhang, J. Dai, L. Liu, S. Nie, L. Hu, Forensic genetic polymorphisms of 16 X-STR loci in the Yunnan Miao population and their relationship to other Chinese groups, Leg. Med. 53 (2021) 101961. https://doi.org/10.1016/j.legalmed.2021.101961.

[176] X.Y. Yang, W.W. Wu, L.L. Chen, C.H. Liu, X.F. Zhang, L. Chen, X.L. Feng, H.J. Wang, C. Liu, Development of the 19 X-STR loci multiplex system and genetic analysis of a Zhejiang Han population in China, Electrophoresis. 37 (2016) 2260–2272. https://doi.org/10.1002/elps.201500540.

[177] J. Zhang, Z. Yang, R. Tao, S. Zhang, C. Li, Genetic investigation of Chinese she ethnic based on autosomal STRs and X-STRs, Forensic Sci. Int. Genet. Suppl. Ser. 7 (2019) 38–40. https://doi.org/10.1016/j.fsigss.2019.09.017.

[178] Z. Yang, C. Chen, J. Zhang, R. Tao, R. Xia, X. Zhang, J. Zhang, L. Yu, S. Zhang, C. Li,

Genetic polymorphisms in 16 X-STR loci analyzed in the She population from Zhejiang Province, China, Leg. Med. 39 (2019) 25–28. https://doi.org/10.1016/j.legalmed.2019.06.002.

[179] C. Xiao, S. Li, X. Zhang, X. Yang, C. Liu, L. Chen, Population genetic analysis of Chinese Zhuang and Mulao minorities using AGCU-X19 STR kit, Int. J. Legal Med. 134 (2020) 501–503. https://doi.org/https://doi.org/10.1007/s00414-019-02004-5.

[180] S. Mukerjee, T. Ghosh, D. Kalpana, M. Mukherjee, A.K. Sharma, Genetic variation of 10 X chromosomal STR loci in Indian population, Int. J. Legal Med. 124 (2010) 327–330. https://doi.org/10.1007/s00414-010-0456-2.

[181] S. Mukerjee, M. Mukherjee, T. Ghosh, D. Kalpana, A.K. Sharma, Population genetic data for 11 X-STR loci in eleven populations of India, Leg. Med. 14 (2012) 163–165. https://doi.org/10.1016/j.legalmed.2012.01.004.

[182] L. Poulsen, M.S. Farzad, C. Børsting, C. Tomas, V. Pereira, N. Morling, Population and forensic data for three sets of forensic genetic markers in four ethnic groups from Iran: Persians, Lurs, Kurds and Azeris, Forensic Sci. Int. Genet. 17 (2015) 43–46. https://doi.org/10.1016/j.fsigen.2015.03.010.

[183] T. Fracasso, M. Schürenkamp, B. Brinkmann, C. Hohoff, An X-STR meiosis study in Kurds and Germans: Allele frequencies and mutation rates, Int. J. Legal Med. 122 (2008) 353–356. https://doi.org/10.1007/s00414-008-0231-9.

[184] L. Poulsen, C. Tomas, K. Drobnič, V. Ivanova, H.S. Mogensen, A. Kondili, P. Miniati, D. Bunokiene, J. Jankauskiene, V. Pereira, N. Morling, NGMSElect™ and Investigator® Argus X-12 analysis in population samples from Albania, Iraq, Lithuania, Slovenia, and Turkey, Forensic Sci. Int. Genet. 22 (2016) 110–112. https://doi.org/10.1016/j.fsigen.2016.02.004.

[185] H. Asamura, H. Sakai, M. Ota, H. Fukushima, Japanese population data for eight X-STR loci using two new quadruplex systems, Int. J. Legal Med. 120 (2006) 303–309. https://doi.org/10.1007/s00414-006-0103-0.

[186] M. Hashiyada, Y. Itakura, M. Funayama, Polymorphism of eight X-chromosomal STRs in a Japanese population, Forensic Sci. Int. Genet. Suppl. Ser. 1 (2008) 150–152. https://doi.org/10.1016/j.fsigss.2007.10.020.

[187] A. Tamura, H. Tsutsumi, M. Hara, A. Takada, K. Saito, K. Suzuki, T. Komuro, Genetic studies of eight X-STRs in a Japanese population, Leg. Med. 11 (2009) S451–S452. https://doi.org/10.1016/j.legalmed.2009.01.102.

[188] Y. Nakamura, K. Minaguchi, Sixteen X-chromosomal STRs in two octaplex PCRs in Japanese population and development of 15-locus multiplex PCR system, Int. J. Legal Med. 124 (2010) 405–414. https://doi.org/10.1007/s00414-010-0467-z.

[189] M. Fukuta, M.H. Gaballah, H. Kato, Y. Aoki, A simple method for calculating the likelihood ratio in a kinship test using X-chromosomal markers incorporating linkage, linkage disequilibrium, and mutation, Leg. Med. 32 (2018) 9–18. https://doi.org/10.1016/j.legalmed.2018.02.002.

[190] M. Samejima, Y. Nakamura, K. Minaguchi, Population genetic study of six closely

linked groups of X-STRs in a Japanese population, Int. J. Legal Med. 125 (2011) 895–900. https://doi.org/10.1007/s00414-011-0618-x.

[191] Y. Nakamura, M. Samejima, K. Tamaki, K. Minaguchi, Multiplex PCR for 18 X-chromosomal STRs in Japanese population, Leg. Med. 15 (2013) 164–170. https://doi.org/10.1016/j.legalmed.2012.10.006.

[192] T. Nishi, A. Kurosu, Y. Sugano, J. Kaminiwa, Y. Sekine, S. Yano, K. Honda, Application of a novel multiplex polymerase chain reaction system for 12 X-chromosomal short tandem repeats to a Japanese population study, Leg. Med. 15 (2013) 43–46. https://doi.org/10.1016/j.legalmed.2012.07.001.

[193] J. Tie, S. Uchigasaki, S. Oshida, Genetic polymorphisms of eight X-chromosomal STR loci in the population of Japanese, Forensic Sci. Int. Genet. 4 (2010) e105–e108. https://doi.org/10.1016/j.fsigen.2009.09.002.

[194] K.J. Shin, B.K. Kwon, S.S. Lee, J.E. Yoo, M.J. Park, U. Chung, H.Y. Lee, G.R. Han, J.H. Choi, C.Y. Kim, Five highly informative X-chromosomal STRs in Koreans, Int. J. Legal Med. 118 (2004) 37–40. https://doi.org/10.1007/s00414-003-0415-2.

[195] H.Y. Lee, M.J. Park, C.K. Jeong, S.Y. Lee, J.E. Yoo, U. Chung, J.H. Choi, C.Y. Kim, K.J. Shin, Genetic characteristics and population study of 4 X-chromosomal STRs in Koreans: Evidence for a null allele at DXS9898, Int. J. Legal Med. 118 (2004) 355–360. https://doi.org/10.1007/s00414-004-0456-1.

[196] S.Y. Yoo, N.S. Cho, S.W. Park, J.H. Hwang, J.N. Kim, K.W. Chung, M.S. Han, Genetic polymorphisms of eight X-STR loci of Mentype Argus X-8 kit in Koreans, Forensic Sci. Int. Genet. Suppl. Ser. 3 (2011) e33–e34. https://doi.org/10.1016/j.fsigss.2011.08.016.

[197] E.J. Lim, H.Y. Lee, J.E. Sim, W.I. Yang, K.J. Shin, Genetic polymorphism and haplotype analysis of 4 tightly linked X-STR duos in Koreans, Croat. Med. J. 50 (2009) 305–312. https://doi.org/10.3325/cmj.2009.50.305.

[198] J.E. Sim, H.Y. Lee, W.I. Yang, K.J. Shin, Population genetic study of four closely-linked X-STR trios in Koreans, Mol. Biol. Rep. 37 (2010) 333–337. https://doi.org/10.1007/s11033-009-9733-x.

[199] H.M. Hakim, H. Omar, K. Siti, A. Ismail, J. Lalung, A. Edward, M. Yusmaidie, A. Siddhartha, B.R. Nelson, G.K. Chambers, H.A. Edinur, Population data and genetic characteristics of 12 X - STR loci using the Investigator ® Argus X - 12 Quality Sensor kit for the Kedayan population of Borneo in Malaysia, Int. J. Legal Med. 135 (2021) 1433–1435. https://doi.org/10.1007/s00414-021-02577-0.

[200] M.A. Tariq, O. Ullah, S.A. Riazuddin, S. Riazuddin, Allele frequency distribution of 13 X-chromosomal STR loci in Pakistani population, Int. J. Legal Med. 122 (2008) 525–528. https://doi.org/10.1007/s00414-008-0263-1.

[201] M.A. Tariq, M.F. Sabir, S.A. Riazuddin, S. Riazuddin, Haplotype analysis of two X-chromosome STR clusters in the Pakistani population, Int. J. Legal Med. 123 (2009) 85–87. https://doi.org/10.1007/s00414-008-0294-7.

[202] M. Israr, A.A. Shahid, A. Rakha, M.S. Zar, M.S. Shahzad, Z. Rahman, T. Husnain,

Baluchi and Pakhtun population data of 9 X-chromosomal short tandem repeat loci, J. Forensic Leg. Med. 37 (2016) 45–49. https://doi.org/10.1016/j.jflm.2015.10.006.

[203] A. Nadeem, M.E. Babar, M. Hussain, M.A. Tahir, Development of pentaplex PCR and genetic analysis of X chromosomal STRs in Punjabi population of Pakistan, Mol. Biol. Rep. 36 (2009) 1671–1675. https://doi.org/10.1007/s11033-008-9367-4.

[204] M. Israr, A.A. Shahid, Z. Rahman, M.S. Zar, M.S. Shahzad, T. Husnain, C. Pfeifer, P. Wiegand, Development and characterization of a new 12-plex ChrX miniSTR system, Int. J. Legal Med. 128 (2014) 595–598. https://doi.org/10.1007/s00414-014-1009-x.

[205] N. Perera, G. Galhena, G. Ranawaka, Development of a 16 X-STR multiplex PCR system for kinship analysis and its applicability for the Sinhalese population in Sri Lanka, Int. J. Leg. 135 (2021) 161–166.

[206] N. Perera, G. Galhena, G. Ranawaka, X-chromosomal STR based genetic polymorphisms and demographic history of Sri Lankan ethnicities and their relationship with global populations, Sci. Rep. 11 (2021) 1–12. https://doi.org/10.1038/s41598-021-92314-9.

[207] D.P. Chen, C.P. Tseng, S.H. Tsai, M.C. Wang, S.C. Lu, T.L. Wu, P.Y. Chang, C.F. Sun, Use of X-linked short tandem repeats loci to confirm mutations in parentage caseworks, Clin. Chim. Acta. 408 (2009) 29–33. https://doi.org/10.1016/j.cca.2009.06.042.

[208] M.Y. Chen, C.W. Ho, C.E. Pu, F.C. Wu, Genetic polymorphisms of 12 X-chromosomal STR loci in Taiwanese individuals and likelihood ratio calculations applied to case studies of blood relationships, Electrophoresis. 35 (2014) 1912–1920. https://doi.org/10.1002/elps.201300645.

[209] J.C.I. Lee, C.Y. Lin, L.C. Tsai, Y.J. Yu, K.H. Liao, A. Linacre, H.M. Hsieh, Establishment of 11 linked X-STR loci within 1.1 Mb to assist with kinship testing, Int. J. Legal Med. 132 (2018) 967–973. https://doi.org/10.1007/s00414-017-1637-z.

[210] M.Y. Chen, C.E. Pu, Population data on the X chromosome short tandem repeat loci DXS10011, DXS101, DXS6789, DXS7132, DXS8377, and DXS9895 in Taiwan, Forensic Sci. Int. 146 (2004) 65–67. https://doi.org/10.1016/j.forsciint.2004.03.020.

[211] H.L. Hwa, Y.Y. Chang, J.C.I. Lee, H.Y. Yin, Y.H. Chen, L.H. Tseng, Y.N. Su, T.M. Ko, Thirteen X-chromosomal short tandem repeat loci multiplex data from Taiwanese, Int. J. Legal Med. 123 (2009) 263–269. https://doi.org/10.1007/s00414-008-0310-y.

[212] K. Vongpaisarnsin, A. Boonlert, K. Rasmeepaisarn, P. Dangkao, Genetic variation study of 12 X chromosomal STR in central Thailand population, Int. J. Legal Med. 130 (2016) 1497–1499. https://doi.org/10.1007/s00414-016-1363-y.

[213] S. Khacha-ananda, P. Mahawong, Genetic analysis of 12 X-short tandem repeats loci in a northern Thai population, Med. Sci. Law. 61 (2021) 34–43. https://doi.org/10.1177/0025802420965000.

[214] F. Aşicioğlu, F. Akyüz, K. Ozdilli, F. Oguz, M. Çarin, X-Chromosomal short tandem repeat loci in the Turkish population, African J. Biotechnol. 10 (2011) 4334–4338. https://doi.org/10.5897/AJB10.1975.

[215] M. Poetsch, D. Wassenaar, N. Von Wurmb-Schwark, Allele frequencies for 11 X chromosomal short tandem repeats in a population from Turkey, Int. J. Legal Med. 127 (2013) 913–914. https://doi.org/10.1007/s00414-013-0886-8.

[216] E. Acar, G. Filoglu, O. Bulbul, Polymorphism of 8 X-Chromosomal STR loci in Turkish population, Med. Sci. | Int. Med. J. 7 (2018) 1. https://doi.org/10.5455/medscience.2018.07.8778.

[217] E. Kalaoglu, M. Ay, A. Ulubay, H. Canan, A. Serin, B. Alper, Population data of 12 X-STRs in Turkey, Forensic Sci. Int. Genet. Suppl. Ser. 7 (2019) 632–634. https://doi.org/10.1016/j.fsigss.2019.10.118.

[218] M.A. Almarri, R.A. Lootah, Allelic and haplotype diversity of 12 X-STRs in the United Arab Emirates, Forensic Sci. Int. Genet. 33 (2018) e4–e6. https://doi.org/10.1016/j.fsigen.2017.12.013.

[219] K. Re˛bała, S.A. Kotova, V.I. Rybakova, T. V. Zabauskaya, A.A. Shyla, A.A. Spivak, I.S. Tsybovsky, Z. Szczerkowska, Variation of X-chromosomal microsatellites in Belarus within the context of their genetic diversity in Europe, Forensic Sci. Int. Genet. 16 (2015) 105–111. https://doi.org/10.1016/j.fsigen.2014.12.011.

[220] L. Cybulska, J. Wysocka, K. Rebała, E. Kapińska, A.I. Mikulich, I.S. Tsybovsky, D. Siváková, Z. Džupinková, Z. Szczerkowska, Polymorphism of four X-chromosomal STR loci in Belarusians and Slovaks, Forensic Sci. Int. Genet. Suppl. Ser. 1 (2008) 145–146. https://doi.org/10.1016/j.fsigss.2007.10.142.

[221] T.M. Diegoli, L. Kovacevic, N. Pojskic, M.D. Coble, D. Marjanovic, Population study of fourteen X chromosomal short tandem repeat loci in a population from Bosnia and Herzegovina, Forensic Sci. Int. Genet. 5 (2011) 350–351. https://doi.org/10.1016/j.fsigen.2010.01.007.

[222] B. Gršković, A. Zidkova, V. Stenzl, M. Popović, D. Primorac, G. Mršić, Analysis of 8 X-chromosomal markers in the population of central Croatia, Croat. Med. J. 54 (2013) 238–247. https://doi.org/10.3325/cmj.2013.54.238.

[223] J. Crnjac, P. Ozretić, S. Merkaš, M. Ratko, M. Lozanc, S. Roz, M. Korolija, M. Popovic, G. Mršic, D. Špoljaric, Analysis of 12 X-chromosomal markers in the population of central Croatia, Leg. Med. 21 (2016) 77–84. https://doi.org/10.1016/j.legalmed.2016.07.001.

[224] G. Mršić, P. Ozretić, J. Crnjac, S. Merkaš, V. Sukser, I. Račića, S. Rožić, L. Barbarić, M. Popović, M. Korolija, Expanded Croatian 12 X-STR loci database with an overview of anomalous profiles, Forensic Sci. Int. Genet. 34 (2018) 249–256. https://doi.org/10.1016/j.fsigen.2018.03.004.

[225] A. Zidkova, P. Capek, A. Horinek, P. Coufalova, Investigator® Argus X-12 study on the population of Czech Republic: Comparison of linked and unlinked X-STRs for kinship analysis, Electrophoresis. 35 (2014) 1989–1992. https://doi.org/10.1002/elps.201400046.

[226] A. Zidkova, P. Coufalova, P. Capek, X-STR decaplex study on the population of Czech Republic, Int. J. Legal Med. 128 (2014) 271–272. https://doi.org/10.1007/s00414-013-

0860-5.

[227] M. Hedman, J.U. Palo, A. Sajantila, X-STR diversity patterns in the Finnish and the Somali population, Forensic Sci. Int. Genet. 3 (2009) 173–178. https://doi.org/10.1016/j.fsigen.2009.02.005.

[228] D. Athanasiadou, B. Stradmann-Bellinghausen, C. Rittner, K.W. Alt, P.M. Schneider, Development of a quadruplex PCR system for the genetic analysis of X-chromosomal STR loci, Int. Congr. Ser. 1239 (2003) 311–314. https://doi.org/10.1016/S0531-5131(02)00479-X.

[229] J. Edelmann, R. Lessig, S. Hering, N. Brundirs, E. Kuhlisch, R. Szibor, Allele frequencies for X-chromosomal microsatellites in different populations, Int. Congr. Ser. 1261 (2004) 263–265. https://doi.org/10.1016/S0531-5131(03)01837-5.

[230] M. Poetsch, H. Petersmann, A. Repenning, E. Lignitz, Development of two pentaplex systems with X-chromosomal STR loci and their allele frequencies in a northeast German population, Forensic Sci. Int. 155 (2005) 71–76. https://doi.org/10.1016/j.forsciint.2004.11.016.

[231] J. Edelman, S. Hering, M. Michael, R. Lessig, D. Deischel, G. Meier-Sundhausen, L. Roewer, I. Plate, R. Szibor, 16 X-chromosome STR loci frequency data from a German population, Forensic Sci. Int. 124 (2001) 215–218. https://doi.org/10.1016/S0379-0738(01)00565-5.

[232] J. Edelmann, S. Hering, C. Augustin, S. Kalis, R. Szibor, Validation of six closely linked STRs located in the chromosome X centromere region, Int. J. Legal Med. 124 (2010) 83–87. https://doi.org/10.1007/s00414-009-0328-9.

[233] S. Tetzlaff, R. Wegener, I. Lindner, Population genetic investigation of eight X-chromosomal short tandem repeat loci from a northeast German sample, Forensic Sci. Int. Genet. 6 (2012) e155–e156. https://doi.org/10.1016/j.fsigen.2012.03.007.

[234] J. Edelmann, S. Lutz-Bonengel, J. Naue, S. Hering, X-chromosomal haplotype frequencies of four linkage groups using the Investigator Argus X-12 Kit, Forensic Sci. Int. Genet. 6 (2012) 24–34. https://doi.org/10.1016/j.fsigen.2011.01.001.

[235] S. Hering, A. Klimova, J. Edelmann, German population data for 18 X-STRs: a hexaplex PCR adding two clusters of X-STRs to the Argus X-12 set and expanding the German haplotype databases, Int. J. Legal Med. 134 (2020) 2061–2062. https://doi.org/10.1007/s00414-020-02306-z.

[236] H. Rodig, F. Kloep, L. Weißbach, C. Augustin, J. Edelmann, S. Hering, R. Szibor, F. Götz, W. Brabetz, Evaluation of seven X-chromosomal short tandem repeat loci located within the Xq26 region, Forensic Sci. Int. Genet. 4 (2010) 194–199. https://doi.org/10.1016/j.fsigen.2009.08.010.

[237] C. Tomas, I. Skitsa, E. Steinmeier, L. Poulsen, A. Ampati, C. Børsting, N. Morling, Results for five sets of forensic genetic markers studied in a Greek population sample, Forensic Sci. Int. Genet. 16 (2015) 132–137. https://doi.org/10.1016/j.fsigen.2015.01.001.

[238] A. Zalán, A. Völgyi, M. Jung, O. Peterman, H. Pamjav, Hungarian population data of

four X-linked markers: DXS8378, DXS7132, HPRTB, and DXS7423, Int. J. Legal Med. 121 (2007) 74–77. https://doi.org/10.1007/s00414-005-0051-0.

[239] A. Zalán, A. Völgyi, W. Brabetz, D. Schleinitz, H. Pamjav, Hungarian population data of eight X-linked markers in four linkage groups, Forensic Sci. Int. 175 (2008) 73–78. https://doi.org/10.1016/j.forsciint.2007.05.012.

[240] G. Horváth, A. Zalán, Z. Kis, H. Pamjav, A genetic study of 12 X-STR loci in the Hungarian population, Forensic Sci. Int. Genet. 6 (2012) 10–12. https://doi.org/10.1016/j.fsigen.2011.03.007.

[241] M. Gelabert-Besada, C. Alves, S. Ferreira, M. García-Magariños, L. Gusmão, P. Sánchez-Diz, Genetic characterization of Western Iberia using Mentype ® Argus X-8 kit, Forensic Sci. Int. Genet. 6 (2012) 2010–2012. https://doi.org/10.1016/j.fsigen.2011.02.008.

[242] C. Toni, S. Presciuttini, I. Spinetti, R. Domenici, Population data of four x-chromosome markers in Tuscany and their use in a deficiency paternity case, Forensic Sci. Int. 137 (2003) 215–216. https://doi.org/10.1016/j.forsciint.2003.07.004.

[243] G. Peloso, P. Grignani, C. Previderè, Allele distribution of five X-chromosome STR loci in an Italian population sample, Int. Congr. Ser. 1261 (2004) 260–262. https://doi.org/10.1016/S0531-5131(03)01814-4.

[244] C. Bini, S. Ceccardi, G. Ferri, S. Pelotti, M. Alù, E. Roncaglia, G. Beduschi, L. Caenazzo, E. Ponzano, P. Tasinato, C. Turchi, L. Buscemi, M. Mazzanti, A. Tagliabracci, C. Toni, I. Spinetti, R. Domenici, S. Presciuttini, Development of a heptaplex PCR system to analyse X-chromosome STR loci from five Italian population samples: A collaborative study, Forensic Sci. Int. 153 (2005) 231–236. https://doi.org/10.1016/j.forsciint.2005.05.013.

[245] N. Cerri, A. Verzeletti, F. Gasparini, B. Bandera, F. De Ferrari, Population data for four X-chromosomal STR loci in a population sample from Brescia (northern Italy), Int. Congr. Ser. 1288 (2006) 286–288. https://doi.org/10.1016/j.ics.2005.08.028.

[246] C. Robino, A. Giolitti, S. Gino, C. Torre, Development of two multiplex PCR systems for the analysis of 12 X-chromosomal STR loci in a northwestern Italian population sample, Int. J. Legal Med. 120 (2006) 315–318. https://doi.org/10.1007/s00414-006-0115-9.

[247] S. Turrina, R. Atzei, G. Filippini, D. De Leo, Development and forensic validation of a new multiplex PCR assay with 12 X-chromosomal short tandem repeats, Forensic Sci. Int. Genet. 1 (2007) 201–204. https://doi.org/10.1016/j.fsigen.2007.01.011.

[248] N. Cerri, A. Verzeletti, F. Gasparini, A. Poglio, E. Mazzeo, F. De Ferrari, Population data for 8 X-chromosome STR loci in a population sample from Northern Italy and from the Sardinia island, Forensic Sci. Int. Genet. Suppl. Ser. 1 (2008) 173–175. https://doi.org/10.1016/j.fsigss.2007.10.209.

[249] S. Massetti, E. Carnevali, M. Lancia, A. Coletti, M. Dobosz, M. Bacci, V. Argiolas, E. D'Aloja, Analysis of 8 STR of the X-chromosome in two Italian regions (Umbria and Sardinia), Forensic Sci. Int. Genet. Suppl. Ser. 1 (2008) 157–159.

https://doi.org/10.1016/j.fsigss.2007.10.022.

[250] A. Barbaro, P. Cormaci, S. Votano, A. Barbaro, Population data of 8 X-STRs in South Italy (Calabria) using the Mentype 1 Argus X-8 PCR Amplification Kit (Biotype), Forensic Sci. Int. Genet. 1 (2008) 135–139. https://doi.org/10.1016/j.fsigss.2007.10.109.

[251] S. Turrina, G. Filippini, D. De Leo, Genetic studies of eight X-STRs in a Northeast Italian population, Forensic Sci. Int. Genet. Suppl. Ser. 2 (2009) 396–397. https://doi.org/10.1016/j.fsigss.2009.08.146.

[252] S. Inturri, S. Menegon, A. Amoroso, C. Torre, C. Robino, Linkage and linkage disequilibrium analysis of X-STRs in Italian families, Forensic Sci. Int. Genet. 5 (2011) 152–154. https://doi.org/10.1016/j.fsigen.2010.10.012.

[253] S. Turrina, G. Filippini, D. De Leo, Population genetic evaluation of 12 X-chromosomal short tandem repeats of Investigator Argus X-12 kit in North-East Italy, Forensic Sci. Int. Genet. Suppl. Ser. 3 (2011) e327–e328. https://doi.org/10.1016/j.fsigss.2011.09.026.

[254] C. Bini, L.N. Riccardi, S. Ceccardi, F. Carano, S. Sarno, D. Luiselli, S. Pelotti, Expanding X-chromosomal forensic haplotype frequencies database: Italian population data of four linkage groups, Forensic Sci. Int. Genet. 15 (2015) 127–130. https://doi.org/10.1016/j.fsigen.2014.11.008.

[255] C. Robino, D. Lacerenza, S. Aneli, C. Di Gaetano, G. Matullo, R. Robledo, C. Calò, Allele and haplotype diversity of 12 X-STRs in Sardinia, Forensic Sci. Int. Genet. 33 (2018) e1–e3. https://doi.org/10.1016/j.fsigen.2017.12.002.

[256] M. Poetsch, A. Sabule, H. Petersmann, V. Volksone, E. Lignitz, Population data of 10 X-chromosomal loci in Latvia, Forensic Sci. Int. 157 (2006) 206–209. https://doi.org/10.1016/j.forsciint.2005.04.006.

[257] W. Pepinski, M. Skawronska, A. Niemcunowicz-Janica, E. Koc-Zorawska, J. Janica, I. Soltyszewski, Polymorphism of four X-chromosomal STRs in a Polish population sample, Forensic Sci. Int. 151 (2005) 93–95. https://doi.org/10.1016/j.forsciint.2004.09.079.

[258] M. Jêdrzejczyk, R. Jacewicz, J. Berent, Distribution of chromosome X str markers DXS10135 , DXS10074 , DXS10101 and DXS10134 and their usefulness in forensic genetics, Probl. Forensic Sci. LXXVII (2009) 89–97.

[259] S. Łuczak, U. Rogalla, B.A. Malyarchuk, T. Grzybowski, Diversity of 15 human X chromosome microsatellite loci in Polish population, Forensic Sci. Int. Genet. 5 (2011). https://doi.org/10.1016/j.fsigen.2010.12.009.

[260] W. Pepinski, A. Niemcunowicz-Janica, M. Skawronska, J.R. Janica, E. Koc-Zorawska, J. Janica, I. Soltyszewski, Polymorphism of four X-chromosomal STRs in a religious minority of Old Believers residing in northeastern Poland, Int. Congr. Ser. 1288 (2006) 307–309. https://doi.org/10.1016/j.ics.2005.08.031.

[261] D. Ruivo, T. Ribeiro, R. Espinheira, H. Geada, Use of eight X-chromosomal STRs in paternity investigation, Forensic Sci. Int. Genet. Suppl. Ser. 1 (2008) 522–524.

https://doi.org/10.1016/j.fsigss.2007.10.001.

[262] L. Cainé, R. Carvalho, S. Costa, M.F. Pereira, M.F. Pinheiro, Interest of X chromosome (Argus X-12 kit) in complex kinship analysis, Forensic Sci. Int. Genet. Suppl. Ser. 3 (2011) 206–207. https://doi.org/10.1016/j.fsigss.2011.08.103.

[263] L. Cainé, S. Costa, M.F. Pinheiro, Population data of 12 X-STR loci in a North of Portugal sample, Int. J. Legal Med. 127 (2013) 63–64. https://doi.org/10.1007/s00414-012-0672-z.

[264] J.C. Pinto, V. Pereira, S.L. Marques, A. Amorim, L. Alvarez, M.J. Prata, Mirandese language and genetic differentiation in Iberia: A study using X chromosome markers, Ann. Hum. Biol. 42 (2015) 20–25. https://doi.org/10.3109/03014460.2014.944215.

[265] R. Pereira, I. Gomes, A. Amorim, L. Gusmão, Genetic diversity of 10 X chromosome STRs in northern Portugal, Int. J. Legal Med. 121 (2007) 192–197. https://doi.org/10.1007/s00414-006-0144-4.

[266] L. Gusmão, P. Sánchez-Diz, C. Alves, I. Gomes, M.T. Zarrabeitia, M. Abovich, I. Atmetlla, C. Bobillo, L. Bravo, J. Builes, L. Cainé, R. Calvo, E. Carvalho, M. Carvalho, R. Cicarelli, L. Catelli, D. Corach, M. Espinoza, Ó. García, M. Malaghini, J. Martins, F. Pinheiro, M. João Porto, E. Raimondi, J.A. Riancho, A. Rodríguez, A. Rodríguez, B. Rodríguez Cardozo, V. Schneider, S. Silva, C. Tavares, U. Toscanini, C. Vullo, M. Whittle, I. Yurrebaso, Á. Carracedo, A. Amorim, A GEP-ISFG collaborative study on the optimization of an X-STR decaplex: Data on 15 Iberian and Latin American populations, Int. J. Legal Med. 123 (2009) 227–234. https://doi.org/10.1007/s00414-008-0309-4.

[267] K. V. Vagaitseva, V.N. Kharkov, K. V. Cherpinskaya, I.Y. Khitrinskaya, V.A. Stepanov, Genetic variability of X-linked STR markers in Siberian populations, Mol. Biol. 49 (2015) 267–274. https://doi.org/10.1134/S0026893315020132.

[268] I. Veselinović, G. Petrić, D. Vapa, M. Djan, N. Veličković, T. Veljović, Genetic analysis of 12 X-STR loci in the serbian population from Vojvodina province, Int. J. Legal Med. 132 (2018) 405–408. https://doi.org/10.1007/s00414-017-1677-4.

[269] M.T. Zarrabeitia, T. Amigo, C. Sañudo, A. Zarrabeitia, D. González-Lamuño, J.A. Riancho, A new pentaplex system to study short tandem repeat markers of forensic interest on X chromosome, Forensic Sci. Int. 129 (2002) 85–89. https://doi.org/10.1016/S0379-0738(02)00228-1.

[270] M.T. Zarrabeitia, A. Alonso, A. Zarrabeitia, A. Castro, I. Fernández, M. Martínez De Pancorbo, X-linked microsatellites in two Northern Spain populations, Forensic Sci. Int. 145 (2004) 57–59. https://doi.org/10.1016/j.forsciint.2004.02.025.

[271] M.T. Zarrabeitia, A. Alonso, J. Martin, M.A. Gonzalez-Gay, J.C. Martin-Escudero, M.M. De Pancorbo, P. Sanz, F. Ruiz-Cabello, J.A. Riancho, Study of six X-linked tetranucleotide microsatellites: Population data from five Spanish regions, Int. J. Legal Med. 120 (2006) 147–150. https://doi.org/10.1007/s00414-005-0057-7.

[272] M. Aler, P. Sánchez-Diz, I. Gomes, M. Gisbert, A. Carracedo, A. Amorim, L. Gusmão, Genetic data of 10 X-STRs in a Spanish population sample, Forensic Sci. Int. 173 (2007)

193–196. https://doi.org/10.1016/j.forsciint.2006.10.023.

[273] M.T. Zarrabeitia, F. Pinheiro, M.M. de Pancorbo, L. Cainé, S. Cardoso, L. Gusmão, J.A. Riancho, Analysis of 10 X-linked tetranucleotide markers in mixed and isolated populations, Forensic Sci. Int. Genet. 3 (2009) 63–66. https://doi.org/10.1016/j.fsigen.2008.10.001.

[274] M.J. Illescas, J.M. Aznar, S. Cardoso, A. López-Oceja, D. Gamarra, J.F. Sánchez-Romera, L. Colodro, J.R. Ordoñana, M.M. de Pancorbo, Genetic diversity of 10 X-STR markers in a sample population from the region of Murcia in Spain, Forensic Sci. Int. Genet. Suppl. Ser. 3 (2011) 437–438. https://doi.org/10.1016/j.fsigss.2011.09.080.

[275] B. García, M. Crespillo, M. Paredes, J.L. Valverde, Population data for 10 X-chromosome STRs from north-east of Spain, Forensic Sci. Int. Genet. 6 (2012) 19–21. https://doi.org/10.1016/j.fsigen.2010.12.010.

[276] M.J. Illescas, J.M. Aznar, S. Cardoso, A. López-Oceja, D. Gamarra, J.F. Sánchez-Romera, L. Colodro-Conde, J.R. Ordoñana, M.M. De Pancorbo, Genetic characterization of ten X-STRs in a population from the Spanish Levant, Forensic Sci. Int. Genet. 6 (2012) 180–181. https://doi.org/10.1016/j.fsigen.2012.06.010.

[277] M.J. Illescas, A. Pérez, J.M. Aznar, L. Valverde, S. Cardoso, J. Algorta, M.M. De Pancorbo, Population genetic data for 10 X-STR loci in autochthonous Basques from Navarre (Spain), Forensic Sci. Int. Genet. 6 (2012) 146–148. https://doi.org/10.1016/j.fsigen.2012.02.014.

[278] E. Prieto-Fernández, C. Núñez, M. Baeta, S. Jiménez-Moreno, B. Martínez-Jarreta, M.M. de Pancorbo, Forensic Spanish allele and haplotype database for a 17 X-STR panel, Forensic Sci. Int. Genet. 24 (2016) 120–123. https://doi.org/10.1016/j.fsigen.2016.06.016.

[279] J.M. Susana, G. Celia, L. Ester, B. Miriam, B. Eladio, M. de Pancorbo Marian, Genetic analysis of 12 X-chromosomal STRs an autochthonous population of Southeast Spain, Forensic Sci. Int. Genet. Suppl. Ser. 7 (2019) 482–484. https://doi.org/10.1016/j.fsigss.2019.10.060.

[280] A.O. Tillmar, P. Mostad, T. Egeland, B. Lindblom, G. Holmlund, K. Montelius, Analysis of linkage and linkage disequilibrium for eight X-STR markers, Forensic Sci. Int. Genet. 3 (2008) 37–41. https://doi.org/10.1016/j.fsigen.2008.09.006.

[281] C. Oguzturun, C.R. Thacker, D. Syndercombe Court, Population study of four X-chromosomal STR loci in the UK and Irish population, Int. Congr. Ser. 1288 (2006) 283–285. https://doi.org/10.1016/j.ics.2005.09.175.

[282] J. Santamaría, M.M. Álvarez-Álvarez, M.E. Esteban, E. Ramon-Gurrea, P. Moral, Dinucleotide (CA)n tandem repeats on the human X-chromosome and the history of the Mediterranean populations, Ann. Hum. Biol. 45 (2018) 72–76. https://doi.org/10.1080/03014460.2017.1414877.

[283] J.F. Ferragut, K. Bentayebi, J.A. Castro, C. Ramon, A. Picornell, Genetic analysis of 12 X-chromosome STRs in Western Mediterranean populations, Int. J. Legal Med. 129 (2015) 253–255. https://doi.org/10.1007/s00414-014-1071-4.

[284] J.F. Ferragut, K. Bentayebi, A. Barbaro, M. Ramírez, A.Y. Saguillo, C. Ramon, A. Picornell, Exploring the Western Mediterranean through X-chromosome, Int. J. Legal Med. 135 (2021) 787–790.

[285] M.G. García, C.I. Catanesi, G.A. Penacino, L. Gusmão, N. Pinto, X-chromosome data for 12 STRs : Towards an Argentinian database of forensic haplotype frequencies, Forensic Sci. Int. Genet. 41 (2019) e8–e13. https://doi.org/10.1016/j.fsigen.2019.04.005.

[286] G. Paula Di Santo Meztler, L.A. Glesmann, M.E. Esteban, S. Del Palacio, M.G. Méndez, C.I. Catanesi, Comparative study of 10 X-STR markers in populations of Northeast Argentina, Hum. Biol. 91 (2019) 9–20. https://doi.org/10.13110/humanbiology.91.1.02.

[287] G. Martinez, C. Schaller, P. Nazar, A. Brondani, N. Gomez, M. Bolea, B. Martinez-jarreta, X-chromosomal haplotype frequencies of four linkage groups in a population of Argentina, Forensic Sci. Int. Genet. Suppl. Ser. 5 (2015) e524–e526.

[288] J.F. Ferragut, M. Bassitta, V. Torrens, V. Albeza, N. Acreche, J.A. Castro, C. Ramon, A. Picornell, Analysis of 21 X-chromosome polymorphisms in urban and rural populations in Salta province (north-western Argentina), Int. J. Legal Med. 133 (2019) 1043–1047.

[289] U. Toscanini, L. Gusmão, G. Berardi, E. Raimondi, Genetic data of 10 X-STR in two Native American populations of Argentina, Forensic Sci. Int. Genet. Suppl. Ser. 2 (2009) 405–406. https://doi.org/10.1016/j.fsigss.2009.08.170.

[290] E.M. Ribeiro-Rodrigues, T.D.J.B.F. Palha, E.A. Bittencourt, Â. Ribeiro-Dos-Santos, S. Santos, Extensive survey of 12 X-STRs reveals genetic heterogeneity among Brazilian populations, Int. J. Legal Med. 125 (2011) 445–452. https://doi.org/10.1007/s00414-011-0561-x.

[291] L.M. Cainé, L. Pontes, D. Abrantes, G. Lima, F. Pinheiro, Genetic data of four X-chromosomal STRs in a population sample of Santa Catarina, Brazil, J. Forensic Sci. 52 (2007) 502–503. https://doi.org/10.1111/j.1556-4029.2007.00397.x.

[292] C.C. Tavares, L. Gusmão, C. Domingues, P. Domingues, D.A. Silva, J. Aquino, C. Peixe, A. Amorim, E.F. de Carvalho, Population data for six X-chromosome STR loci in a Rio de Janeiro (Brazil) sample: Usefulness in forensic casework, Forensic Sci. Int. Genet. Suppl. Ser. 1 (2008) 164–166. https://doi.org/10.1016/j.fsigss.2007.10.100.

[293] E.M. Ribeiro Rodrigues, F.P. das N. Leite, M.H. Hutz, T. de J.B.F. Palha, Â.K.C. Ribeiro dos Santos, S.E.B. dos Santos, A multiplex PCR for 11 X chromosome STR markers and population data from a Brazilian Amazon Region, Forensic Sci. Int. Genet. 2 (2008) 154–158. https://doi.org/10.1016/j.fsigen.2007.10.179.

[294] J.A. Martins, R.H.A. Silva, A. Freschi, G.G. Paneto, R.N. Oliveira, R.M.B. Cicarelli, Population genetic data of five X-chromosomal loci in Bauru (São Paulo, Brazil), Forensic Sci. Int. Genet. Suppl. Ser. 1 (2008) 155–156. https://doi.org/10.1016/j.fsigss.2007.08.011.

[295] J.A. Martins, J.C. Costa, G.G. Paneto, L. Gusmão, P. Sánchez-Diz, A. Carracedo, R.M.B.

Cicarelli, Genetic data of 10 X-chromosomal loci in Vitória population (Espírito Santo State, Brazil), Forensic Sci. Int. Genet. Suppl. Ser. 2 (2009) 394–395. https://doi.org/10.1016/j.fsigss.2009.08.174.

[296] F.P.N. Leite, S.E.B. Santos, E.M.R. Rodríguez, S.M. Callegari-Jacques, D.A. Demarchi, L.T. Tsuneto, M.L. Petzl-Erler, F.M. Salzano, M.H. Hutz, Linkage disequilibrium patterns and genetic structure of Amerindian and non-Amerindian Brazilian populations revealed by long-range X-STR markers, Am. J. Phys. Anthropol. 139 (2009) 404–412. https://doi.org/10.1002/ajpa.20998.

[297] I.H. Ferreira Da Silva, A.G. Barbosa, D.A. Azevedo, P. Sánchez-Diz, L. Gusmão, C.C. Tavares, E.F. Carvalho, L.A. Ferreira Da Silva, An X-chromosome pentaplex in two linkage groups: Haplotype data in Alagoas and Rio de Janeiro populations from Brazil, Forensic Sci. Int. Genet. 4 (2010). https://doi.org/10.1016/j.fsigen.2009.08.002.

[298] E.M.R. Rodrigues, T. de J.B.F. Palha, Â.K.C.R. dos Santos, S.E.B. dos Santos, Genetic data of twelve X-STRs in a Japanese immigrant population resident in Brazil, Forensic Sci. Int. Genet. 4 (2010) 2009–2010. https://doi.org/10.1016/j.fsigen.2009.05.004.

[299] L.M. Cainé, M.T. Zarrabeitia, J.A. Riancho, M.F. Pinheiro, Genetic data of a Brazilian population sample (Santa Catarina) using an X-STR decaplex, J. Forensic Leg. Med. 17 (2010) 272–274. https://doi.org/10.1016/j.jflm.2010.04.002.

[300] J.A. Martins, J.C. Costa, G.G. Paneto, R.F. Figueiredo, L. Gusmão, P. Sánchez-Diz, Á. Carracedo, R.M.B. Cicarelli, Genetic profile characterization of 10 X-STRs in four populations of the southeastern region of Brazil, Int. J. Legal Med. 124 (2010) 427–432. https://doi.org/10.1007/s00414-010-0478-9.

[301] L.S. Penna, F.G. Silva, P.H. Salim, G. Ewald, M. Jobim, J.A. De Azevedo Magalhães, L.F. Jobim, Development of two multiplex PCR systems for the analysis of 14 X-chromosomal STR loci in a southern Brazilian population sample, Int. J. Legal Med. 126 (2012) 327–330. https://doi.org/10.1007/s00414-011-0629-7.

[302] J.A. Martins, D.P. Martins, C.I.F. Oliveira-brancati, J. Martinez, R.M.B. Cicarelli, D.R.S. Souza, Genetic characterization of an X-STR decaplex system in the State of Mato Grosso , Brazil : distribution , forensic efficiency and population structure, Int. J. Legal Med. 131 (2017) 1523–1530. https://doi.org/10.1007/s00414-017-1578-6.

[303] J.J. Builes, L. Mendoza, A. Gaviria, A.K. Zambrano, N.D. Suarez, J.A. Gutierrez, A. Ibarra, J.D. Granda, A. Castillo, A.M. Gil, A.L. Pico, D.P. Aguirre, Genetic characterization of four Colombian populations using Investigator® Argus X-12 kit, Forensic Sci. Int. Genet. Suppl. Ser. 6 (2017) e263–e264. https://doi.org/10.1016/j.fsigss.2017.09.090.

[304] M. Lopez, A. Manrique, D.P. Aguirre, L. Mendoza, M.L.J. Bravo, M. Salgar, Y. Puerto, L. Gusmão, J.J. Builes, Genetic data of 10 X-STR in an Afro-descendant population sample of the Department of Chocó—Colombia, Forensic Sci. Int. Genet. Suppl. Ser. 5 (2015) e506–e507. https://doi.org/10.1016/j.fsigss.2015.09.200.

[305] B. Martínez, J.J. Builes, L. Gusmão, M. Manrique, D. Aguirre, Y. Puerto, L. Caraballo, M.L. Bravo, Genetic data of 10 X-STR in a Colombian population of Bolivar Department, Forensic Sci. Int. Genet. Suppl. Ser. 3 (2011) 59–60.

https://doi.org/10.1016/j.fsigss.2011.08.029.

[306] A. Pico, A. Castillo, C. Vargas, A. Amorim, L. Gusmão, Genetic profile characterization and segregation analysis of 10 X-STRs in a sample from Santander, Colombia, Int. J. Legal Med. 122 (2008) 347–351. https://doi.org/10.1007/s00414-007-0215-1.

[307] M. Baeta, C. Núñez, J.M. Aznar, C. Sosa, Y. Casalod, M. Bolea, F. González-Andrade, M.M. De Pancorbo, B. Martínez-Jarreta, Analysis of 10 X-STRs in three population groups from Ecuador, Forensic Sci. Int. Genet. 7 (2013) 19–20. https://doi.org/10.1016/j.fsigen.2012.08.004.

[308] A.K. Zambrano, G. Morejón, J. Galarza, V. Pastas, G. Castillo, M. Vela, A. Gaviria, Genetic data of an X-STR decaplex in Ecuadorian population (P), Forensic Sci. Int. Genet. Suppl. Ser. 5 (2015) e91–e92. https://doi.org/10.1016/j.fsigss.2015.09.037.

[309] A. Gaviria, L. Boada, C. Rodríguez-pólit, M. Vela, G. Fiallos, C. Gruezo, C. Paz-y-miño, A.K. Zambrano, Genetic polymorphisms of 12 X-STRs in the Ecuadorian population, Forensic Sci. Int. Genet. Suppl. Ser. 7 (2019) 677–679. https://doi.org/10.1016/j.fsigss.2019.10.135.

[310] A.K. Zambrano, M. Vaca-Pólit, L. Boada, M. Vela, C. Rodríguez-Pólit, G. Fiallos, C. Gruezo, C. Paz-y-Miño, A. Gaviria, X-STR decaplex study in the population of Imbabura-Ecuador, Forensic Sci. Int. Genet. Suppl. Ser. 7 (2019) 288–290. https://doi.org/10.1016/j.fsigss.2019.09.116.

[311] R. Flores-Espinoza, E. Paz-Cruz, V. Ruiz-Pozo, M. Lopez-Carrera, A. Cabrera-Andrade, L. Gusmao, G. Burgos, Investigating genetic diversity in admixed populations from Ecuador, Am. J. Phys. Anthropol. 176 (2021) 109–119. https://doi.org/10.1002/ajpa.24341.

[312] A. Gaviria, A.K. Zambrano, G. Morejon, V. Aguirre, M. Vela, J.J. Builes, G. Burgos, Genetic characterization of an X-STR decaplex on the population of Pichincha (Ecuador), Forensic Sci. Int. Genet. Suppl. Ser. 4 (2013) e144–e145. https://doi.org/10.1016/j.fsigss.2013.10.075.

[313] G.C. Iannacone, R. Parra, M. Bermejo, Y. Rojas, C. Valencia, L. Portugues, M. Medina, A.R. Vallejo, A. Prochanow, Peruvian genetic structure and their impact in the identification of Andean missing persons: A perspective from Ayacucho, Forensic Sci. Int. Genet. Suppl. Ser. 3 (2011) e291–e292. https://doi.org/10.1016/j.fsigss.2011.09.008.

[314] C. Barletta, J.J. Builes, M.L. Bravo, D. Aguirre, J. Descailleaux, L. Gusmão, Genetic data of 10 X-STRs in a population sample from Lima, Perú, Forensic Sci. Int. Genet. Suppl. Ser. 4 (2013) 168–169. https://doi.org/10.1016/j.fsigss.2013.10.087.

[315] C. Mariscal Ramos, G. Martínez-Cortes, B. Ramos-González, H. Rangel-Villalobos, Forensic parameters of the X-STR Decaplex system in Mexican populations, Leg. Med. 31 (2018) 38–41. https://doi.org/10.1016/j.legalmed.2017.12.013.

[316] I. Cortés-Trujillo, B. Ramos-González, O. Salas-Salas, F. Zuñiga-Chiquette, A. Zetina Hernández, G. Martínez-Cortés, M. Ruiz-Hernández, A. González-Martín, J.F. Ferragut, H. Rangel-Villalobos, Forensic efficiency parameters of the Investigator Argus X-12 kit

in women from two Mestizo and seven Amerindian populations from Mexico, Leg. Med. 26 (2017) 62–64. https://doi.org/10.1016/j.legalmed.2017.03.006.

[317] C. Núñez, M. Baeta, J.M. Aznar, C. Sosa, Y. Casalod, M. Bolea, M.M. De Pancorbo, B. Martínez Jarreta, Genetic diversity of 10 X chromosome STRs in an admixed population of Nicaragua, Forensic Sci. Int. Genet. 7 (2013) 95–96. https://doi.org/10.1016/j.fsigen.2013.02.008.

[318] M. Baeta, E. Prieto-fernández, C. Núñez, T. Kleinbielen, P. Villaescusa, L. Palencia-madrid, O. Alvarez-gila, B. Martínez-jarreta, M.M. De Pancorbo, Study of 17 X-STRs in Native American and Mestizo populations of Central America for forensic and population purposes, Int. J. Legal Med. 135 (2021) 1773–1776.

[319] M.J. Illescas, J.M. Aznar, A. Odriozola, D. Celorrio, M.M. De Pancorbo, X-STR admixture analysis of two populations of the Basque Diaspora in America, Forensic Sci. Int. Genet. Suppl. Ser. 3 (2011) e441–e442. https://doi.org/10.1016/j.fsigss.2011.09.082.

[320] T.M. Diegoli, A. Linacre, M.D. Coble, Population genetic data for 15 X chromosomal short tandem repeat markers in three U.S. populations, Forensic Sci. Int. Genet. 8 (2014) 64–67. https://doi.org/10.1016/j.fsigen.2013.07.008.

[321] A. Bekada, S. Benhamamouch, A. Boudjema, M. Fodil, S. Menegon, C. Torre, C. Robino, Analysis of 12 X-chromosomal STRs in an Algerian population sample, Forensic Sci. Int. Genet. Suppl. Ser. 2 (2009) 400–401. https://doi.org/10.1016/j.fsigss.2009.08.021.

[322] A. Bekada, S. Benhamamouch, A. Boudjema, M. Fodil, S. Menegon, C. Torre, C. Robino, Analysis of 21 X-chromosomal STRs in an Algerian population sample, Int. J. Legal Med. 124 (2010) 287–294.

[323] M. Poetsch, D. El-Mostaqim, F. Tschentscher, E.N.L. Browne, C. Timmann, R.D. Horstmann, N. Von Wurmb-Schwark, Allele frequencies of 11 X-chromosomal loci in a population sample from Ghana, Int. J. Legal Med. 123 (2009) 81–83. https://doi.org/10.1007/s00414-008-0251-5.

[324] K. Thiele, S. Löffler, J. Löffler, F. Günthner, K. Nitschke, J. Edelmann, R. Lessig, Population data of eight X-chromosomal STR markers in Ewe individuals from Ghana, Forensic Sci. Int. Genet. Suppl. Ser. 1 (2008) 167–169. https://doi.org/10.1016/j.fsigss.2007.10.059.

[325] S. Pasino, S. Caratti, M. Del Pero, A. Santovito, C. Torre, C. Robino, Allele and haplotype diversity of X-chromosomal STRs in Ivory Coast, Int. J. Legal Med. 125 (2011) 749–752. https://doi.org/10.1007/s00414-011-0591-4.

[326] K. Bentayebi, A. Picornell, M. Bouabdeallah, J.A. Castro, R. Aboukhalid, D. Squalli, M. Misericordia, S. Amzazi, Genetic diversity of 12 X-chromosomal short tandem repeats in the Moroccan population, Forensic Sci. Int. Genet. 6 (2012) e48–e49. https://doi.org/10.1016/j.fsigen.2011.03.008.

[327] A. Picornell, K. Bentayebi, M. Bouabdeallah, R. Aboukhalid, D. Squalli, J.A. Castro, M.M. Ramon, S. Amzazi, X-chromosomal haplotype frequencies of four linkage groups

in a North African population, Forensic Sci. Int. Genet. Suppl. Ser. 3 (2011) e19–e20. https://doi.org/10.1016/j.fsigss.2011.08.009.

[328] A. Laouina, J.M. Aznar, F. Chbel, M.M. De Pancorbo, Genetic data of X-chromosomal STRs in a Moroccan population sample (Casablanca) using an X-STR decaplex, Forensic Sci. Int. Genet. 7 (2013) 90–92. https://doi.org/10.1016/j.fsigen.2013.02.006.

[329] M. Poetsch, A. Knop, D. El-Mostaqim, N. Rakotomavo, N. Von Wurmb-Schwark, Allele frequencies of 11 X-chromosomal loci of two population samples from Africa, Int. J. Legal Med. 125 (2011) 307–314. https://doi.org/10.1007/s00414-010-0451-7.

[330] C. Gomes, A. Amorim, V.O. Okolie, S.O. Keshinro, A. Starke, C. Vullo, L. Gusmão, I. Gomes, Genetic insight into Nigerian population groups using an X-chromosome decaplex system, Forensic Sci. Int. Genet. Suppl. Ser. 7 (2019) 501–503. https://doi.org/10.1016/j.fsigss.2019.10.067.

[331] L. Lin, J. Li, Y. Hu, H. Wang, F.A. Marah, M. Moseray, A. Kureshi, C. Wang, M.M.J. Zeye, L. Zha, Genetic characterization of 19 X-STRs in Sierra Leone population from Freetown, Int. J. Legal Med. 134 (2020) 1659–1661. https://doi.org/10.1007/s00414-019-02243-6.

[332] D. Kling, B. Dell'Amico, P.J.T. Haddeland, A.O. Tillmar, Population genetic analysis of 12 X-STRs in a Somali population sample, Forensic Sci. Int. Genet. 11 (2014) e7–e8. https://doi.org/10.1016/j.fsigen.2014.02.013.

[333] I. Gomes, V. Pereira, V. Gomes, M.J. Prata, N. Pinto, A. Carracedo, A. Amorim, L. Gusmao, The Karimojong from Uganda: Genetic characterization using an X-STR decaplex system, Forensic Sci. Int. Genet. 3 (2009) e127–e128.

[334] J.F. Ferragut, J.A. Castro, C. Ramon, A. Picornell, Genetic diversity of 12 X-chromosomal short tandem repeats in Jewish populations, Forensic Sci. Int. Genet. Suppl. Ser. 5 (2015) e327–e329. https://doi.org/10.1016/j.fsigss.2015.09.130.

[335] J.F. Ferragut, K. Bentayebi, R. Pereira, J.A. Castro, A. Amorim, C. Ramon, A. Picornell, Genetic portrait of Jewish populations based on three sets of X-chromosome markers: Indels, Alu insertions and STRs, Forensic Sci. Int. Genet. 31 (2017) e5–e11. https://doi.org/10.1016/j.fsigen.2017.09.008.

[336] E. Prieto-Fernández, A. Díaz-de Usera, M. Baeta, C. Núñez, F. Chbel, S. Nadifi, K. Rouault, C. Férec, O. Hardiman, F. Pinheiro, M.M. de Pancorbo, A genetic overview of Atlantic coastal populations from Europe and North-West Africa based on a 17 X-STR panel, Forensic Sci. Int. Genet. 27 (2017) 167–171. https://doi.org/10.1016/j.fsigen.2016.11.011.

Appendices:

Appendix A:

Table A1 *List of all publications included within the systematic literature review.*

Objective	Authors	Title	Journal	Publication Year	Volume	Issue
X-STR applications	Schmidt, D., Hummel, S., Herrmann, B	Brief communication: Multiplex X/Y-PCR improves sex identification in aDNA analysis	American Journal of Physical Anthropology	2003	121	4
	Szibor, R., Plate, I., Edelmann, J., Hering, S., Kuhlisch, E., Michael, M., Krause, D.	Chromosome X haplotyping in deficiency paternity testing principles and case report	International Congress Series	2003	1239	
	Edelmann, J., Lessig, R., Klintschar, M., Szibor, R.	Advantages of X-chromosomal microsatellites in deficiency paternity testing: Presentation of cases	International Congress Series	2004	1261	
	Szibor, R., Hering, S., Kuhlisch, E., Plate, I., Demberger, S., Krawczak, M., Edelmann, J.	Haplotyping of STR cluster DXS6801-DXS6809-DXS6789 on Xq21 provides a powerful tool for kinship testing	International Journal of Legal Medicine	2005	199	6
	Toni, C., Presciuttini, S., Spinetti, I., Rocchi, A., Domenici, R.	Usefulness of X-chromosome markers in resolving relationships: Report of a court case involving presumed half sisters	International Congress Series	2006	1288	
	Asamura, H., Sakai, H., Kobayashi, K., Ota, M., Fukushima, H.	MiniX-STR multiplex system population study in Japan and application to degraded DNA analysis	International Journal of Legal Medicine	2006	120	3
	Barbaro, A., Cormaci, P., Barbaro, A.	X-STR typing for an identification casework	International Congress Series	2006	1288	
	Hatsch, D., Keyser, C., Hienne, R., Bertrand, L.	Resolving paternity relationships using X-chromosome STRs and Bayesian networks	Journal of Forensic Sciences	2007	52	4
	Krawczak, M.	Kinship testing with X-chromosomal markers: Mathematical and statistical issues	Forensic Science International: Genetics	2007	1	
	Silveira, Debora., Silva, F., Jesus, P., Whittle, M.	Use of X-linked short tandem repeat loci in routine parentage casework	Transfusion	2007	47	6
	Branicki, W., Wolańska-Nowak, P., Parys-Proszek, A., Kupiec, T.	Application of the mentype ARGUS X-8 kit to forensic casework	Problems of Forensic Sciences	2008	73	
	Serra, A., Bento, A. M., Carvalho, M., Andrade, L., Batista, L., Oliveira, M. C., Lopes, V., Balsa, F., Corte-Real, F., Anjos, M. J.	X-chromosome STR typing in deficiency paternity cases	Forensic Science International: Genetics Supplement Series	2008	1	
	Bobillo, C., Marino, M., Sala, A., Gusmão, L., Corach, D.	X-STRs: Relevance in complex kinship cases	Forensic Science International: Genetics Supplement Series	2008	1	

Objective	Authors	Title	Journal	Publication Year	Volume	Issue
X-STR applications	Builes, J. J., Manrique, A., Aguirre, D., Puerto, Y., Bravo, M. L., Gusmão, L.	Utility of Y- and X-STRs in the research of complex biological relationship	Forensic Science International: Genetics Supplement Series	2009	2	
	Aquino, J., Peixe, C., Silva, D., Tavares, C., de Carvalho, E.	A X-chromosome STR hexaplex as a powerful tool in deficiency paternity cases	Forensic Science International: Genetics Supplement Series	2009	2	
	Toscanini, U., Berardi, G., Gómez, A., Raimondi, E.	X-STRs analysis in paternity testing when the alleged father is related to the biological father	Forensic Science International: Genetics Supplement Series	2009	2	
	Silva, D., Manta, F., Desidério, M., Tavares, C., de Carvalho, E.	Paternity testing involving human remains identification and putative half sister: Usefulness of an X-hexaplex STR markers	Forensic Science International: Genetics Supplement Series	2009	2	
	Pinto, N., Gusmão, L., Amorim, A.	X-chromosome markers in kinship testing: A generalisation of the IBD approach identifying situations where their contribution is crucial	Forensic Science International: Genetics	2011	5	
	Lancia, M., Severini, S., Coletti, A., Margiotta, G., Dobosz, M., Carnevali, E.	Using X-chromosomal markers in rape investigation	Forensic Science International: Genetics Supplement Series	2011	3	
	Gomes, C., Magalhães, M., Amorim, A., Alves, C., Pinto, N., Gusmão, L.	How useful is your X in discerning pedigrees?	Forensic Science International: Genetics Supplement Series	2011	3	
	Gomes, C., Magalhaes, M., Alves, C., Amorim, A., Pinto, N., Gusmao, L.	Comparative evaluation of alternative batteries of genetic markers to complement autosomal STRs in kinship investigations: Autosomal indels vs. X-chromosome STRs	nternational Journal of Legal Medicine	2012	126	6
	Diegoli, T., Linacre, A., Coble, M.	A gonosomal marker multiplex to aid in mixture interpretation	Forensic Science International: Genetics Supplement Series	2013	4	
	Pinto, N., Gusmão, L., Egeland, T., Amorim, A.	Paternity exclusion power: Comparative behaviour of autosomal and X-chromosomal markers in standard and deficient cases with inbreeding	Forensic Science International: Genetics	2013	7	
	Trindade-Filho, A., Ferreira, S., Oliveira, S.	Impact of a chromosome X STR Decaplex in deficiency paternity cases	Genetics and Molecular Biology	2013	36	4
	Tavares, C., Loiola, S., Pontes, I., Silva, D. A., Carvalho, E. F.	A multiplex typing system composed of autosomal and X-chromosomal STR markers	Forensic Science International: Genetics Supplement Series	2013	4	
	Shyla, A., Borovko, S., Tillmar, A., Kuzub, N., Kotova, S., Tsybovsky, I., Rębała, K.	Belarusian experience of the use of FamLinkX for solving complex kinship cases involving X-STR markers	Forensic Science International: Genetics Supplement Series	2015	5	

Objective	Authors	Title	Journal	Publication Year	Volume	Issue
X-STR applications	Hering, S., Edelmann, J., Haas, S., Grasern, N.	Paternity testing of two female siblings with Investigator Argus X-12 kit: A case with several rare mutation and recombination events	Forensic Science International: Genetics Supplement Series	2015	5	
	Auler-Bittencourt, E., Iwamura, E., Lima, M., da Silva, I., dos Santos, S.	Exploring the applicability of analysing X chromosome STRs in Brazilian admixed population	Science and Justice	2015	55	5
	Liu, Q., Xue, L., Zhao, H., Lu, D.	A Case of Maternal Half-sisters Sharing Alleles at 18 X-chromosomal Short Tandem Repeat Loci	Journal of Forensic Science and Medicine	2016	2	2
	Votrubova, J., Saskova, L., Frolik, J., Vanek, D.	DNA identification of a 10th century female skeleton from the Prague Castle belonging to a member of the Przemyslids Dynasty	Forensic Science International: Genetics Supplement Series	2017	6	
	Tillmar, A., Kling, D., Butler, J., Parson, W., Prinz, M., Schneider, P., Egeland, T., Gusmão, L.	DNA Commission of the International Society for Forensic Genetics (ISFG): Guidelines on the use of X-STRs in kinship analysis	Forensic Science International: Genetics	2017	29	
	Palomo-Díez, S., Esparza Arroyo, Á., Tirado-Vizcaíno, M., Velasco Vázquez, J., López-Parra, A., Gomes, C., Baeza-Richer, C., Arroyo-Pardo, E.	Kinship analysis and allelic dropout: a forensic approach on an archaeological case	Annals of Human Biology	2018	45	4
	Kling, D.	Curiosities of X chromosomal markers and haplotypes	nternational Journal of Legal Medicine	2018	132	2
	Dumache, R., Puiu, M., Parvanescu, R., Rogobete, A., Enache, A.	Advantages of chromosome X-STRS markers in solving a father-daughter paternity case with one mismatch on SE33 locus	Clinical Laboratory	2019	65	9
	Spitzer, A., Sapir, L., Amiel, M.	What is she doing here? Klinefelter syndrome in forensic casework	Science and Justice	2021	61	4
	Zhang, J., Hao, S., Liu, Y., Yuan, L.	Identification of half-sisters from different mothers by autosomal and X chromosomal short tandem repeats: A case study	Journal of Forensic Science and Medicine	2021	7	2
X-STR kits	Gehrig, C., Teyssier, A.	Validation of the Mentype® Argus X-UL kit	International Congress Series	2006	1288	
	Gusmão, L., *et al.*	Results of the GEP-ISFG collaborative study on an X-STR Decaplex	Forensic Science International: Genetics Supplement Series	2008	1	
	Scherer, M., König, M., Bussmann, M., Prochnow, A., Peist, R.	Development and validation of the new Investigator® Argus X-12 QS Kit	Forensic Science International: Genetics Supplement Series	2015	5	
X-STR databases	Szibor, R., Hering, S., Edelmann, J.	A new Web site compiling forensic chromosome X research is now online	International Journal of Legal Medicine	2006	120	4

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X-STR databases	Martins, J., Kawamura, B., Cardoso, A., Cicarelli, M., Regina B.	Brazilian genetic database of chromosome X	Molecular Biology Reports	2014	41	
	Kling, D., Dell'Amico, B., Tillmar, A.	FamLinkX - Implementation of a general model for likelihood computations for X-chromosomal marker data	Forensic Science International: Genetics	2015	17	
X-STR population studies	Edelman, J., Hering, S., Michael, M., Lessig, R., Deischel, D., Meier-Sundhausen, G., Roewer, L., Plate, I., Szibor, R.	16 X-chromosome STR loci frequency data from a German population	Forensic Science International	2001	124	
	Zarrabeitia, M., Amigo, T., Sañudo, C., Zarrabeitia, A., González-Lamuño, D., Riancho, J.	A new pentaplex system to study short tandem repeat markers of forensic interest on X chromosome	Forensic Science International	2002	129	2
	Athanasiadou, D., Stradmann-Bellinghausen, B., Rittner, C., Alt, K. W., Schneider, P. M.	Development of a quadruplex PCR system for the genetic analysis of X-chromosomal STR loci	International Congress Series	2003	1239	
	Toni, C., Presciuttini, S., Spinetti, I., Domenici, R.	Population data of four x-chromosome markers in Tuscany and their use in a deficiency paternity case	Forensic Science International	2003	137	
	Shin, K., Kwon, B., Lee, S., Yoo, J., Park, M., Chung, U., Lee, H., Han, G., Choi, J., Kim, C.	Five highly informative X-chromosomal STRs in Koreans	International Journal of Legal Medicine	2004	118	
	Zarrabeitia, M. T., Alonso, A., Zarrabeitia, A., Castro, A., Fernández, I., Martínez De Pancorbo, M.	X-linked microsatellites in two Northern Spain populations	Forensic Science International	2004	145	
	Edelmann, J., Lessig, R., Hering, S., Brundirs, N., Kuhlisch, E., Szibor, R.	Allele frequencies for X-chromosomal microsatellites in different populations	International Congress Series	2004	1261	
	Chen, M., Pu, C	Population data on the X chromosome short tandem repeat loci DXS10011, DXS101, DXS6789, DXS7132, DXS8377, and DXS9895 in Taiwan	Forensic Science International	2004	146	
	Peloso, G., Grignani, P., Previderè, C.	Allele distribution of five X-chromosome STR loci in an Italian population sample	International Congress Series	2004	1261	
	Lee, H., Park, M., Jeong, C., Lee, S., Yoo, J., Chung, U., Choi, J., Kim, C., Shin, K.	Genetic characteristics and population study of 4 X-chromosomal STRs in Koreans: Evidence for a null allele at DXS9898	International Journal of Legal Medicine	2004	118	6
	Bini, C., Ceccardi, S., Ferri, G., Pelotti, S., Alù, M., Roncaglia, E., Beduschi, G., Caenazzo, L., Ponzano, E., Tasinato, P., Turchi, C., Buscemi, L., Mazzanti, M., Tagliabracci, A., Toni, C., Spinetti, I., Domenici, R., Presciuttini, S.	Development of a heptaplex PCR system to analyse X-chromosome STR loci from five Italian population samples: A collaborative study	Forensic Science International	2005	153	

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X-STR population studies	Poetsch, M., Petersmann, H., Repenning, A., Lignitz, E.	Development of two pentaplex systems with X-chromosomal STR loci and their allele frequencies in a northeast German population	Forensic Science International	2005	155	
	Pepinski, W., Skawronska, M., Niemcunowicz-Janica, A., Koc-Zorawska, E., Janica, J., Soltyszewski, I.	Polymorphism of four X-chromosomal STRs in a Polish population sample	Forensic Science International	2005	151	
	Shin, S., Yu, J., Park, S., Min, G., Chung, K.	Genetic analysis of 18 X-linked short tandem repeat markers in Korean population	Forensic Science International	2005	147	
	Tabbada, K., De Ungria, M., Faustino, L., Athanasiadou, D., Stradmann-Bellinghausen, B., Schneider, P.	Development of a pentaplex X-chromosomal short tandem repeat typing system and population genetic studies	Forensic Science International	2005	154	
	Zarrabeitia, M., Alonso, A., Martin, J., Gonzalez-Gay, M., Martin-Escudero, J. De Pancorbo, M., Sanz, P., Ruiz-Cabello, F., Riancho, J.	Study of six X-linked tetranucleotide microsatellites: Population data from five Spanish regions	International Journal of Legal Medicine	2006	120	
	Oguzturun, C., Thacker, C. R., Syndercombe Court, D.	Population study of four X-chromosomal STR loci in the UK and Irish population	International Congress Series	2006	1288	
	Pepinski, W., Niemcunowicz-Janica, A., Skawronska, M., Janica, J. R., Koc-Zorawska, E.,Janica, J., Soltyszewski, I.	Polymorphism of four X-chromosomal STRs in a religious minority of Old Believers residing in northeastern Poland	International Congress Series	2006	1288	
	Cerri, N., Verzeletti, A., Gasparini, F., Bandera, B., De Ferrari, F.	Population data for four X-chromosomal STR loci in a population sample from Brescia (northern Italy)	International Congress Series	2006	1288	
	Edelmann, J., Lessig, R., Willenberg, A., Wildgrube, R., Hering, S., Szibor, R.	Forensic validation of the X-chromosomal STR-markers GATA165B12, GATA164A09, DXS9908 and DXS7127 in German population	International Congress Series	2006	1288	
	Tang, W. M., To, K. Y.	Four X-chromosomal STRs and their allele frequencies in a Chinese population	Forensic Science International	2006	162	
	Asamura, H., Sakai, H., Kobayashi, K., Ota, M., Fukushima, H.	MiniX-STR multiplex system population study in Japan and application to degraded DNA analysis	International Journal of Legal Medicine	2006	120	
	Poetsch, M., Sabule, A., Petersmann, H., Volksone, V., Lignitz, E.	Population data of 10 X-chromosomal loci in Latvia	Forensic Science International	2006	157	
	Robino, C., Giolitti, A., Gino, S., Torre, C.	Development of two multiplex PCR systems for the analysis of 12 X-chromosomal STR loci in a northwestern Italian population sample	International Journal of Legal Medicine	2006	120	
	Asamura, H., Sakai, H., Ota, M., Fukushima, H.	Japanese population data for eight X-STR loci using two new quadruplex systems	International Journal of Legal Medicine	2006	120	

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X-STR population studies	Aler, M., Sánchez-Diz, P., Gomes, I., Gisbert, M., Carracedo, A., Amorim, A., Gusmão, L.	Genetic data of 10 X-STRs in a Spanish population sample	Forensic Science International	2007	173	
	Cainé, L., Pontes, L., Abrantes, D., Lima, G., Pinheiro, F.	Genetic data of four X-chromosomal STRs in a population sample of Santa Catarina, Brazil	Journal of Forensic Sciences	2007	52	2
	Gomes, I., Prinz, M., Pereira, R., Meyers, C., Mikulasovich, R., Amorim, A., Carracedo, A., Gusmão, L.	Genetic analysis of three US population groups using an X-chromosomal STR decaplex	International Journal of Legal Medicine	2007	121	
	Zalán, A., Völgyi, A., Jung, M., Peterman, O., Pamjav, H.	Hungarian population data of four X-linked markers: DXS8378, DXS7132, HPRTB, and DXS7423	International Journal of Legal Medicine	2007	121	
	Gomes, I., Alves, C., Maxzud, K., Pereira, R., Prata, M., Sánchez-Diz, P., Carracedo, A., Amorim, A., Gusmão, L.	Analysis of 10 X-STRs in three African populations	Forensic Science International: Genetics	2007	1	
	Pereira, R., Gomes, I., Amorim, A., Gusmão, L.	Genetic diversity of 10 X chromosome STRs in northern Portugal	International Journal of Legal Medicine	2007	121	
	Turrina, S., Atzei, R., Filippini, G., De Leo, D.	Development and forensic validation of a new multiplex PCR assay with 12 X-chromosomal short tandem repeats	Forensic Science International: Genetics	2007	1	
	Cerri, N., Verzeletti, A., Gasparini, F., Poglio, A., Mazzeo, E., De Ferrari, F.	Population data for 8 X-chromosome STR loci in a population sample from Northern Italy and from the Sardinia island	Forensic Science International: Genetics Supplement Series	2008	1	
	Massetti, S., Carnevali, E., Lancia, M., Coletti, A., Dobosz, M., Bacci, M., Argiolas, V., D'Aloja, E.	Analysis of 8 STR of the X-chromosome in two Italian regions (Umbria and Sardinia)	Forensic Science International: Genetics Supplement Series	2008	1	
	Tavares, C., Gusmão, L., Domingues, C., Domingues, P., Silva, D., Aquino, J., Peixe, C., Amorim, A., de Carvalho, E.	Population data for six X-chromosome STR loci in a Rio de Janeiro (Brazil) sample: Usefulness in forensic casework	Forensic Science International: Genetics Supplement Series	2008	1	
	Ribeiro Rodrigues, E., Leite, F., Hutz, M., Palha, T., Ribeiro dos Santos, Â., dos Santos, S.	A multiplex PCR for 11 X chromosome STR markers and population data from a Brazilian Amazon Region	Forensic Science International: Genetics	2008	2	
	Thiele, K., Löffler, S., Löffler, J., Günthner, F., Nitschke, K., Edelmann, J., Lessig, R.	Population data of eight X-chromosomal STR markers in Ewe individuals from Ghana	Forensic Science International: Genetics Supplement Series	2008	1	
	Tariq, M., Ullah, O., Riazuddin, S., Riazuddin, S.	Allele frequency distribution of 13 X-chromosomal STR loci in Pakistani population	International Journal of Legal Medicine	2008	122	
	Fracasso, T., Schürenkamp, M., Brinkmann, B., Hohoff, C.	An X-STR meiosis study in Kurds and Germans: Allele frequencies and mutation rates	International Journal of Legal Medicine	2008	122	

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X-STR population data	Ruivo, D., Ribeiro, T., Espinheira, R., Geada, H.	Use of eight X-chromosomal STRs in paternity investigation	Forensic Science International: Genetics Supplement Series	2008	1	
	Tillmar, A., Mostad, P., Egeland, T., Lindblom, B., Holmlund, G., Montelius, K.	Analysis of linkage and linkage disequilibrium for eight X-STR markers	Forensic Science International: Genetics	2008	3	
	Branicki, W., Wolańska-Nowak, P., Parys-Proszek, A., Kupiec, T.	Application of the mentype ARGUS X-8 kit to forensic casework	Problems of Forensic Sciences	2008	73	
	Liu, Q., Lv, D., Wu, X., Sun, H., Wu, X., Lu, H.	Development of a five ChX STRs loci typing system	International Journal of Legal Medicine	2008	122	
	Zalán, A., Völgyi, A., Brabetz, W., Schleinitz, D., Pamjav, H.	Hungarian population data of eight X-linked markers in four linkage groups	Forensic Science International	2008	175	
	Hashiyada, M., Itakura, Y., Funayama, M.	Polymorphism of eight X-chromosomal STRs in a Japanese population	Forensic Science International: Genetics Supplement Series	2008	1	
	Cybulska, L., Wysocka, J., Rebała, K., Kapińska, E., Mikulich, A., Tsybovsky, I., Siváková, D., Džupinková, Z., Szczerkowska, Z.	Polymorphism of four X-chromosomal STR loci in Belarusians and Slovaks	Forensic Science International: Genetics Supplement Series	2008	1	
	Barbaro, A., Cormaci, P., Votano, S., Barbaro, A.	Population data of 8 X-STRs in South Italy (Calabria) using the Mentype 1 Argus X-8 PCR Amplification Kit (Biotype)	Forensic Science International: Genetics	2008	1	
	Martins, J. A., Silva, R. H.A., Freschi, A., Paneto, G. G., Oliveira, R. N., Cicarelli, R. M.B.	Population genetic data of five X-chromosomal loci in Bauru (São Paulo, Brazil)	Forensic Science International: Genetics Supplement Series	2008	1	
	Becker, D., Rodig, H., Augustin, C., Edelmann, J., Götz, F., Hering, S., Szibor, R., Brabetz, W.	Population genetic evaluation of eight X-chromosomal short tandem repeat loci using Mentype Argus X-8 PCR amplification kit	Forensic Science International: Genetics	2008	2	
	Pico, A., Castillo, A., Vargas, C., Amorim, A., Gusmão, L.	Genetic profile characterization and segregation analysis of 10 X-STRs in a sample from Santander, Colombia	International Journal of Legal Medicine	2008	122	
	Tamura, A., Tsutsumi, H., Hara, M., Takada, A., Saito, K., Suzuki, K., Komuro, T.	Genetic studies of eight X-STRs in a Japanese population	Legal Medicine	2009	11	
	Poetsch, M., El-Mostaqim, D., Tschentscher, F., Browne, E., Timmann, C., Horstmann, R., Von Wurmb-Schwark, N.	Allele frequencies of 11 X-chromosomal loci in a population sample from Ghana	International Journal of Legal Medicine	2009	123	
	Gusmão, L., Sánchez-Diz, P., Alves, C., Gomes, I., Zarrabeitia, M., Abovich, M.	A GEP-ISFG collaborative study on the optimization of an X-STR decaplex: Data on 15 Iberian and Latin American populations	International Journal of Legal Medicine	2009	123	
	Bekada, A., Benhamamouch, S., Boudjema, A., Fodil, M., Menegon, S., Torre, C., Robino, C	Analysis of 12 X-chromosomal STRs in an Algerian population sample	Forensic Science International : Genetics Supplement Series	2009	2	

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X-STR population data	Li, H., Tang, H., Zhang, Q., Jiao, Z., Bai, J., Chang, S.	A multiplex PCR for 4 X chromosome STR markers and population data from Beijing Han ethnic group	Legal Medicine	2009	11	
	Nadeem, A., Babar, M., Hussain, M., Tahir, M.	Development of pentaplex PCR and genetic analysis of X chromosomal STRs in Punjabi population of Pakistan	Molecular Biology Reports	2009	36	7
	Jêdrzejczyk, M., Jacewicz, R., Berent, J.	Distribution of chromosome X str markers DXS10135 , DXS10074 , DXS10101 and DXS10134 and their usefulness in forensic genetics	Problems of Forensic Sciences	2009	77	
	Martins, J. A., Costa, J. C., Paneto, G. G., Gusmão, L., Sánchez-Diz, P., Carracedo, A., Cicarelli, R. M.B.	Genetic data of 10 X-chromosomal loci in Vitória population (Espírito Santo State, Brazil)	Forensic Science International: Genetics Supplement Series	2009	2	
	Toscanini, U., Gusmão, L., Berardi, G., Raimondi, E.	Genetic data of 10 X-STR in two Native American populations of Argentina	Forensic Science International: Genetics Supplement Series	2009	2	
	Gomes, I., Amorim, A., Pereira, V., Carracedo, A., Gusmão, L.	Genetic patterns of 10 X chromosome short tandem repeats in an Asian population from Macau	Forensic Science International: Genetics Supplement Series	2009	2	
	Lim, E., Lee, H., Sim, J., Yang, W., Shin, K.	Genetic polymorphism and haplotype analysis of 4 tightly linked X-STR duos in Koreans	Croatian Medical Journal	2009	50	
	Turrina, S., Filippini, G., De Leo, D.	Genetic studies of eight X-STRs in a Northeast Italian population	Forensic Science International: Genetics Supplement Series	2009	2	
	Tariq, M., Sabir, M., Riazuddin, S., Riazuddin, S.	Haplotype analysis of two X-chromosome STR clusters in the Pakistani population	International Journal of Legal Medicine	2009	123	
	Leite, F., Santos, S., Rodríguez, E., Callegari-Jacques, S., Demarchi, D., Tsuneto, L., Petzl-Erler, M., Salzano, F. , Hutz, M.	Linkage disequilibrium patterns and genetic structure of Amerindian and non-Amerindian Brazilian populations revealed by long-range X-STR markers	American Journal of Physical Anthropology	2009	139	
	Gomes, I., Pereira, V., Gomes, V., Prata, M., Pinto, N., Carracedo, A., Amorim, A., Gusmao, L.	The Karimojong from Uganda: Genetic characterization using an X-STR decaplex system	Forensic Science International: Genetics	2009	3	
	Hwa, H., Chang, Y., Lee, J., Yin, H., Chen, Y., Tseng, L., Su, Y., Ko, T.	Thirteen X-chromosomal short tandem repeat loci multiplex data from Taiwanese	International Journal of Legal Medicine	2009	123	
	Chen, D., Tseng, C., Tsai, S., Wang, M., Lu, S., Wu, T., Chang, P., Sun, C.	Use of X-linked short tandem repeats loci to confirm mutations in parentage caseworks	Clinica Chimica Acta	2009	408	
	Hedman, M., Palo, J. U., Sajantila, A.	X-STR diversity patterns in the Finnish and the Somali population	Forensic Science International: Genetics	2009	3	
	Zarrabeitia, M., Pinheiro, F., de Pancorbo, M., Cainé, L., Cardoso, S., Gusmão, L., Riancho, J.	Analysis of 10 X-linked tetranucleotide markers in mixed and isolated populations	Forensic Science International: Genetics	2009	3	

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X-STR population data	Ferreira Da Silva, I., Barbosa, A., Azevedo, D., Sánchez-Diz, P., Gusmão, L., Tavares, C., Carvalho, E., Ferreira Da Silva, L.	An X-chromosome pentaplex in two linkage groups: Haplotype data in Alagoas and Rio de Janeiro populations from Brazil	Forensic Science International: Genetics	2010	4	
	Rodrigues, E., Palha, T., Santos, Â., Santos, S.	Genetic data of twelve X-STRs in a Japanese immigrant population resident in Brazil	Forensic Science International: Genetics	2010	4	
	Mukerjee, S., Ghosh, T., Kalpana, D., Mukherjee, M., Sharma, A.	Genetic variation of 10 X chromosomal STR loci in Indian population	International Journal of Legal Medicine	2010	124	
	Bekada, A., Benhamamouch, S., Boudjema, A., Fodil, M., Menegon, S., Torre, C., Robino, C.	Analysis of 21 X-chromosomal STRs in an Algerian population sample	International Journal of Legal Medicine	2010	124	
	Cainé, L., Zarrabeitia, M., Riancho, J., Pinheiro, M.	Genetic data of a Brazilian population sample (Santa Catarina) using an X-STR decaplex	Journal of Forensic and Legal Medicine	2010	17	
	Martins, J., Costa, J., Paneto, G., Figueiredo, R., Gusmão, L., Sánchez-Diz, P., Carracedo, Á., Cicarelli, R.	Genetic profile characterization of 10 X-STRs in four populations of the southeastern region of Brazil	International Journal of Legal Medicine	2010	124	
	Tie, J., Uchigasaki, S., Oshida, S.	Genetic polymorphisms of eight X-chromosomal STR loci in the population of Japanese	Forensic Science International: Genetics	2010	4	
	Sim, J., Lee, H., Yang, W., Shin, K.	Population genetic study of four closely-linked X-STR trios in Koreans	Molecular Biology Reports	2010	37	
	Nakamura, Y., Minaguchi, K.	Sixteen X-chromosomal STRs in two octaplex PCRs in Japanese population and development of 15-locus multiplex PCR system	International Journal of Legal Medicine	2010	124	
	Edelmann, J., Hering, S., Augustin, C., Kalis, S., Szibor, R.	Validation of six closely linked STRs located in the chromosome X centromere region	International Journal of Legal Medicine	2010	124	
	Rodig, H., Kloep, F., Weißbach, L., Augustin, C., Edelmann, J., Hering, S., Szibor, R., Götz, F., Brabetz, W.	Evaluation of seven X-chromosomal short tandem repeat loci located within the Xq26 region	Forensic Science International: Genetics	2010	4	
	Pasino, S., Caratti, S., Pero, M., Santovito, A., Torre, C., Robino, C.	Allele and haplotype diversity of X-chromosomal STRs in Ivory Coast	International Journal of Legal Medicine	2011	125	
	Diegoli, T. Coble, M.	Development and characterization of two mini-X chromosomal short tandem repeat multiplexes	Forensic Science International: Genetics	2011	5	
	Diegoli, T., Linacre, A., Vallone, P.,Butler, J., Coble, M.	Allele frequency distribution of twelve X-chromosomal short tandem repeat markers in four U.S. population groups	Forensic Science International: Genetics Supplement Series	2011	3	
	Luo, H., Ye, Y., Wang, Y., Liang, W., Yun, L., Liao, M., Yan, J.,Wu, J. Li, Ying B., Hou, Y.	Characteristics of eight X-STR loci for forensic purposes in the Chinese population	International Journal of Legal Medicine	2011	125	
	Li, C., Ma, T., Zhao, S., Zhang, S., Xu, J., Zhao, Z., Jin, L., Li, S.	Development of 11 X-STR loci typing system and genetic analysis in Tibetan and Northern Han populations from China	International Journal of Legal Medicine	2011	125	

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X-STR population data	Liu, Q., Lu, D., Li, X., Zhao, H., Zhang, J., Lai, Y., Chen, Y.	Development of the nine X-STR loci typing system and genetic analysis in three nationality populations from China	International Journal of Legal Medicine	2011	125	
	Łuczak, S., Rogalla, U., Malyarchuk, B., Grzybowski, T.	Diversity of 15 human X chromosome microsatellite loci in Polish population	Forensic Science International: Genetics	2011	5	
	Ribeiro-Rodrigues, E., Palha, T., Bittencourt, E., Ribeiro-Dos-Santos, Â., Santos, S.	Extensive survey of 12 X-STRs reveals genetic heterogeneity among Brazilian populations	International Journal of Legal Medicine	2011	125	
	Li, C., Zhang, S., Zhao, Z., Li, L., Liu, Y., Zhao, S.	Genetic analysis of the 11 X-STR loci in Uigur and Northern Han populations from China	Forensic Science International: Genetics Supplement Series	2011	3	
	Poetsch, M., Knop, A., El-Mostaqim, D., Rakotomavo, N., Von Wurmb-Schwark, N.	Allele frequencies of 11 X-chromosomal loci of two population samples from Africa	International Journal of Legal Medicine	2011	125	
	Martínez, B., Builes, J. J., Gusmão, L., Manrique, M., Aguirre, D., Puerto, Y., Caraballo, L., Bravo, M. L.	Genetic data of 10 X-STR in a Colombian population of Bolivar Department	Forensic Science International: Genetics Supplement Series	2011	3	
	Illescas, M. J., Aznar, J. M., Cardoso, S., López-Oceja, A., Gamarra, D., Sánchez-Romera, J. F., Colodro, L., Ordoñana, J. R., de Pancorbo, M. M.	Genetic diversity of 10 X-STR markers in a sample population from the region of Murcia in Spain	Forensic Science International: Genetics Supplement Series	2011	3	
	Yoo, S., Cho, N., Park, S., Hwang, J., Kim, J., Chung, K., Han, M.	Genetic polymorphisms of eight X-STR loci of Mentype Argus X-8 kit in Koreans	Forensic Science International: Genetics Supplement Series	2011	3	
	Zeng, X., Ren, Z., Chen, J., Lv, D., Tong, D., Chen, H.	Genetic polymorphisms of twelve X-chromosomal STR loci in Chinese Han population from Guangdong Province	Forensic Science International: Genetics	2011	4	
	Cainé, L., Carvalho, R., Costa, S., Pereira, M., Pinheiro, M.	Interest of X chromosome (Argus X-12 kit) in complex kinship analysis	Forensic Science International: Genetics Supplement Series	2011	3	
	Inturri, S., Menegon, S., Amoroso, A., Torre, C., Robino, C.	Linkage and linkage disequilibrium analysis of X-STRs in Italian families	Forensic Science International: Genetics	2011	5	
	Iannacone, G. C., Parra, R., Bermejo, M., Rojas, Y., Valencia, C., Portugues, L., Medina, M., Vallejo, A. R., Prochanow, A.	Peruvian genetic structure and their impact in the identification of Andean missing persons: A perspective from Ayacucho	Forensic Science International: Genetics Supplement Series	2011	3	
	Turrina, S., Filippini, G., De Leo, D.	Population genetic evaluation of 12 X-chromosomal short tandem repeats of Investigator Argus X-12 kit in North-East Italy	Forensic Science International: Genetics Supplement Series	2011	3	
	Samejima, M., Nakamura, Y., Minaguchi, K.	Population genetic study of six closely linked groups of X-STRs in a Japanese population	International Journal of Legal Medicine	2011	125	

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X-STR population data	Picornell, A., Bentayebi, K., Bouabdeallah, M., Aboukhalid, R., Squalli, D., Castro, J. A., Ramon, M. M., Amzazi, S.	X-chromosomal haplotype frequencies of four linkage groups in a North African population	Forensic Science International: Genetics Supplement Series	2011	3	
	Aşicioğlu, F., Akyüz, F., Ozdilli, K., Oguz, F., Çarin, M.	X-Chromosomal short tandem repeat loci in the Turkish population	African Journal of Biotechnology	2011	10	
	Illescas, M. J., Aznar, J. M., Odriozola, A., Celorrio, D., De Pancorbo, M. M.	X-STR admixture analysis of two populations of the Basque Diaspora in America	Forensic Science International: Genetics Supplement Series	2011	3	
	Zhang, S., Li, C., Zhao, S., Li, L.	Genetic polymorphism of eight X-linked STRs of Mentype® Argus X-8 Kit in Chinese population from Shanghai	Forensic Science International: Genetics	2011	5	
	Diegoli, T., Kovacevic, L., Pojskic, N., Coble, M., Marjanovic, D.	Population study of fourteen X chromosomal short tandem repeat loci in a population from Bosnia and Herzegovina	Forensic Science International: Genetics	2011	5	
	Zeng, X. P., Ren, Z., Wu, X. J., Ou, X. L., Tong, D. Y., Chen, W. J., Zhang, Y. M., Liu, S. J., Chen, Y., Sun, H. Y.	Development of a 12-plex X chromosomal STR loci typing system	Forensic Science International: Genetics Supplement Series	2011	3	
	Tetzlaff, S., Wegener, R., Lindner, I.	Population genetic investigation of eight X-chromosomal short tandem repeat loci from a northeast German sample	Forensic Science International: Genetics	2012	6	
	Gelabert-Besada, M., Alves, C., Ferreira, S., García-Magariños, M., Gusmão, L., Sánchez-Diz, P.	Genetic characterization of Western Iberia using Mentype ® Argus X-8 kit	Forensic Science International: Genetics	2012	6	
	García, B., Crespillo, M., Paredes, M., Valverde, J.	Population data for 10 X-chromosome STRs from north-east of Spain	Forensic Science International: Genetics	2012	6	
	Illescas, M., Aznar, J., Cardoso, S., López-Oceja, A., Gamarra, D., Sánchez-Romera, J., Colodro-Conde, L., Ordoñana, J., De Pancorbo, M.	Genetic characterization of ten X-STRs in a population from the Spanish Levant	Forensic Science International: Genetics	2012	6	
	Horváth, G., Zalán, A., Kis, Z., Pamjav, H.	A genetic study of 12 X-STR loci in the Hungarian population	Forensic Science International: Genetics	2012	6	
	Tomas, C., Pereira, V., Morling, N.	Analysis of 12 X-STRs in greenlanders, danes and somalis using argus X-12	International Journal of Legal Medicine	2012	126	
	Liu, Q., Zhao, H., Chen, J., Wang, X., Lu, D., Quan, L.	Development and population study of the 12 X-STR loci multiplexes PCR systems	International Journal of Legal Medicine	2012	126	
	Liu, Q., Lu, D., Quan, L., Chen, Y., Shen, M., Zhao, H.	Development of multiplex PCR system with 15 X-STR loci and genetic analysis in three nationality populations from China	Electrophoresis	2012	33	8
	Li, C., Xu, J., Zhao, S., Zhang, S., Ma, T., Zhao, Z., Yang, Y., Jin, L., Li, S.	Genetic analysis of the 11 X-STR loci in Uigur population from China	Forensic Science International: Genetics	2012	6	

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X-STR population data	Bentayebi, K., Picornell, A., Bouabdeallah, M., Castro, J., Aboukhalid, R., Squalli, D., Misericordia, M., Amzazi, S.	Genetic diversity of 12 X-chromosomal short tandem repeats in the Moroccan population	Forensic Science International: Genetics	2012	6	
	Zhang, S., Zhao, S., Zhu, R., Li, C.	Genetic polymorphisms of 12 X-STR for forensic purposes in Shanghai Han population from China	Molecular Biology Reports	2012	39	
	Samejima, M., Nakamura, Y., Nambiar, P., Minaguchi, K.	Genetic study of 12 X-STRs in Malay population living in and around Kuala Lumpur using Investigator Argus X-12 kit	International Journal of Legal Medicine	2012	126	
	Tillmar, A.	Population genetic analysis of 12 X-STRs in Swedish population	Forensic Science International: Genetics	2012	6	
	Illescas, M., Pérez, A., Aznar, J., Valverde, L., Cardoso, S., Algorta, J., De Pancorbo, M.	Population genetic data for 10 X-STR loci in autochthonous Basques from Navarre (Spain)	Forensic Science International: Genetics	2012	6	
	Penna, L., Silva, F., Salim, P., Ewald, G., Jobim, M., De Azevedo Magalhães, J., Jobim, L.	Development of two multiplex PCR systems for the analysis of 14 X-chromosomal STR loci in a southern Brazilian population sample	International Journal of Legal Medicine	2012	126	
	Mukerjee, S., Mukherjee, M., Ghosh, T., Kalpana, D., Sharma, A.	Population genetic data for 11 X-STR loci in eleven populations of India	Legal Medicine	2012	14	3
	Edelmann, J., Lutz-Bonengel, S., Naue, J., Hering, S.	X-chromosomal haplotype frequencies of four linkage groups using the Investigator Argus X-12 Kit	Forensic Science International: Genetics	2012	6	
	Núñez, C., Baeta, M., Aznar, J., Sosa, C., Casalod, Y., Bolea, M., De Pancorbo, M., Martínez Jarreta, B.	Genetic diversity of 10 X chromosome STRs in an admixed population of Nicaragua	Forensic Science International: Genetics	2013	7	
	Barletta, C., Builes, J. J., Bravo, M. L., Aguirre, D., Descailleaux, J., Gusmão, L.	Genetic data of 10 X-STRs in a population sample from Lima, Perú	Forensic Science International: Genetics Supplement Series	2013	4	
	Cainé, L., Costa, S., Pinheiro, M.	Population data of 12 X-STR loci in a North of Portugal sample	International Journal of Legal Medicine	2013	127	
	Gaviria, A., Zambrano, A. K., Morejon, G., Aguirre, V., Vela, M., Builes, J. J., Burgos, G.	Genetic characterization of an X-STR decaplex on the population of Pichincha (Ecuador)	Forensic Science International: Genetics Supplement Series	2013	4	
	Gršković, B., Zidkova, A., Stenzl, V., Popović, M., Primorac, D., Mršić, G.	Analysis of 8 X-chromosomal markers in the population of central Croatia	Croatian Medical Journal	2013	54	3
	Laouina, A., Aznar, J., Chbel, F., De Pancorbo, M.	Genetic data of X-chromosomal STRs in a Moroccan population sample (Casablanca) using an X-STR decaplex	Forensic Science International: Genetics	2013	7	
	Liu, Q., Wang, J., Quan, L., Zhao, H., Wu, Y., Huang, X., Lu, D.	Allele and Haplotype Diversity of 26 X-STR Loci in Four Nationality Populations from China	PLoS ONE	2013	8	6
	Nakamura, Y., Samejima, M., Tamaki, K., Minaguchi, K.	Multiplex PCR for 18 X-chromosomal STRs in Japanese population	Legal Medicine	2013	15	

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X-STR population data	Nishi, T., Kurosu, A., Sugano, Y., Kaminiwa, J., Sekine, Y., Yano, S., Honda, K.	Application of a novel multiplex polymerase chain reaction system for 12 X-chromosomal short tandem repeats to a Japanese population study	Legal Medicine	2013	15	
	Ren, Z., Zeng, X. P., Hong, L., Peng, S., Chen, Y., Sun, H. Y.	The polymorphisms of 12 X-STR loci in six ethnic populations in China	Forensic Science International: Genetics Supplement Series	2013	4	
	Poetsch, M., Wassenaar, D., Von Wurmb-Schwark, N.	Allele frequencies for 11 X chromosomal short tandem repeats in a population from Turkey	International Journal of Legal Medicine	2013	127	
	Sun, K., Zhao, S., Tian, H., Zhang, S., Li, C.	Development of the 16 X-STR loci typing system and genetic analysis in a Shanghai Han population from China	Electrophoresis	2013	34	
	Baeta, M., Núñez, C., Aznar, J., Sosa, C., Casalod, Y.,Bolea, M., González-Andrade, F., De Pancorbo, M., Martínez-Jarreta, B.	Analysis of 10 X-STRs in three population groups from Ecuador	Forensic Science International: Genetics	2013	7	
	Uchigasaki, S., Tie, J., Takahashi, D.	Genetic analysis of twelve X-chromosomal STRs in Japanese and Chinese populations	Molecular Biology Reports	2013	40	
	Li, X., Zheng, J., Yao, J., Ding, M., Pang, H., Wang, B.	Population data of 12 X-chromosome STR loci in Yanbian Korean samples from China	Forensic Science International: Genetics	2014	13	
	Afonso Costa, H., Morais, P., Vieira Da Silva, C., Matos, S., Marques Santos, R., Espinheira, R., Costa Santos, J., Amorim, A.	X-Chromosome STR markers data in a Cabo Verde immigrant population of Lisboa	Molecular Biology Reports	2014	41	
	Israr, M., Shahid, A., Rahman, Z., Zar, M., Shahzad, M., Husnain, T., Pfeifer, C., Wiegand, P.	Development and characterization of a new 12-plex ChrX miniSTR system	International Journal of Legal Medicine	2014	128	
	Meng, H., Han, J., Zhang, Y., Liu, W., Wang, T., Yan, J., Huang, J., Du, W., Guo, J., Wang, H., Zhang, Y., Zhou, R., Zhu, B., Wei, X.	Diversity study of 12 X-chromosomal STR loci in Hui ethnic from China	Electrophoresis	2014	35	14
	Chen, M., Ho, C., Pu, C., Wu, F.	Genetic polymorphisms of 12 X-chromosomal STR loci in Taiwanese individuals and likelihood ratio calculations applied to case studies of blood relationships	Electrophoresis	2014	35	14
	Elakkary, S., Hoffmeister-Ullerich, S., Schulze, C., Seif, E., Sheta, A., Hering, S., Edelmann, J., Augustin, C.	Genetic polymorphisms of twelve X-STRs of the investigator Argus X-12 kit and additional six X-STR centromere region loci in an Egyptian population sample	Forensic Science International: Genetics	2014	11	
	Zidkova, A., Capek, P., Horinek, A., Coufalova, P.	Investigator® Argus X-12 study on the population of Czech Republic: Comparison of linked and unlinked X-STRs for kinship analysis	Electrophoresis	2014	35	14
	Kling, D., Dell'Amico, B., Haddeland, P., Tillmar, A.	Population genetic analysis of 12 X-STRs in a Somali population sample	Forensic Science International: Genetics	2014	11	

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X-STR population data	Diegoli, T., Linacre, A., Coble, M.	Population genetic data for 15 X chromosomal short tandem repeat markers in three U.S. populations	Forensic Science International: Genetics	2014	8	
	Zidkova, A., Coufalova, P., Capek, P.	X-STR decaplex study on the population of Czech Republic	International Journal of Legal Medicine	2014	128	
	Zhang, S., Bian, Y., Li, L., Sun, K., Wang, Z., Zhao, Q., Zha, L., Cai, J., Gao, Y., Ji, C., Li, C.	Population genetic study of 34 X-Chromosome markers in 5 main ethnic groups of China	Scientific Reports	2015	5	
	Prieto-Fernández, E., Baeta, M., Núñez, C., Jiménez-Moreno, S., de Pancorbo, M.	A new 17 X-STR multiplex for forensic purposes	Forensic Science International: Genetics Supplement Series	2015	5	
	Tomas, C., Skitsa, I., Steinmeier, E., Poulsen, L., Ampati, A., Børsting, C., Morling, N.	Results for five sets of forensic genetic markers studied in a Greek population sample	Forensic Science International: Genetics	2015	16	
	Bini, C., Riccardi, L., Ceccardi, S., Carano, F., Sarno, S., Luiselli, D., Pelotti, S.	Expanding X-chromosomal forensic haplotype frequencies database: Italian population data of four linkage groups	Forensic Science International: Genetics	2015	15	
	Ferragut, J. F., Bentayebi, K., Castro, J. A., Ramon, C., Picornell, A.	Genetic analysis of 12 X-chromosome STRs in Western Mediterranean populations	International Journal of Legal Medicine	2015	129	
	Ferragut, J. F., Castro, J. A.,Ramon, C., Picornell, A.	Genetic diversity of 12 X-chromosomal short tandem repeats in Jewish populations	Forensic Science International: Genetics Supplement Series	2015	5	
	Lopez, M., Manrique, A., Aguirre, D. P., Mendoza, L., Bravo, M. L.J., Salgar, M.	Genetic data of 10 X-STR in an Afro-descendant population sample of the Department of Chocó—Colombia	Forensic Science International: Genetics Supplement Series	2015	5	
	Zambrano, A. K., Morejón, G., Galarza, J., Pastas, V., Castillo, G., Vela, M.	Genetic data of an X-STR decaplex in Ecuadorian population (P)	Forensic Science International: Genetics Supplement Series	2015	5	
	Shrivastava, P., Jain, T., Gupta, U., Trivedi, V.	Genetic polymorphism study on 12 X STR loci of investigator Argus X STR kit in Bhil tribal population of Madhya Pradesh, India	Legal Medicine	2015	17	
	Vagaitseva, K. V., Kharkov, V. N., Cherpinskaya, K. V., Khitrinskaya, I. Y., Stepanov, V. A.	Genetic variability of X-linked STR markers in Siberian populations	Molecular Biology	2015	49	2
	Moreira, H., Costa, H., Tavares, F., Souto, L.	Genetic variation of 12 X-chromosomal STR loci in an East Timor sample	International Journal of Legal Medicine	2015	129	
	Re˛bała, K., Kotova, S., Rybakova, V., Zabauskaya, T., Shyla, A., Spivak, A., Tsybovsky, I., Szczerkowska, Z.	Variation of X-chromosomal microsatellites in Belarus within the context of their genetic diversity in Europe	Forensic Science International: Genetics	2015	16	

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X-STR population data	Poulsen, L., Farzad, M., Børsting, C., Tomas, C., Pereira, V., Morling, N.	Population and forensic data for three sets of forensic genetic markers in four ethnic groups from Iran: Persians, Lurs, Kurds and Azeris	Forensic Science International: Genetics	2015	17	
	Pinto, J. C., Pereira, V., Marques, S. L., Amorim, A., Alvarez, L., Prata, M. J.	Mirandese language and genetic differentiation in Iberia: A study using X chromosome markers	Annals of Human Biology	2015	42	
	Martinez, G., Schaller, C., Nazar, P., Brondani, A., Gomez, N., Bolea, M., Martinez-jarreta, B.	X-chromosomal haplotype frequencies of four linkage groups in a population of Argentina	Forensic Science International: Genetics Supplement Series	2015	5	
	Zhang, Y., Shen, C., Meng, H., Guo, Y., Dong, Q., Yang, G.	Allele and haplotype diversity of new multiplex of 19 ChrX-STR loci in Han population from Guanzhong region (China)	Electrophoresis	2016	37	12
	Crnjac, J., Ozretić, P., Merkaš, S., Ratko, M., Lozančić, M., Rožić, S., Špoljarić, D., Korolija, M., Popović, M., Mršić, G.	Analysis of 12 X-chromosomal markers in the population of central Croatia	Legal Medicine	2016	21	
	Yang, X., Wu, W., Chen, L., Liu, C., Zhang, X., Chen, L., Feng, X., Wang, H., Liu, C.	Development of the 19 X-STR loci multiplex system and genetic analysis of a Zhejiang Han population in China	Electrophoresis	2016	37	
	Israr, M., Shahid, A., Rakha, A., Zar, Mian S., Shahzad, Muhammad S., Rahman, Z., Husnain, T.	Baluchi and Pakhtun population data of 9 X-chromosomal short tandem repeat loci	Journal of Forensic and Legal Medicine	2016	37	
	Prieto-fernández, E., Núñez, C., Baeta, M., Jiménez-moreno, S., Martínez-jarreta, B., De Pancorbo, M.	Forensic Spanish allele and haplotype database for a 17 X-STR panel	Forensic Science International: Genetics	2016	24	
	Guo, Y., Chen, J., Wang, Y., Yan, J., Chen, J., Yao, T., Zhang, L., Yang, G., Meng, H., Zhang, Y., Mei, T., Liu, Y., Dong, Q., Zhu, B.	Genetic polymorphism analyses of a novel panel of 19 X-STR loci in the Chinese Uygur ethnic minority	Journal of Zhejiang University: Science B	2016	17	6
	Vongpaisarnsin, K., Boonlert, A., Rasmeepaisarn, K., Dangkao, P.	Genetic variation study of 12 X chromosomal STR in central Thailand population	International Journal of Legal Medicine	2016	130	
	Poulsen, L., Tomas, C., Drobnič, K., Ivanova, V., Mogensen, H. S., Kondili, A., Miniati, P., Bunokiene, D., Jankauskiene, J., Pereira, V., Morling, N.	NGMSElect™ and Investigator® Argus X-12 analysis in population samples from Albania, Iraq, Lithuania, Slovenia, and Turkey	Forensic Science International: Genetics	2016	22	
	Builes, J J., Mendoza, L., Gaviria, A., Zambrano, A K., Suarez, N D., Gutierrez, J A., Ibarra, A., Granda, J D., Castillo, A., Gil, A M., Pico, A L., Aguirre, D P.	Genetic characterization of four Colombian populations using Investigator ® Argus X-12 kit	Forensic Science International: Genetics Supplement Series	2017	6	
	Cortés-Trujillo, I., Ramos-González, B., Salas-Salas, O., Zuñiga-Chiquette, F., Zetina Hernández, A., Martínez-Cortés, G., *et al.*	Forensic efficiency parameters of the Investigator Argus X-12 kit in women from two Mestizo and seven Amerindian populations from Mexico	Legal Medicine	2017	26	

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X-STR population data	Crnjac, J., Ozretić, P., Merkaš, S., Ratko, M., Lozančić, M., Korolija, M., Popović, M., Mršić, G.	Investigator argus X-12 study on the population of northern Croatia	Genetics and Molecular Biology	2017	40	1
	Deng, C., Song, F., Li, J., Ye, Y., Zhang, L., Liang, W., Luo, H., Li, Y.	Forensic parameters of 19 X-STR polymorphisms in two Chinese populations	International Journal of Legal Medicine	2017	131	
	Ferragut, J. F., Bentayebi, K., Pereira, R., Castro, J. A., Amorim, A., Ramon, C., Picornell, A.	Genetic portrait of Jewish populations based on three sets of X-chromosome markers: Indels, Alu insertions and STRs	Forensic Science International: Genetics	2017	31	
	Gao, H. M., Wang, C., Han, S. Y., Sun, S. H., Xiao, D. J., Wang, Y. S., Li, C. T., Zhang, M. X.	Analysis of the 19 Y-STR and 16 X-STR loci system in the Han population of Shandong province, China	Genetics and Molecular Research	2017	16	1
	Gomes, I., Pereira, P., Harms, S., Oliveira, A., Schneider, P., Brehm, A.	Genetic characterization of Guinea-Bissau using a 12 X-chromosomal STR system : Inferences from a multiethnic population	Forensic Science International: Genetics	2017	31	
	Guo, F.	Population genetic data for 12 X-STR loci in the Northern Han Chinese and StatsX package as tools for population statistics on X-STR	Forensic Science International: Genetics	2017	26	
	He, G., Li, Y., Zou, X., Li, P., Chen, P., Song, F., Gao, T., Liao, M., Yan, J., Wu, J.	Forensic characteristics and phylogenetic analyses of the Chinese Yi population via 19 X-chromosomal STR loci	International Journal of Legal Medicine	2017	131	
	He, G., Li, Y., Zou, X., Wang, M., Chen, P., Liao, M., Wu, J.	Genetic polymorphisms for 19 X-STR loci of Sichuan Han ethnicity and its comparison with Chinese populations	Legal Medicine	2017	29	
	Liu, Y., Meng, H., Mei, T., Zhang, L., Chen, J., Zhang, Y., Chen, J., Guo, Y., Dong, Q., Yan, J., Zhu, B.	Genetic diversity and haplotypic structure of Chinese Kazak ethnic group revealed by 19 STRs on the X chromosome	Gene	2017	600	
	Martins, J., Martins, D., Oliveira-brancati, C., Martinez, J., Cicarelli, R., Souza, D.	Genetic characterization of an X-STR decaplex system in the State of Mato Grosso , Brazil : distribution , forensic efficiency and population structure	International Journal of Legal Medicine	2017	131	
	Meng, H., Shen, C., Zhang, Y., Dong, Q., Guo, Y., Yang, G.	Chinese Xibe population genetic composition according to linkage groups of X-chromosomal STRs: population genetic variability and interpopulation comparisons	Annals of Human Biology	2017	44	6
	Mršić, G., Ozretić, P., Crnjac, J., Merkaš, S., Račić, I., Rožić, S., Sukser, V., Popović, M., Korolija, M.	Analysis of 12 X-STR loci in the population of south Croatia	Molecular Biology Reports	2017	44	
	Prieto-Fernández, E., Díaz-de Usera, A., Baeta, M., Núñez, C., Chbel, F., Nadifi, S., Rouault, K., Férec, C., Hardiman, O., Pinheiro, F., de Pancorbo, M.	A genetic overview of Atlantic coastal populations from Europe and North-West Africa based on a 17 X-STR panel	Forensic Science International: Genetics	2017	27	

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X-STR population data	Sufian, A., Hosen, M., Fatema, K., Hossain, T., Hasan, M., Mazumder, A., Akhteruzzaman, S.	Genetic diversity study on 12 X-STR loci of investigator® Argus X STR kit in Bangladeshi population	International Journal of Legal Medicine	2017	131	
	Sun, M., Zhang, Y., Zhang, X., Fu, S., Wu, Y.	Genetic polymorphisms of 12 X STR loci in Shaanxi Han population from China	Legal Medicine	2017	26	
	Yang, X., Zhang, X., Zhu, J., Chen, L., Liu, C., Feng, X., Chen, L., Wang, H., Liu, C.	Genetic analysis of 19 X chromosome STR loci for forensic purposes in four Chinese ethnic groups	Scientific Reports	2017	7	
	Almarri, M., Lootah, R.	Allelic and haplotype diversity of 12 X-STRs in the United Arab Emirates	Forensic Science International: Genetics	2018	33	
	Chen, P., He, G., Zou, X., Wang, M., Jia, F., Bai, H., Li, J., Yu, J., Han, Y.	Forensic characterization and genetic polymorphisms of 19 X-chromosomal STRs in 1344 Han Chinese individuals and comprehensive population relationship analyses among 20 Chinese groups	PLoS ONE	2018	13	9
	Chen, L., Guo, Y., Xiao, C., Wu, W., Lan, Q., Fang, Y., Chen, J., Zhu, B.	Genetic polymorphisms and forensic efficiency of 19 X-chromosomal STR loci for Xinjiang Mongolian population	PeerJ	2018	6	
	Chen, P., He, G., Zou, X., Wang, M., Luo, H., Yu, L., Hu, X., Xia, M., Gao, H., Yu, J., Hou, Y., Han, Y.	Genetic structure and polymorphisms of Gelao ethnicity residing in southwest china revealed by X-chromosomal genetic markers	Scientific Reports	2018	8	
	He, G., Li, Y., Zou, X., Zhang, Y., Li, H., Wang, M., Wu, J.	X-chromosomal STR-based genetic structure of sichuan tibetan minority ethnicity group and its relationships to various groups	International Journal of Legal Medicine	2018	132	
	Fukuta, M., Gaballah, M., Kato, H., Aoki, Y.	A simple method for calculating the likelihood ratio in a kinship test using X-chromosomal markers incorporating linkage, linkage disequilibrium, and mutation	Legal Medicine	2018	32	
	Lee, J., Lin, C., Tsai, L., Yu, Y., Liao, K., Linacre, A., Hsieh, H.	Establishment of 11 linked X-STR loci within 1.1 Mb to assist with kinship testing	International Journal of Legal Medicine	2018	132	
	Mršić, G., Ozretić, P., Crnjac, J., Merkaš, S., Sukser, V., Račića, I., Rožić, S., Barbarić, L., Popović, M., Korolija, M.	Expanded Croatian 12 X-STR loci database with an overview of anomalous profiles	Forensic Science International: Genetics	2018	34	
	Mariscal Ramos, C., Martínez-Cortes, G., Ramos-González, B., Rangel-Villalobos, H.	Forensic parameters of the X-STR Decaplex system in Mexican populations	Legal Medicine	2018	31	
	Robino, C., Lacerenza, D., Aneli, S., Di Gaetano, C., Matullo, G., Robledo, R., Calò, C.	Allele and haplotype diversity of 12 X-STRs in Sardinia	Forensic Science International: Genetics	2018	33	
	Salvador, J., Apaga, D., Delfin, F., Calacal, G., Dennis, S., De Ungria, M.	Filipino DNA variation at 12 X-chromosome short tandem repeat markers	Forensic Science International: Genetics	2018	36	
	Santamaría, J., Álvarez-Álvarez, M., Esteban, M., Ramon-Gurrea, E., Moral, P.	Dinucleotide (CA)n tandem repeats on the human X-chromosome and the history of the Mediterranean populations	Annals of Human Biology	2018	45	

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X-STR population data	Tao, R., Zhang, J., Bian, Y., Dong, R., Liu, X., Jin, C., Zhu, R., Zhang, S., Li, C.	Investigation of 12 X-STR loci in Mongolian and Eastern Han populations of China with comparison to other populations	Scientific Reports	2018	8	
	Acar, E., Filoglu, G., Bulbul, O.	Polymorphism of 8 X-Chromosomal STR loci in Turkish population	Medicine Science International Medical Journal	2018	7	3
	Veselinović, I., Petrić, G., Vapa, D., Djan, M., Veličković, N., Veljović, T.	Genetic analysis of 12 X-STR loci in the serbian population from Vojvodina province	International Journal of Legal Medicine	2018	132	
	Ferragut, J F., Bassitta, M., Torrens, V., Albeza, V., Acreche, N., Castro, J A., Ramon, C., Picornell, A.	Analysis of 21 X-chromosome polymorphisms in urban and rural populations in Salta province (north-western Argentina)	International Journal of Legal Medicine	2019	133	
	García, M G., Catanesi, C I., Penacino, G A., Gusmão, L., Pinto, N.	X-chromosome data for 12 STRs : Towards an Argentinian database of forensic haplotype frequencies	Forensic Science International: Genetics	2019	41	
	Gaviria, A., Boada, L., Rodríguez-pólit, C., Vela, M., Fiallos, G., Gruezo, C., Paz-y-miño, C., Zambrano, A.	Genetic polymorphisms of 12 X-STRs in the Ecuadorian population	Forensic Science International: Genetics Supplement Series	2019	7	
	Gomes, C., Amorim, A., Okolie, V. O., Keshinro, S. O., Starke, A., Vullo, C., Gusmão, L., Gomes, I.	Genetic insight into Nigerian population groups using an X-chromosome decaplex system	Forensic Science International: Genetics Supplement Series	2019	7	
	Guo, J., Ji, J., He, G., Ren, Z., Zhang, H., Wang, Q., Yang, M., Nabijiang, Y., Zhang, Z., Zhang, J., Huang, J., Wang, C.	Genetic structure and forensic characterisation of 19 X-chromosomal STR loci in Guizhou Sui population	Annals of Human Biology	2019	46	3
	Han, Y., He, G., Gong, S., Chen, J., Jiang, Z., Chen, P.	Genetic diversity and haplotype analysis of Guizhou Miao identified with 19 X-chromosomal short tandem repeats	International Journal of Legal Medicine	2019	133	
	Kalaoglu, E., Ay, M., Ulubay, A., Canan, H., Serin, A., Alper, B.	Population data of 12 X-STRs in Turkey	Forensic Science International: Genetics Supplement Series	2019	7	
	Li, Y., Zeng, J., Fan, Y., He, G., Xie, M., Gao, T., Wang, S., Wu, J.	Genetic portrait and phylogenetic analysis of an Aksu Uyghur population based on the 19 X-STR system	International Journal of Legal Medicine	2019	133	
	Messoussi, M., Prieto-Fernández, E., Baeta, M., Núñez, C., Gaaied, A., de Pancorbo, M., Fadhlaoui-Zid, K.	Genetic variation of 17 X-chromosome STR loci in Tunisian population of Nabeul	International Journal of Legal Medicine	2019	133	
	Di Santo Meztler, G., Glesmann, A., Esteban, M., Del Palacio, S., Méndez, M., Catanesi, C.	Comparative study of 10 X-STR markers in populations of Northeast Argentina	Human Biology	2019	91	
	Ren, Z., Guo, J., He, G., Zhang, H., Zou, X., Zhang, H., Wang, Q., Ji, J., Yang, M., Zhang, J., Zhang, Z., Nabijiang, Y., Huang, J., Wang, C.	Forensic genetic polymorphisms and population structure of the Guizhou Bouyei people based on 19 X-STR loci	Annals of Human Biology	2019	46	

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X-STR population data	Sun, S., Yang, Z., Wen, D., Lan, L., Xie, P., Xiao, J., Li, G., Zhu, W., Zha, L.	Genetic polymorphism investigation of 16 X-STR loci in a Han population in Central South China	Forensic Science International: Genetics	2019	39	
	Susana, J., Celia, G., Ester, L., Miriam, B., Eladio, B., Marian, M.	Genetic analysis of 12 X-chromosomal STRs an autochthonous population of Southeast Spain	Forensic Science International: Genetics Supplement Series	2019	7	
	Xing, J., Adnan, A., Rakha, A., Kasim, K., Noor, A., Xuan, J., Zhang, X., Yao, J., McNevin, D., Wang, B.	Genetic analysis of 12 X-STRs for forensic purposes in Liaoning Manchu population from China	Gene	2019	683	
	Yang, Z., Chen, C., Zhang, J., Tao, R., Xia, R., Zhang, X., Zhang, J., Yu, L., Zhang, S., Li, C.	Genetic polymorphisms in 16 X-STR loci analyzed in the She population from Zhejiang Province, China	Legal Medicine	2019	39	
	Zambrano, A., Vaca-Pólit, M., Boada, L., Vela, M., Rodríguez-Pólit, C., Fiallos, G., Gruezo, C., Paz-y-Miño, C., Gaviria, A.	X-STR decaplex study in the population of Imbabura-Ecuador	Forensic Science International: Genetics Supplement Series	2019	7	
	Zhang, J., Yang, Z., Tao, R., Zhang, S., Li, C.	Genetic investigation of Chinese she ethnic based on autosomal STRs and X-STRs	Forensic Science International: Genetics Supplement Series	2019	7	
	Luo, L., Gao, H., Zhang, L., Liu, Y., Yao, L., Long, F., Zhang, H.	Genetic diversity, forensic feature, and phylogenetic analysis of Guizhou Tujia population via 19 X-STRs	Molecular Genetics & Genomic Medicine	2020		
	Chen, M., Ren, H., Liu, Z., Zhao, J., Chen, C., Shi, Y., Jia, L., Cheng, F., Chen, T., Fan, Q., Yang, Y.	Genetic polymorphisms and mutation rates of 16 X-STRs in a Han Chinese population of Beijing and application examples in second-degree kinship cases	International Journal of Legal Medicine	2020	134	
	Lin, L., Li, J., Hu, Y., Wang, H., Marah, F., Moseray, M., Kureshi, A., Wang, C., Zeye, M., Zha, L.	Genetic characterization of 19 X-STRs in Sierra Leone population from Freetown	International Journal of Legal Medicine	2020	134	
	Hering, S., Klimova, A., Edelmann, J.	German population data for 18 X-STRs: a hexaplex PCR adding two clusters of X-STRs to the Argus X-12 set and expanding the German haplotype databases	International Journal of Legal Medicine	2020	134	
	He, G., Zou, X., Wang, M., Liu, J., Wang, F., Hou, Y., Wang, Z.	Population genetics, diversity, forensic characteristics of four Chinese populations inferred from X-chromosomal short tandem repeats	Legal Medicine	2020	43	
	Kakkar, S., Shrivastava, P., Sahajpal, V., Sharma, A., Devi, N., Mandal, S. P.	Genetic diversity of X-STR markers in Jat Sikh population of Punjab, India and its comparison with other 39 global populations	Annals of Human Biology	2020	47	
	Tao, R., Zhang, J., Xia, R., Yang, Z., Wang, S., Zhang, X., Yang, Q., Zhang, S., Li, C.	Genetic investigation and phylogenetic analysis of three Chinese ethnic groups using 16 X chromosome STR loci	Annals of Human Biology	2020	47	
	Xiao, C., Li, S., Zhang, X., Yang, X., Liu, C., Chen, L.	Population genetic analysis of Chinese Zhuang and Mulao minorities using AGCU-X19 STR kit	International Journal of Legal Medicine	2020	134	

Objective	Authors	Title	Journal	Publication Year	Volume	Issue
X-STR population data	Baeta, M., Prieto-fernández, E., Núñez, C., Kleinbielen, T., Villaescusa, P., Palencia-madrid, L.	Study of 17 X-STRs in Native American and Mestizo populations of Central America for forensic and population purposes	International Journal of Legal Medicine	2021	135	
	Bini, C., Sarno, S., Tangorra, E., Iuvaro, A., Tseghereda, Y., Pelotti, S., Luiselli, D.	Haplotype data and forensic evaluation of 23 Y-STR and 12 X-STR loci in eight ethnic groups from Eritrea	International Journal of Legal Medicine	2021	135	
	Ferragut, J.F., Bentayebi, K., Barbaro, A., Ramírez, M., Saguillo, A.Y., Ramon, C., Picornell, A.	Exploring the Western Mediterranean through X-chromosome	International Journal of Legal Medicine	2021	135	
	Flores-Espinoza, R., Paz-Cruz, E., Ruiz-Pozo, V., Lopez-Carrera, M., Cabrera-Andrade, A., Gusmão, L., Burgos, G.	Investigating genetic diversity in admixed populations from Ecuador	American Journal of Physical Anthropology	2021	176	
	Hakim, H., Omar, H., Siti, K., Ismail, A., Lalung, J., Edward, A., Yusmaidie, M., Siddhartha, A., Nelson, B., Chambers, G., Edinur, H.	Population data and genetic characteristics of 12 X - STR loci using the Investigator ® Argus X - 12 Quality Sensor kit for the Kedayan population of Borneo in Malaysia	International Journal of Legal Medicine	2021	135	
	Jia, J., Liu, X., Fan, Q., Fang, C., Wang, M., Zhang, J., Li, W., Shi, L., Zhang, X., Chen, C., Yu, Z., Li, C., Yun, K., Yan, J.	Development and validation of a multiplex 19 X-chromosomal short tandem repeats typing system for forensic purposes	Scientific Reports	2021	11	
	Khacha-ananda, S., Mahawong, P.	Genetic analysis of 12 X-short tandem repeats loci in a northern Thai population	Medicine, Science and the Law	2021	61	
	Messaoudi, S., Babu, S., Alsaleh, A., Albujja, M., Al-Snan, N., Chaudhary, A., Kassab, A., Assidi, M.	Population genetic data for 12 X-STR loci in the Central Saudi region using investigator Argus X-12 amplification kit	Annals of Human Biology	2021	48	4
	Perera, N., Galhena, G., Ranawaka, G.	Development of a 16 X-STR multiplex PCR system for kinship analysis and its applicability for the Sinhalese population in Sri Lanka	International Journal of Legal	2021	135	
	Perera, N., Galhena, G., Ranawaka, G.	X-chromosomal STR based genetic polymorphisms and demographic history of Sri Lankan ethnicities and their relationship with global populations	Scientific Reports	2021	11	
	Semikhodskii, A., Krassotkin, Y., Makarova, T., Zavarin, V., Ilina, V., Sutyagina, D.	Genetic diversity and forensic parameters of 12 X-STR included in Argus X-12® marker panel in the population of the Russian Federation	Annals of Human Biology	2021	48	5
	Xiao, C., Yang, X., Liu, H., Liu, C., Yu, Z., Chen, L., Liu, C.	Validation and forensic application of a new 19 X-STR loci multiplex system	Legal Medicine	2021	53	
	Yang, Q., Qian, J., Shao, C., Yao, Y., Zhou, Z., Xu, H.	Identification and Characterization of Nine Novel X-Chromosomal Short Tandem Repeats on Xp21.1, Xq21.31, and Xq23 Regions	Frontiers in Genetics	2021	12	

Objective	Authors	Title	Journal	Publication Year	Volume	Issue
X-STR population data	Yang, M., Jin, X., Ren, Z., Wang, Q., Zhang, H., Zhang, H., Chen, J., Ji, J., Liu, Y., Huang, J.	X-chromosomal STRs for genetic composition analysis of Guizhou Dong group and its phylogenetic relationships with other reference populations	Annals of Human Biology	2021	48	
	Zhang, Y., Yu, Z., Mo, X., Zhao, X., Li, W., Liu, H., Liu, C., Wu, R., Sun, H.	Development and validation of a new 18 X-STR typing assay for forensic applications	Electrophoresis	2021	42	
	Zhang, X., Yuan, X., Huang, Y., Yao, J., Zhang, J., Dai, J., Liu, L., Nie, S., Hu, L.	Forensic genetic polymorphisms of 16 X-STR loci in the Yunnan Miao population and their relationship to other Chinese groups	Legal Medicine	2021	53	
	Liu, L., Yao, J., Huang, Y., Gao, L., Dai, J., Yuan, X., Zhang, X., Nie, S., Hu, L.	Genetic polymorphisms of 16 X-STR loci in the Hani population from Southwest China	Forensic Sciences Research	2021		
	Qing, L., Li, Y., Liu, L., Chen, D., Han, J., Shi, Y., Huang, R., Zhang, X.	Genetic polymorphism investigation of 16 X-STR loci in the Bai ethnic minority in Yunnan Province , Southwest China	International Journal of Legal Medicine	2022	136	
	Bottinelli, M., Gouy, A., Utz, S., Zieger, M.	Population genetic analysis of 12 X - chromosomal STRs in a Swiss sample	International Journal of Legal Medicine	2022	136	
	Curtis, R., Ward, D., Taylor, D., Henry, J.	Investigation of X-STR haplotype diversity in the Australian Aboriginal population	Australian Journal of Forensic Sciences	2022		
	Haddish, K., Chierto, E., Vella, G., Lacerenza, D.,Raddi, S., Aneli, S., Bogale, A L., Kidane, E., Yizengaw, A., Getaneh, Y., Tewelemedhin, G., Kumar, H R S., Robino, C.	A reference database of forensic autosomal and gonosomal STR markers in the Tigray population of Ethiopia	Forensic Science International: Genetics	2022	56	
	Liu, Y., Ye, Y., Yi, X., Zhang, J., Fan, G., Hao, D.	Phylogenetic analyses of the 19 STR loci in X chromosome revealed discriminant forensic characteristics for Chinese Daur and Oroqen minorities	International Journal of Legal Medicine	2022	136	
	Liu, L., Yuan, J., Miao, L., Huang, R., Zhang, X., Nie, S., Hu, L.	Genetic polymorphisms of 16 X-STR loci analyzed in the Han population of Yunnan Province, Southwest China	Legal Medicine	2022	54	
	Yang, M., Zhang, R., Jin, X., Ren, Z., Wang, Q., Luo, W.	Forensic characteristic of 19 X-STRs in Chuanqing, Tujia and Yi groups from Guizhou province and their genetic relationships with other reference populations	Gene Reports	2022	27	

Appendix B:

Table B1 *Summary of the available global X-STR population data publications*

Continent	Country (Region/Population)	Sample size used	Multiplex system used	Reference
Asia	Bangladesh	102 males, 107 females	Investigator Argus X-12	[81]
	China	80 males, 10 females	In-house (5 X-STRs)	[121]
	China (Aksu Uyghur)	229 males, 271 females	AGCU X19	[68]
	China (Beijing Han)	200 males, 200 females	In-house (4 X-STRs)	[122]
	China (Beijing Han)	592 males, 655 females, 770 families	Goldeneye 17X	[123]
	China (Beijing Han)	494 males, 591 females	In-house (19 X-STRs)	[124]
	China (Chinese Han)	500 males, 327 females	In-house (5 X-STRs)	[125]
	China (Chinese Han)	203 males, 100 females	Mentype Argus X-8	[126]
	China (Daur and Oroqen)	141 males, 110 females	AGCU X19	[127]
	China (Gelao)	248 males, 265 females	AGCU X19	[128]
	China (Guangdong Han, Xinjiang Uigur, Inner Mongolia Mongol)	484 males, 406 females, 210 family trios, 170 family duos	In-house (9 X-STRs)	[129]
	China (Guangdong Han)	144 males, 128 females	Investigator Argus X-12	[130]
	China (Guangdong Han)	191 males, 169 females	In-house (12 X-STRs)	[131]
	China (Guangdong Han)	65 males, 135 females	Microreader 19X Direct ID System	[132]
	China (Guangdong Han and Xinjiang Kazakh)	574 males, 431 females, 310 family trios, 170 family duos, 40 three-generation families	In-house (12 X-STRs)	[133]
	China (Guangdong Han, Uigur and Kazakh)	670 males, 581 females	In-house (15 X-STRs)	[134]
	China (Guangdong Han, Xinjiang Uigur, Tacheng Kazakh, Mongolia Mongol)	876 males, 646 females, 325 family trios, 286 family duos, 40 three-generation families	In-house (26 X-STRs)	[135]
	China (Guangdong Han, Tibetan, Mongolian, Korean, Uighur, Hui)	1298 individuals	Investigator Argus X-12	[136]
	China (Guangdong Han, Tibetan, Uighur, Hui)	631 males, 301 females	AGCU X19	[137]
	China (Guanzhong Han)	252 males, 222 females	AGCU X19	[138]
	China (Guizhou Bouyei)	188 males, 165 females	AGCU X19	[139]
	China (Guizhou Chuanqing, Tujia and Yi)	306 males, 208 females	AGCU X19	[140]

Continent	Country (Region/Population)	Sample size used	Multiplex system used	Reference
Asia	China (Guizhou Dong)	272 males, 235 females	AGCU X19	[141]
	China (Guizhou Han)	819 males, 525 females	AGCU X19	[142]
	China (Guizhou Miao)	151 males, 117 females	AGCU X19	[143]
	China (Guizhou Sui)	195 males, 205 females	AGCU X19	[144]
	China (Guizhou Tujia)	258 males, 249 females	AGCU X19	[145]
	China (Hainan Li, Hainan Han, Dujiangyan Tibetan and Wuzhong Hui)	712 individuals	AGCU X19	[146]
	China (Han)	508 males	Goldeneye 17X	[147]
	China (Han, Hui, Uygur, Mongolian and Tibetab)	250 males, 250 females	In-house (16 X-STRs)	[148]
	China (Hani)	116 males, 335 females	Goldeneye 17X	[149]
	China (Hong Kong)	250 males, 250 females	Mentype Argus X-UL	[150]
	China (Kazak)	149 males, 151 females	AGCU X19	[151]
	China (Liaoning Manchu)	514 males, 258 females	Investigator Argus X-12	[101]
	China (Macau)	46 males, 22 females	GHEP-ISFG X-STR decaplex	[152]
	China (Mongolian and Eastern Han)	316 males, 225 females	Investigator Argus X-12	[153]
	China (Northern Han)	268 males, 248 females	Investigator Argus X-12 QS	[97]
	China (Shaanxi Han)	312 males, 206 females	AGCU X12	[154]
	China (Shandong Han)	97 males, 214 females	Goldeneye 17X	[155]
	China (Shanghai Han)	106 males, 92 females	Mentype Argus X-8	[156]
	China (Shanghai Han)	200 males, 109 females	Investigator Argus X-12	[157]
	China (Shanghai Han)	293 males, 298 females, 400 two-generation families	In-house (16 X-STRs)	[64]
	China (Shanghai Han)	127 males, 71 females, 43 families	In-house (9 X-STRs)	[158]
	China (Sichuan Han)	93 males, 108 females	AGCU X19	[159]
	China (Sichuan Tibetan)	117 males, 118 females	AGCU X19	[160]
	China (Southern Han)	199 males, 199 females	TYPER X19	[161]
	China (Tibetan and Northern Han)	742 males, 863 females	In-house (11 X-STRs)	[162]
	China (Tibetan and Uygur)	490 males	AGCU X19	[163]
	China (Tibetan, Mongolian and Kazakh)	259 males, 259 females	Goldeneye 17X	[164]

Continent	Country (Region/Population)	Sample size used	Multiplex system used	Reference
Asia	China (Tongxin Hui and Wuzhong Hui)	131 males, 100 females	ZJGA-X12 STR	[165]
	China (Uigur and Northern Han)	470 males, 780 females	In-house (11 X-STRs)	[166]
	China (Xibe)	87 males, 92 females	AGCU X19	[167]
	China (Xinjiang Mongolian)	156 males, 111 females	AGCU X19	[168]
	China (Xinjiang Uygur)	78 males, 231 females	In-house (11 X-STRs)	[169]
	China (Xinjiang Uygur)	94 males, 139 females	AGCU X19	[170]
	China (Yanbian, Korean)	257 males, 316 females	Investigator Argus X-12	[171]
	China (Yi)	133 males, 198 females	AGCU X19	[172]
	China (Yunnan Bai)	202 males, 222 females	Goldeneye 17X	[173]
	China (Yunnan Han)	247 males, 168 females	Goldeneye 17X	[174]
	China (Yunnan Miao)	260 males, 180 females	Goldeneye 17X	[175]
	China (Zhejiang Han)	121 males, 60 females	AGCU X19	[176]
	China (Zhejiang She)	129 males, 167 females	Goldeneye 17X	[177]
	China (Zhejiang)	129 males, 167 females	Goldeneye 17X	[178]
	China (Zhuang and Mulao)	388 males, 251 females	AGCU X19	[179]
	East Timor	101 males, 48 females	Investigator Argus X-12	[79]
	India	749 males	In-house (10 X-STRs)	[180]
	India	749 males	In-house (11 X-STRs)	[181]
	India (Bhil, Madhya Pradesh)	100 males, 83 females	Investigator Argus X-12	[84]
	India (Jat Sikh, Punjab)	100 males, 100 females	Investigator Argus X-12 QS	[85]
	Iran (Persians, Lurs, Kurds, Azeris)	255 individuals	Investigator Argus X-12	[182]
	Iraq	105 males, 103 females	In-house (5 X-STRs)	[183]
	Iraq	96 males	Investigator Argus X-12	[184]
	Japan	195 males, 138 females	In-house (8 mini X-STRs)	[39]
	Japan	229 males, 172 females	In-house (8 X-STRs)	[185]
	Japan	144 males, 114 females	Mentype Argus X-8	[186]
	Japan	313 males, 181 females	Mentype Argus X-8	[187]
	Japan	95 males	In-house (5 X-STRs)	[121]
	Japan	339 males, 173 females	In-house (16 X-STRs)	[188]

Continent	Country (Region/Population)	Sample size used	Multiplex system used	Reference
Asia	Japan	425 males, 323 females	In-house (27 X-STRs)	[189]
	Japan	390 males, 179 females	Mentype Argus X-8	[190]
	Japan	37 males, 175 females	In-house (18 X-STRs)	[191]
	Japan	290 males, 160 females, 34 family trios	In-house (12 X-STRs)	[192]
	Japan (Fukuoka)	93 male	Mentype Argus X-8	[65]
	Japan (Tokoyo)	283 males, 209 females	Mentype Argus X-8	[193]
	Japan (Tokoyo), China (Shenyang)	438 males, 232 females (Japan), 263 males, 225 females (China)	Investigator Argus X-12	[72]
	Korea	150 males, 150 females	In-house (5 X-STRs)	[194]
	Korea	150 males, 150 females	In-house (4 X-STRs)	[195]
	Korea	220 males, 181 females, 95 family trios	In-house (18 X-STRs)	[90]
	Korea	41 families (138 individuals)	Mentype Argus X-8	[196]
	Korea (Seoul)	300 males, 150 females	Mentype Argus X-8	[197]
	Korea (Seoul)	300 males, 150 females	In-house (4 X-STRs)	[198]
	Malaysia (Kedayan, Borneo)	127 males, 72 females	Investigator Argus X-12 QS	[199]
	Malaysia (Kuala Lumpur)	160 males, 123 females	Investigator Argus X-12	[117]
	Pakistan	285 males, 147 females	In-house (13 X-STRs)	[200]
	Pakistan	302 males	In-house (5 X-STRs)	[201]
	Pakistan (Baluchi and Pakhtun)	250 males, 250 females	In-house (9 mini X-STRs)	[202]
	Pakistan (Punjabi)	94 males, 118 females, 84 family trios	In-house (5 X-STRs)	[203]
	Pakistan (Punjab, Sindh)	712 individuals	In-house (11 mini X-STRs)	[204]
	Philippines	57 males, 58 females	In-house (5 X-STRs)	[121]
	Philippines	143 males	Investigator Argus X-12	[106]
	Saudi Arabia	105 males, 95 females	Investigator Argus X-12	[82]
	Sri Lanka (Sinhalese)	120 males, 80 females	In-house (16 X-STRs)	[205]
	Sri Lanka (Sinhalese, Sri Lankan Tamils, Indian Tamils and Moors)	838 individuals	In-house (16 X-STRs)	[206]
	Taiwan	101 males, 99 females	In-house (5 X-STRs)	[207]
	Taiwan	327 males, 187 females	Investigator Argus X-12	[208]

Continent	Country (Region/Population)	Sample size used	Multiplex system used	Reference
Asia	Taiwan	208 males, 197 females	In-house (11 X-STRs)	[209]
	Taiwan (Chinese)	N/A	In-house (6 X-STRs)	[210]
	Taiwan (Han)	113 males, 108 females	In-house (13 X-STRs)	[211]
	Thailand	116 males, 41 females	In-house (5 X-STRs)	[121]
	Thailand	50 individuals	In-house (17 X-STRs)	[49]
	Thailand	282 males, 109 females	Investigator Argus X-12	[212]
	Thailand	61 males, 150 females	Investigator Argus X-12	[213]
	Turkey	135 males, 129 females	In-house (5 X-STRs)	[214]
	Turkey	175 males, 52 females	In-house (11 X-STRs)	[215]
	Turkey	56 males, 73 females	Mentype Argus X-8	[216]
	Turkey	100 males, 91 females	Investigator Argus X-12	[217]
	Turkey	61 males	Investigator Argus X-12	[184]
	United Arab Emirates	501 males	Investigator Argus X-12 QS	[218]
Europe	Albania	180 males, 77 females	Investigator Argus X-12	[184]
	Belarus	360 males, 423 females	In-house (19 X-STRs)	[219]
	Belarus, Slovakia	180 males (Belarus), 116 males (Slovakia)	In-house (4 X-STRs)	[220]
	Bosnia and Herzegovina	86 males, 86 females	In-house (15 mini X-STRs)	[221]
	Croatia	78 males, 99 females	Mentype Argus X-8	[222]
	Croatia	100 males, 100 females	Investigator Argus X-12	[223]
	Croatia	102 males, 100 females	Investigator Argus X-12	[103]
	Croatia	99 males, 98 females	Investigator Argus X-12	[104]
	Croatia	249 males, 148 females	Investigator Argus X-12	[224]
	Czech Republic	307 males, 216 females	Investigator Argus X-12	[225]
	Czech Republic	234 males, 197 females	GHEP-ISFG X-STR decaplex	[226]
	Denmark	210 individuals	Investigator Argus X-12	[83]
	Finland	200 males, 100 females	Mentype Argus X-8	[227]
	Germany	60 family trios	In-house (4 X-STRs)	[228]
	Germany	N/A	In-house (5 X-STRs)	[229]
	Germany	105 males, 100 females	In-house (10 X-STRs)	[230]

Continent	Country (Region/Population)	Sample size used	Multiplex system used	Reference
Europe	Germany	50 males, 55 females	In-house (5 X-STRs)	[121]
	Germany	574 individuals	In-house (4 X-STRs)	[91]
	Germany	N/A	In-house (16 X-STRs)	[231]
	Germany	110 males, 107 females	In-house (5 X-STRs)	[183]
	Germany	354 males, 184 females	In-house (6 X-STRs)	[232]
	Germany	159 males, 159 females	Mentype Argus X-8	[233]
	Germany	1037 males	Investigator Argus X-12	[234]
	Germany	700 males	Investigator Argus X-12	[235]
	Germany (Dresden)	80 males, 52 females	In-house (7 X-STRs)	[236]
	Germany (Dresden, Leipzig, Magdeburg, Hamburg)	439 male, 556 female	Mentype Argus X-8	[65]
	Greece	223 individuals	Investigator Argus X-12	[237]
	Hungary	219 males, 165 females, 96 family trios	Mentype Argus X-UL	[238]
	Hungary	219 males, 165 females	Mentype Argus X-8	[239]
	Hungary	219 males, 188 females	Investigator Argus X-12	[240]
	Iberia (western)	244 males, 83 females	Mentype Argus X-8	[241]
	Ireland	N/A	In-house (5 X-STRs)	[229]
	Italy (Tuscany)	80 males, 80 females	In-house (4 X-STRs)	[242]
	Italy (Pavia)	60 males, 60 females, 40 family trios	In-house (5 X-STRs)	[243]
	Italy (Bologna, Modena, Padova, Ancona, Pisa)	288 males, 268 females	In-house (7 X-STRs)	[244]
	Italy (Brescia)	30 males, 90 females	Mentype Argus X-UL	[245]
	Italy (Piedmont)	80 males, 80 females	In-house (12 X-STRs)	[246]
	Italy	100 males, 100 females	In-house (12 X-STRs)	[247]
	Italy (Brescia), Sardinia island	131 individuals	Mentype Argus X-8	[248]
	Italy (Umbria and Sardinia island)	200 individuals	In-house (5 X-STRs)	[249]
	Italy (Calabria)	25 males, 75 females	Mentype Argus X-8	[250]
	Italy	29 males, 147 females	Mentype Argus X-8	[251]
	Italy	80 families	Mentype Argus X-8, In-house (12 X-STRs)	[252]

Continent	Country (Region/Population)	Sample size used	Multiplex system used	Reference
Europe	Italy	118 males, 89 females	Investigator Argus X-12	[253]
	Italy	200 males	Investigator Argus X-12	[254]
	Sardinia	318 males, 198 females	Investigator Argus X-12	[255]
	Lativa (Riga, Liepaja, Ogre, Jelgava, Aizkraukle, Rezenkne, Preili, Balvi, Kuldiga, Madona	78 males, 45 females	In-house (10 X-STRs)	[256]
	Lithuania	33 males, 77 females	Investigator Argus X-12	[184]
	Poland	120 males, 120 females	Mentype Argus X-UL	[257]
	Poland	103 males, 101 females	Mentype Argus X-8	[33]
	Poland	60 males, 60 females	Mentype Argus X-8	[258]
	Poland (Kuyavua-Pomerania)	152 males, 159 females	Mentype Argus X-8, In-house (7 X-STRs)	[259]
	Poland (Old Believers)	140 males, 70 females	Mentype Argus X-UL	[260]
	Portugal	53 males, 48 females	Mentype Argus X-8	[261]
	Portugal	150 males	Investigator Argus X-12	[262]
	Portugal	150 males, 73 females	Investigator Argus X-12	[263]
	Portugal (Cabo Verde, Lisboa)	95 males, 54 females	Investigator Argus X-12	[113]
	Portugal (Miranda do Douri) and Spain (Zamora)	121 individuals (Portugal), 202 individuals (Spain)	Investigator Argus X-12	[264]
	Portugal (Porto, Braga, Viana do Castelo, Vila Real, Bragança)	347 males	In-house (10 X-STRs)	[265]
	Portugal, Spain	1492 males, 1467 females (total)	GHEP-ISFG X-STR decaplex	[266]
	Russian Federation	803 females	Investigator Argus X-12	[86]
	Serbia	604 males	In-house (10 X-STRs)	[267]
	Serbia (Vojvodina)	220 males, 105 females	Investigator Argus X-12	[268]
	Slovenia	136 males, 21 females	Investigator Argus X-12	[184]
	Spain	63 males, 68 females	In-house (5 X-STRs)	[269]
	Spain (Cantabria and Basque Country)	244 individuals	In-house (5 X-STRs)	[270]
	Spain (Cantabria, Basque Country, Galicia, Castilla, Andalucia)	324 males, 298 females	In-house (6 X-STRs)	[271]
	Spain (Castellón, Valencia, Alicante)	145 females	In-house (10 X-STRs)	[272]

Continent	Country (Region/Population)	Sample size used	Multiplex system used	Reference
Europe	Spain (Cantabria, Pas Valley, Basque Country), Portugal	252 males, 273 females	GHEP-ISFG X-STR decaplex	[273]
	Spain (Murcia)	311 sets of female twins, 4 sets of triplets	GHEP-ISFG X-STR decaplex	[274]
	Spain	192 males	In-house (10 X-STRs)	[275]
	Spanish Levant	172 individuals	GHEP-ISFG X-STR decaplex	[276]
	Spain (Basque, Navarre)	91 males, 94 females	GHEP-ISFG X-STR decaplex	[277]
	Spain	50 individuals	In-house (17 X-STRs)	[49]
	Spain (Alicante, Basque Country, Andalusia, Galicia, Madrud, Barcelona)	391 males, 202 females	In-house (17 X-STRs)	[278]
	Spain (Alicante)	62 males, 59 females	Investigator Argus X-12	[279]
	Sweden	718 males, 106 females	Mentype Argus X-8	[280]
	Sweden	652 males	Investigator Argus X-12	[112]
	Switzerland	606 males, 592 females	Investigator Argus X-12 QS	[118]
	UK and Irish	600 individuals	Mentype Argus X-UL	[281]
	Mediterranean	672 individuals	In-house (15 X-STRs)	[282]
	Western Mediterranean (Valencia, Majorca, Minorca, Ibiza)	160 males, 95 females	Investigator Argus X-12	[283]
	Western Mediterranean	716 individuals	Investigator Argus X-12	[284]
South America	Argentina	457 father-daughter duos	Investigator Argus X-12	[285]
	Argentina	419 individuals	GHEP-ISFG X-STR decaplex	[286]
	Argentina (Entre Rios)	110 males	Investigator Argus X-12	[287]
	Argentina (Salta)	78 males, 100 females	Investigator Argus X-12	[288]
	Argentina (Toba and Colla)	72 males	GHEP-ISFG X-STR decaplex	[289]
	Argentina, Brazil, Colombia	1492 males, 1467 females (total)	GHEP-ISFG X-STR decaplex	[266]
	Brazil	1355 males, 879 females	In-house (12 X-STRs)	[290]
	Brazil (Santa Catarina)	114 males, 70 females	Mentype Argus X-UL	[291]
	Brazil (Rio de Janeiro)	129 males, 134 females	In-house (6 X-STRs)	[292]
	Brazilian Amazon (Pará City)	182 males, 142 females	In-house (11 X-STRs)	[293]
	Brazil (Bauru, São Paulo)	90 males and females	In-house (5 X-STRs)	[294]
	Brazil (Espírito Santo State)	77 males, 147 females	GHEP-ISFG X-STR decaplex	[295]

Continent	Country (Region/Population)	Sample size used	Multiplex system used	Reference
South America	Brazil (Rio Grande do Sul)	200 males	In-house (11 X-STRs)	[296]
	Brazil (Alagoas, Rio de Janeiro)	423 males, 323 females	In-house (5 X-STRs)	[297]
	Brazil (Japanese)	102 males, 130 females	In-house (12 X-STRs)	[298]
	Brazil (Santa Catarina)	112 males, 72 females	GHEP-ISFG X-STR decaplex	[299]
	Brazil (São Paulo, Rio de Janeriro, Vitória and Belo Horizonte)	424 males, 577 females	GHEP-ISFG X-STR decaplex	[300]
	Brazil (Rio Grande do Sul)	141 males, 124 females	In-house (14 X-STRs)	[301]
	Brazil (Mato Grosso)	174 males, 100 females	GHEP-ISFG X-STR decaplex	[302]
	Colombia (Antioquia, Cauca, Santander, Cundiboyacense)	806 males	Investigator Argus X-12	[303]
	Colombia	50 individuals	In-house (17 X-STRs)	[49]
	Colombia (Chocó)	285 individuals	GHEP-ISFG X-STR decaplex	[304]
	Colombia, Bolivar	101 males, 89 females	GHEP-ISFG X-STR decaplex	[305]
	Colombia (Santander)	108 males, 110 females	In-house (10 X-STRs)	[306]
	Ecuador	72 males, 67 females	GHEP-ISFG X-STR decaplex	[307]
	Ecuador	200 males	GHEP-ISFG X-STR decaplex	[308]
	Ecuador	100 males, 100 females	Investigator Argus X-12	[309]
	Ecuador (Imbabura)	51 males, 49 females	GHEP-ISFG X-STR decaplex	[310]
	Ecuador (Mestizos)	377 males, 209 females	Investigator Argus X-12	[311]
	Ecuador (Pichincha)	52 males, 48 females	GHEP-ISFG X-STR decaplex	[312]
	Peru	N/A	In-house (5 X-STRs)	[229]
	Peru (Ayacucho)	203 individuals	Investigator Argus X-12	[313]
	Peru (Lima)	141 males, 141 females	GHEP-ISFG X-STR decaplex	[314]
North America	Costa Rica	1492 males, 1467 females (total)	GHEP-ISFG X-STR decaplex	[266]
	Greenland	198 individuals	Investigator Argus X-12	[83]
	Mexico	529 females	GHEP-ISFG X-STR decaplex	[315]
	Mexico (Mestizos and Amerindian)	641 females	Investigator Argus X-12	[316]
	Nicaragua	164 males	GHEP-ISFG X-STR decaplex	[317]
	America (Native American and Mestizo)	404 males, 237 females	In-house (17 X-STRs)	[318]

Continent	Country (Region/Population)	Sample size used	Multiplex system used	Reference
North America	United States of America (African Americans, Asians, Hispanics)	377 males	In-house (10 X-STRs)	[89]
	United States of America (African American, Asian, Caucasian, Hispanic)	621 males, 742 females	In-house (15 mini X-STRs)	[50]
	United States of America (African American, Asian, Caucasian, Hispanic)	663 males, 38 females	Investigator Argus X-12	[87]
	United States of America (Basque Diaspora)	40 males, 44 females (United States), 60 males, 112 females (Argentina)	GHEP-ISFG X-STR decaplex	[319]
	United States of America (African American, Caucasian, Hispanic)	423 males, 723 females	In-house (15 mini X-STRs)	[320]
Africa	Algeria	104 males, 106 females	In-house (12 X-STRs)	[321]
	Algeria	104 males, 106 females	In-house (21 X-STRs)	[322]
	Angola, Mozambique, Uganda	74 males (Angola), 112 males (Mozambique), 51 males (Uganda)	In-house (10 X-STRs)	[88]
	Eritrea	255 males	Investigator Argus X-12	[109]
	Ethiopia	N/A	In-house (5 X-STRs)	[229]
	Ethiopia (Tigray)	248 individuals	Investigator Argus X-12	[110]
	Eygpt (Alexandria)	250 males	Investigator Argus X-12	[111]
	Ghana	59 male	Mentype Argus X-8	[65]
	Ghana (Ashanti)	129 males, 114 females	In-house (11 X-STRs)	[323]
	Ghana (Ewe)	74 males, 108 females	Mentype Argus X-8	[324]
	Guinea-Bissau	332 males	Investigator Argus X-12	[108]
	Ivory Coast (Ouangolodougou)	51 males, 74 females	Mentype Argus X-8, In-house (13 X-STRs)	[325]
	Malawi and Equatorial Guinea	50 individuals	In-house (17 X-STRs)	[49]
	Morocco	97 males, 48 females	Investigator Argus X-12	[326]
	Morocco (Arabs, Berbers, Sahrawi)	97 males	Investigator Argus X-12	[327]
	Morocco (Casablanca)	246 males	GHEP-ISFG X-STR decaplex	[328]
	Morocco and Madagascar	50 males, 50 females (Morocco), 107 males, 62 females (Madagascar)	In-house (11 X-STRs)	[329]

Continent	Country (Region/Population)	Sample size used	Multiplex system used	Reference
Africa	Nigeria (Igbo, Hausa and Yoruba)	218 males	GHEP-ISFG X-STR decaplex	[330]
	Sierra Leone (Freetown)	265 males, 285 females	Microreader 19X Direct ID System	[331]
	Somalia	200 males, 100 females + 100 additional Somali individuals	Mentype Argus X-8	[227]
	Somalia	692 males	Investigator Argus X-12	[332]
	Somalia	441 individuals	Investigator Argus X-12	[83]
	Tunisia (Nabeul)	26 males, 113 females	In-house (17 X-STRs)	[80]
	Uganda (Karamoja)	117 males, 138 females	GHEP-ISFG X-STR decaplex	[333]
Oceania	Australia (Aboriginal)	298 males	Investigator Argus X-12 QS	[107]
Other	Jewish (Middle Eastern, Ashkenazi, Sephardic, North Africa) and Chuetas	152 males, 161 females	Investigator Argus X-12	[334]
	Jewish (Middle Eastern, Ashkenazi, Sephardic, North Africa) and Chuetas	276 males, 224 females	Investigator Argus X-12	[335]
	Atlantic Coast of Europe and North-West Africa	500 males, 13 females	In-house (17 X-STRs)	[336]

Appendix C:

Ethical approval letter

UNIVERSITY OF CAPE TOWN
Faculty of Health Sciences
Human Research Ethics Committee

Room 45 E-52-E-Floor- Old Main Building
Groote Schuur Hospital
Observatory 7925
Telephone [021] 406 6492
Email: hrec-submissions@uct.ac.za
Website: www.health.uct.ac.za/fhs/research/humanethics/forms

01 March 2022

HREC REF: 136/2022

Dr L Heathfield
Division of Forensic Medicine & Toxicology
Entrance 3 Level 1, Falmouth Building-FHS
Email: Laura.heathfield@uct.ac.za
Student: WHTAMY003@myuct.ac.za

Dear Dr Heathfield

PROJECT TITLE: INVESTIGATION INTO X-STR HAPLOTYPE FREQUENCIES FOR FORENSIC HUMAN IDENTIFICATION IN SOUTH AFRICA-MPHIL CANDIDATE-MISS AMY-LEIGH WHITTAKER-SUB-STUCY LINKED TO 342/2016

Thank you for submitting your study to the Faculty of Health Sciences Human Research Ethics Committee (HREC) for review.

It is a pleasure to inform you that the HREC has **formally approved** the above-mentioned study.

This approval is subject to strict adherence to the HREC recommendations regarding research involving human participants during COVID -19, our letter dated 02 February 2022 provides guidance found on our website:
http://www.health.uct.ac.za/fhs/research/humanethics/forms

Approval is granted for one year until the 30 March 2023.

Please submit a progress form, using the standardised Annual Report Form if the study continues beyond the approval period. Please submit a Standard Closure form if the study is completed within the approval period.
(Forms can be found on our website: www.health.uct.ac.za/fhs/research/humanethics/forms)

The HREC acknowledge that the student: Miss Amy-Leigh Whittaker will also be involved in this study.

Please quote the HREC REF 136/2022 in all your correspondence.

Please note that the ongoing ethical conduct of the study remains the responsibility of the principal investigator.

Please note that for all studies approved by the HREC, the principal investigator **must** obtain appropriate institutional approval, where necessary, before the research may occur.

Yours sincerely

PROFESSOR M BLOCKMAN
CHAIRPERSON, FACULTY OF HEALTH SCIENCES HUMAN RESEARCH ETHICS COMMITTEE
Federal Wide Assurance Number: FWA00001637. Institutional Review Board (IRB) number: IRB00001938 NHREC-registration number: REC-210208-007
This serves to confirm that the University of Cape Town Human Research Ethics Committee complies to the Ethics Standards for Clinical Research with a new drug in patients, based on the Medical Research Council (MRC-SA), Food and Drug Administration (FDA-USA), International Council for Harmonisation of Technical Requirements for Pharmaceuticals for Human Use: Good Clinical Practice (ICH GCP), South African Good Clinical Practice Guidelines (DoH 2020), based on the Association of the British Pharmaceutical Industry Guidelines (ABPI), and Declaration of Helsinki (2013) guidelines. The Human Research Ethics Committee granting this approval is in compliance with the ICH Harmonised Tripartite Guidelines E6: Note for Guidance on Good Clinical Practice (CPMP/ICH/135/95) and FDA Code Federal Regulation Part 50, 56 and 312.

Appendix D:

Table D1 *Non-concordant alleles identified between the Investigator Argus X-12 QS kit (Qiagen, Hilden) and the ForenSeq™ DNA Signature Prep kit (Illumina, CA, USA).*

Locus	Investigator Argus X-12 QS kit allele called	Forenseq DNA Signature Prep kit allele called
DXS10135	23.1	23
	34.1	34
	29	29.1
DXS10074	14.2	14
	17	16
DXS8378	11	12

Appendix E:

Table E1 *Exact test for population differentiation per locus between allele frequencies for male and female individuals using 100000 steps in the Markov chain. Significance level = 0.05.*

Locus	*p*-value
DXS8378	0.71555 ± 0.0235
DXS10135	0.88583 ± 0.0114
DXS10148	0.93992 ± 0.0091
DXS7132	0.65209 ± 0.0149
DXS10074	0.93204 ± 0.0083
DXS10079	0.65388 ± 0.0191
DXS10101	0.89960 ± 0.0095
DXS10103	0.54168 ± 0.0149
HPRTB	0.72595 ± 0.0155
DXS7423	0.86183 ± 0.0081
DXS10134	0.50997 ± 0.0253
DXS10146	0.41480 ± 0.0226

Appendix F:

Table F1 *Pooled allele frequencies and forensic parameters for 781 South African individuals.*

Allele	DXS8378	DXS10135	DXS10148	DXS7132	DXS10074	DXS10079	HPRTB	DXS10101	DXS10103	DXS7423	DXS10134	DXS10146	Combined
7					0.045								
8	0.0029				0.0603					0.0019			
9	0.0278				0.0067		0.0029						
10	0.2096			0.001	0.0029		0.0067						
11	0.3828			0.0153	0.0096		0.0938						
11.2							0.001						
12	0.3292			0.0871	0.0364		0.3502			0.0048			
13	0.045			0.2517	0.0402	0.0105	0.3033			0.0775			
13.2					0.0019								
13.3			0.0354										
14	0.0029	0.001	0.001	0.3378	0.0565	0.0019	0.1732			0.3971			
14.2					0.001		0.001						
15				0.2498	0.1397	0.0278	0.0555		0.0077	0.3732			
15.3					0.001								
16		0.0096	0.0019	0.044	0.199	0.0201	0.0124		0.1483	0.1263			
16.1		0.0048											
16.3			0.001		0.0048								
17		0.0153	0.0124	0.0115	0.1828	0.0699			0.0842	0.0191			
17.1		0.0096											
17.3					0.0019								
18		0.0517	0.1282	0.0019	0.1388	0.1407			0.2182				
18.1		0.0287											
18.2			0.001										
18.3					0.0019								
19		0.0498	0.0383		0.0545	0.2364			0.3914				

Allele	DXS8378	DXS10135	DXS10148	DXS7132	DXS10074	DXS10079	HPRTB	DXS10101	DXS10103	DXS7423	DXS10134	DXS10146	Combined
19.1		0.0201											
19.3			0.001										
20		0.0421	0.0163		0.0144	0.2239			0.1292				
20.1		0.0201	0.0096										
20.3		0.001	0.001										
21		0.0775	0.0077		0.001	0.1799			0.0201			0.001	
21.1		0.0325	0.001										
21.2						0.0029							
22		0.0689	0.0019			0.0641			0.001				
22.1		0.0182	0.0144									0.0019	
22.2								0.001					
22.3			0.001										
23		0.0651	0.0249			0.0144						0.001	
23.1		0.0134	0.0622										
24		0.0699	0.023			0.0057		0.001				0.0182	
24.1		0.0057	0.0842										
24.2								0.0124					
24.3			0.001										
25		0.0584	0.0124			0.0019		0.001				0.0488	
25.1		0.0019	0.1254										
25.2								0.001					
26		0.0555	0.0153					0.0038				0.0852	
26.1			0.0861								0.001		
26.2								0.0153				0.001	
26.3		0.0029	0.001										
27		0.0603	0.0268					0.0048				0.1033	
27.1		0.0019	0.0632								0.001		
27.2								0.0373					
27.3		0.001										0.001	

Allele	DXS8378	DXS10135	DXS10148	DXS7132	DXS10074	DXS10079	HPRTB	DXS10101	DXS10103	DXS7423	DXS10134	DXS10146	Combined
28		0.0459	0.0191					0.0526			0.0029	0.155	
28.1		0.0019	0.0383					0.001					
28.2			0.0019					0.0785			0.001		
28.3		0.0048	0.001										
29		0.0383	0.0211					0.0536			0.001	0.1407	
29.1			0.0211								0.001		
29.2			0.0019					0.0746			0.001	0.0019	
29.3		0.0019											
30		0.0344	0.0105					0.0679			0.0086	0.0909	
30.1		0.001	0.0105								0.0019	0.001	
30.2								0.1072					
31		0.0191	0.0077					0.1321			0.0048	0.0785	
31.1			0.0048										
31.2		0.0019						0.0689				0.0038	
31.3			0.001					0.0019				0.001	
32		0.0086	0.0067					0.134			0.0364	0.0411	
32.1		0.0057	0.0096								0.001		
32.2								0.0325				0.0019	
32.3			0.001										
33		0.0086	0.0029					0.0833			0.0632	0.0172	
33.1		0.0019						0.001					
33.2								0.0105			0.001	0.0086	
33.3											0.0038		
34		0.0077						0.0172			0.1215	0.0057	
34.1		0.0019											
34.2								0.001			0.0038	0.0258	
34.3											0.0067		
35		0.0057						0.0048			0.1646	0.0019	
35.1		0.0019	0.0038								0.001		

Allele	DXS8378	DXS10135	DXS10148	DXS7132	DXS10074	DXS10079	HPRTB	DXS10101	DXS10103	DXS7423	DXS10134	DXS10146	Combined
35.2		0.001										0.0067	
35.3											0.001		
36		0.0038									0.1904	0.0019	
36.1			0.001										
36.2		0.0019									0.0019	0.0191	
36.3											0.0048		
37		0.0048									0.1579		
37.1		0.0019	0.001										
37.2		0.0038									0.0067	0.0067	
37.3											0.0077		
38											0.0861	0.001	
38.1			0.001										
38.2		0.001									0.0029	0.0153	
38.3											0.0077		
39											0.0392		
39.1			0.0086										
39.2		0.0029										0.0153	
39.3											0.0096		
40			0.001								0.0096		
40.1			0.0067										
40.2		0.001										0.0258	
40.3											0.022	0.001	
41											0.001		
41.1			0.0115										
41.2												0.0086	
41.3											0.0124		
42.1			0.0067										
42.2												0.0153	
42.3											0.0057		

Allele	DXS8378	DXS10135	DXS10148	DXS7132	DXS10074	DXS10079	HPRTB	DXS10101	DXS10103	DXS7423	DXS10134	DXS10146	Combined
43.1			0.001										
43.2												0.0115	
43.3											0.0067		
44.1			0.001										
44.2												0.0144	
45.2												0.0105	
46.2												0.0057	
47.2												0.001	
Null allele												0.0038	
MEC_Kruger	0.440	0.907	0.874	0.523	0.747	0.666	0.516	0.831	0.541	0.424	0.764	0.832	1
MEC_Kishida	0.643	0.952	0.934	0.709	0.861	0.810	0.702	0.910	0.719	0.623	0.871	0.910	1
MEC_Desmarais	0.643	0.952	0.933	0.709	0.860	0.810	0.702	0.910	0.718	0.623	0.870	0.910	1
MEC_Desmarais_Duo	0.498	0.910	0.878	0.571	0.766	0.696	0.564	0.841	0.582	0.478	0.781	0.842	1

Abbreviations – MEC: mean exclusion chance.

Appendix G:

Table G1 *Hardy-Weinberg equilibrium test for female samples. Significance level = 0.0042.*

Locus	Observed Heterozygosity	Expected Heterozygosity	*p*-value
DXS8378	0.73485	0.69691	0.30851
DXS10135	0.95455	0.95395	0.00878
DXS10148	0.88636	0.9284	**0.00009**
DXS7132	0.72727	0.75265	0.62951
DXS10074	0.89015	0.87666	0.34980
DXS10079	0.84848	0.83867	0.53975
HPRTB	0.73485	0.73787	0.38804
DXS10101	0.93561	0.91888	0.18347
DXS10103	0.67803	0.74371	0.06018
DXS7423	0.67803	0.68759	0.13571
DXS10134	0.89773	0.8798	0.30600
DXS10146	0.91288	0.90864	0.03020

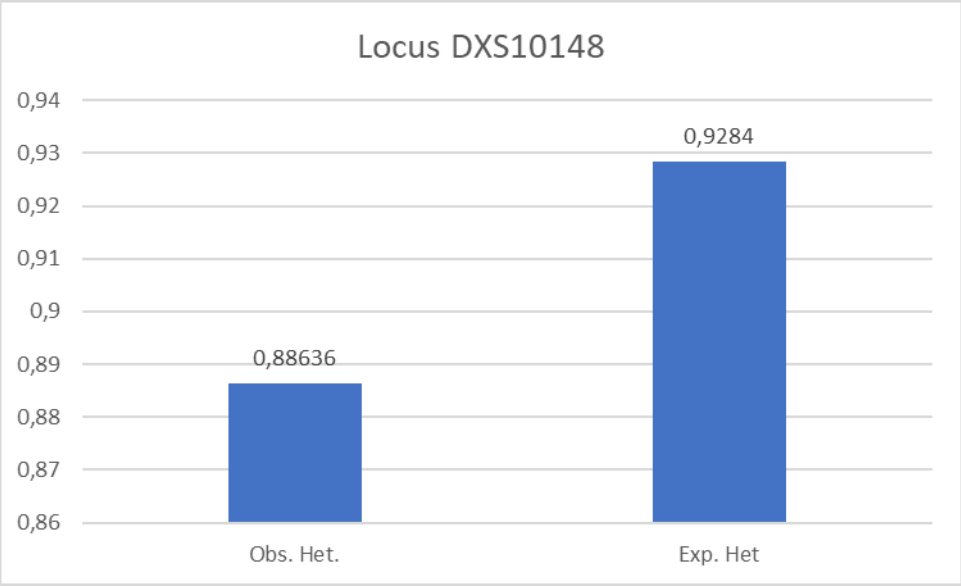

Fig. G1. *Bar graph illustrating the significant difference between observed and expected heterozygosity at locus DXS10148 (p < 0.0042).*

Appendix H:

Table H1 *Haplotype frequencies for 517 South African males.*

LG1			LG2			LG3			LG4		
DXS8378-DXS10135-DXS10148			**DXS7132-DXS10074-DXS10079**			**HPRTB-DXS10101-DXS10103**			**DXS7423-DXS10134-DXS10146**		
Haplotype	**Count**	**Frequency**	**Haplotype**	**Count**	**Frequency**	**Haplotype**	**Count**	**Frequency**	**Haplotype**	**Count**	**Frequency**
10 16 29.1	1	0.0019	10 18 20	1	0.0019	10 24.2 16	1	0.0019	12 35 38.2	2	0.0039
10 16 40.1	1	0.0019	11 12 17	1	0.0019	10 28.2 20	1	0.0019	13 32 30.1	1	0.0019
10 16 42.1	1	0.0019	11 13 20	1	0.0019	10 32 18	1	0.0019	13 34 27	1	0.0019
10 18 22.1	1	0.0019	11 14 18	2	0.0039	10 32 20	1	0.0019	13 34 28	1	0.0019
10 18 26.1	3	0.0058	11 14 19	1	0.0019	11 26.2 18	1	0.0019	13 34 29	1	0.0019
10 18 30.1	1	0.0019	11 15 19	1	0.0019	11 27.2 19	1	0.0019	13 34 30	1	0.0019
10 18.1 13.3	1	0.0019	11 17 20	1	0.0019	11 28.1 19	1	0.0019	13 35 27	3	0.0058
10 18.1 25.1	1	0.0019	11 17 21	1	0.0019	11 28.2 16	1	0.0019	13 35 29	2	0.0039
10 18.1 29.1	2	0.0039	11 18 20	1	0.0019	11 28.2 18	3	0.0058	13 35 30	2	0.0039
10 18.1 30.1	1	0.0019	12 12 19	1	0.0019	11 28.2 19	2	0.0039	13 36 25	3	0.0058
10 18.1 31.1	1	0.0019	12 12 22	1	0.0019	11 28.2 21	3	0.0058	13 36 26	1	0.0019
10 19 22.1	1	0.0019	12 14 19	4	0.0077	11 29.2 19	9	0.0174	13 36 27	2	0.0039
10 19 23.1	1	0.0019	12 14 20	1	0.0019	11 29.2 20	1	0.0019	13 36 28	1	0.0019
10 19.1 28.1	1	0.0019	12 14 22	1	0.0019	11 30 17	1	0.0019	13 36 39.2	1	0.0019
10 19.1 28.2	1	0.0019	12 15 19	1	0.0019	11 30 18	2	0.0039	13 37 25	1	0.0019
10 19.1 44.1	1	0.0019	12 15 20	1	0.0019	11 30 19	1	0.0019	13 37 26	3	0.0058
10 20 28	1	0.0019	12 15 22	1	0.0019	11 30.2 18	1	0.0019	13 37 29	1	0.0019
10 20.1 32.1	1	0.0019	12 16 17	2	0.0039	11 30.2 19	2	0.0039	13 37 34.2	1	0.0019
10 21 18	4	0.0077	12 16 19	2	0.0039	11 31 17	1	0.0019	13 37 35.2	1	0.0019
10 21 24.1	1	0.0019	12 16 20	4	0.0077	11 31 18	2	0.0039	13 38 25	1	0.0019
10 21 25.1	1	0.0019	12 16 21	3	0.0058	11 31 19	2	0.0039	13 38 29	1	0.0019
10 21 26	2	0.0039	12 16 23	1	0.0019	11 31 20	2	0.0039	13 38 30	2	0.0039
10 21 26.1	1	0.0019	12 16.3 22	1	0.0019	11 31.2 18	1	0.0019	13 38 31	1	0.0019

LG1			LG2			LG3			LG4		
DXS8378-DXS10135-DXS10148			DXS7132-DXS10074-DXS10079			HPRTB-DXS10101-DXS10103			DXS7423-DXS10134-DXS10146		
Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency
10 21 27	1	0.0019	12 17 18	1	0.0019	11 31.2 19	3	0.0058	13 38 36.2	1	0.0019
10 21 27.1	1	0.0019	12 17 19	1	0.0019	11 31.2 20	1	0.0019	13 38.3 44.2	1	0.0019
10 21 28.1	1	0.0019	12 17 20	2	0.0039	11 32 17	1	0.0019	13 39 28	1	0.0019
10 21.1 13.3	1	0.0019	12 17 21	2	0.0039	11 32 18	2	0.0039	13 39 40.2	1	0.0019
10 21.1 18	1	0.0019	12 17.3 20	1	0.0019	11 32 19	1	0.0019	13 39 46.2	1	0.0019
10 21.1 23.1	1	0.0019	12 18 19	4	0.0077	11 32 20	2	0.0039	13 40.3 27	1	0.0019
10 21.1 24.1	1	0.0019	12 18 21	1	0.0019	11 33 16	1	0.0019	13 41.3 40.2	1	0.0019
10 22 18	1	0.0019	12 19 15	1	0.0019	11 33 18	2	0.0039	14 29.1 27	1	0.0019
10 22 23	1	0.0019	12 19 17	1	0.0019	11 33 19	1	0.0019	14 30 31	1	0.0019
10 22 23.1	1	0.0019	12 19 18	2	0.0039	11 34 16	1	0.0019	14 30 32	1	0.0019
10 22 24.1	1	0.0019	12 19 20	2	0.0039	11 34 17	1	0.0019	14 32 29	2	0.0039
10 22 25	1	0.0019	12 7 19	2	0.0039	11 34 18	1	0.0019	14 32 29.2	1	0.0019
10 22 25.1	2	0.0039	12 8 18	1	0.0019	11.2 33.2 18	1	0.0019	14 32 30	1	0.0019
10 22 26.1	1	0.0019	13 10 19	1	0.0019	12 22.2 19	1	0.0019	14 32 31.2	1	0.0019
10 22 27.1	1	0.0019	13 11 21	1	0.0019	12 24.2 18	2	0.0039	14 32 32	2	0.0039
10 22 29	1	0.0019	13 12 19	3	0.0058	12 24.2 19	2	0.0039	14 32 36.2	1	0.0019
10 22 29.1	1	0.0019	13 12 20	5	0.0097	12 25 18	1	0.0019	14 32 43.2	1	0.0019
10 22.1 28.1	1	0.0019	13 13 16	1	0.0019	12 25.2 18	1	0.0019	14 32.1 27	1	0.0019
10 22.1 32.1	1	0.0019	13 13 19	1	0.0019	12 26 18	1	0.0019	14 33 25	1	0.0019
10 22.1 39.1	1	0.0019	13 13 20	1	0.0019	12 26.2 16	4	0.0077	14 33 26	1	0.0019
10 23 18	1	0.0019	13 13 21	1	0.0019	12 26.2 18	1	0.0019	14 33 27	3	0.0058
10 23 20	1	0.0019	13 13 22	1	0.0019	12 26.2 20	1	0.0019	14 33 28	2	0.0039
10 23 23	1	0.0019	13 14 19	2	0.0039	12 27 20	1	0.0019	14 33 29	2	0.0039
10 23 24.1	1	0.0019	13 14 20	1	0.0019	12 27.2 19	5	0.0097	14 33 30	2	0.0039
10 23 25.1	2	0.0039	13 14 21	1	0.0019	12 27.2 20	3	0.0058	14 33 31	2	0.0039
10 23 27	1	0.0019	13 14 21.2	1	0.0019	12 28 17	1	0.0019	14 33 32	1	0.0019
10 23 28.1	1	0.0019	13 14 22	1	0.0019	12 28 18	6	0.0116	14 33 38.2	2	0.0039

LG1			LG2			LG3			LG4		
DXS8378-DXS10135-DXS10148			DXS7132-DXS10074-DXS10079			HPRTB-DXS10101-DXS10103			DXS7423-DXS10134-DXS10146		
Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency
10 23 29.1	1	0.0019	13 15 13	2	0.0039	12 28 19	11	0.0213	14 34 25	4	0.0077
10 23 32.1	1	0.0019	13 15 17	1	0.0019	12 28 20	2	0.0039	14 34 26	8	0.0155
10 23.1 25.1	1	0.0019	13 15 18	2	0.0039	12 28.2 16	3	0.0058	14 34 27	1	0.0019
10 24 18	1	0.0019	13 15 19	5	0.0097	12 28.2 17	1	0.0019	14 34 29	5	0.0097
10 24 19	1	0.0019	13 15 20	6	0.0116	12 28.2 18	1	0.0019	14 34 30	3	0.0058
10 24 23	2	0.0039	13 15 21	2	0.0039	12 28.2 19	8	0.0155	14 34 31	2	0.0039
10 24 23.1	1	0.0019	13 15 22	1	0.0019	12 28.2 20	4	0.0077	14 34 34.2	1	0.0019
10 24 24.1	1	0.0019	13 16 13	1	0.0019	12 29 18	1	0.0019	14 34 40.2	1	0.0019
10 24 25	1	0.0019	13 16 16	1	0.0019	12 29 20	1	0.0019	14 34 44.2	1	0.0019
10 24 25.1	2	0.0039	13 16 18	3	0.0058	12 29.2 16	1	0.0019	14 34.3 31	1	0.0019
10 24 28	1	0.0019	13 16 19	3	0.0058	12 29.2 19	5	0.0097	14 34.3 44.2	1	0.0019
10 24 28.1	1	0.0019	13 16 20	8	0.0155	12 29.2 21	1	0.0019	14 35 24	2	0.0039
10 24 29.1	1	0.0019	13 16 21	7	0.0135	12 30 17	1	0.0019	14 35 25	1	0.0019
10 24 42.1	1	0.0019	13 16 21.2	1	0.0019	12 30 18	8	0.0155	14 35 26	2	0.0039
10 24.1 18	1	0.0019	13 16 22	1	0.0019	12 30 19	2	0.0039	14 35 27	1	0.0019
10 25 23.1	1	0.0019	13 16 23	2	0.0039	12 30 20	2	0.0039	14 35 28	12	0.0232
10 25 24.1	1	0.0019	13 16.3 20	1	0.0019	12 30.2 16	1	0.0019	14 35 29	2	0.0039
10 25 25.1	2	0.0039	13 17 15	1	0.0019	12 30.2 18	3	0.0058	14 35 30	2	0.0039
10 25 26.1	1	0.0019	13 17 17	2	0.0039	12 30.2 19	12	0.0232	14 35 31	6	0.0116
10 25 28	1	0.0019	13 17 18	3	0.0058	12 30.2 20	2	0.0039	14 35 32	1	0.0019
10 26 23.1	1	0.0019	13 17 19	5	0.0097	12 30.2 21	1	0.0019	14 35 34.2	2	0.0039
10 26 24.1	1	0.0019	13 17 20	7	0.0135	12 31 16	3	0.0058	14 35 35.2	2	0.0039
10 26 26.1	1	0.0019	13 17 21	5	0.0097	12 31 18	10	0.0193	14 35 40.2	2	0.0039
10 27 17	1	0.0019	13 18 15	2	0.0039	12 31 19	8	0.0155	14 36 24	1	0.0019
10 27 18	1	0.0019	13 18 18	2	0.0039	12 31 20	1	0.0019	14 36 25	3	0.0058
10 27 19	1	0.0019	13 18 19	4	0.0077	12 31.2 16	1	0.0019	14 36 26	1	0.0019
10 27 24.1	1	0.0019	13 18 20	1	0.0019	12 31.2 18	2	0.0039	14 36 27	6	0.0116

LG1			LG2			LG3			LG4		
DXS8378-DXS10135-DXS10148			DXS7132-DXS10074-DXS10079			HPRTB-DXS10101-DXS10103			DXS7423-DXS10134-DXS10146		
Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency
10 27 26.1	3	0.0058	13 18 21	3	0.0058	12 31.2 19	8	0.0155	14 36 28	10	0.0193
10 27 28.1	1	0.0019	13 18 22	2	0.0039	12 31.2 20	4	0.0077	14 36 29	7	0.0135
10 27 43.1	1	0.0019	13 18 23	1	0.0019	12 31.3 20	1	0.0019	14 36 30	1	0.0019
10 28 23.1	1	0.0019	13 18.3 18	1	0.0019	12 32 16	3	0.0058	14 36 31	5	0.0097
10 28 26.1	1	0.0019	13 19 17	1	0.0019	12 32 17	3	0.0058	14 36 32	1	0.0019
10 29 26	1	0.0019	13 19 20	2	0.0039	12 32 18	3	0.0058	14 36 32.2	1	0.0019
10 29 27.1	1	0.0019	13 20 19	1	0.0019	12 32 19	4	0.0077	14 36 33	2	0.0039
10 29 28	1	0.0019	13 20 20	2	0.0039	12 32.2 16	1	0.0019	14 36 33.2	1	0.0019
10 30 18	1	0.0019	13 20 22	1	0.0019	12 32.2 17	1	0.0019	14 36 34.2	1	0.0019
10 30 24.1	1	0.0019	13 7 18	1	0.0019	12 32.2 18	2	0.0039	14 36 36.2	1	0.0019
10 31 28.1	1	0.0019	13 7 19	4	0.0077	12 32.2 19	3	0.0058	14 36 40.2	1	0.0019
10 31 41.1	1	0.0019	13 7 20	2	0.0039	12 33 16	1	0.0019	14 36 42.2	1	0.0019
10 33 23	1	0.0019	13 7 23	1	0.0019	12 33 18	2	0.0039	14 36 44.2	1	0.0019
10 34 18	1	0.0019	13 7 24	1	0.0019	12 33 19	1	0.0019	14 36.3 31	1	0.0019
11 16 19	1	0.0019	13 8 17	2	0.0039	12 33.2 18	1	0.0019	14 36.3 33	2	0.0039
11 17 18	1	0.0019	13 8 18	1	0.0019	12 34 18	1	0.0019	14 37 0	1	0.0019
11 17 25.1	1	0.0019	13 8 20	1	0.0019	12 34 19	2	0.0039	14 37 26	3	0.0058
11 17.1 23.1	1	0.0019	14 12 19	1	0.0019	12 35 16	1	0.0019	14 37 27	5	0.0097
11 17.1 31	1	0.0019	14 12 21	4	0.0077	13 24 19	1	0.0019	14 37 28	4	0.0077
11 18 18	3	0.0058	14 12 22	1	0.0019	13 26.2 16	2	0.0039	14 37 29	3	0.0058
11 18 20	1	0.0019	14 13 18	3	0.0058	13 27.2 16	1	0.0019	14 37 30	3	0.0058
11 18 23	1	0.0019	14 13 20	2	0.0039	13 27.2 18	1	0.0019	14 37 31	5	0.0097
11 18 24.1	1	0.0019	14 13 23	1	0.0019	13 27.2 21	1	0.0019	14 37 31.3	1	0.0019
11 18 26.1	1	0.0019	14 13.2 19	1	0.0019	13 28 16	1	0.0019	14 37 32	1	0.0019
11 18 27.1	1	0.0019	14 13.2 20	1	0.0019	13 28 19	3	0.0058	14 37 33	2	0.0039
11 18.1 13.3	1	0.0019	14 14 18	3	0.0058	13 28.2 16	3	0.0058	14 37 34	1	0.0019
11 18.1 19	1	0.0019	14 14 19	2	0.0039	13 28.2 18	2	0.0039	14 37 34.2	1	0.0019

LG1			LG2			LG3			LG4		
DXS8378-DXS10135-DXS10148			DXS7132-DXS10074-DXS10079			HPRTB-DXS10101-DXS10103			DXS7423-DXS10134-DXS10146		
Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency
11 18.1 24.1	1	0.0019	14 14 20	2	0.0039	13 28.2 19	3	0.0058	14 37 43.2	1	0.0019
11 18.1 27	1	0.0019	14 14 21	1	0.0019	13 28.2 20	2	0.0039	14 37.2 27	1	0.0019
11 18.1 29.2	1	0.0019	14 15 13	1	0.0019	13 29 17	1	0.0019	14 37.2 28	1	0.0019
11 18.1 30.1	1	0.0019	14 15 15	1	0.0019	13 29 18	2	0.0039	14 37.3 43.2	1	0.0019
11 19 18	1	0.0019	14 15 17	1	0.0019	13 29 19	8	0.0155	14 38 26	1	0.0019
11 19 23.1	1	0.0019	14 15 18	2	0.0039	13 29 20	1	0.0019	14 38 27	1	0.0019
11 19 25.1	1	0.0019	14 15 19	13	0.0251	13 29.2 16	4	0.0077	14 38 28	1	0.0019
11 19 28	1	0.0019	14 15 20	7	0.0135	13 29.2 18	2	0.0039	14 38 29	3	0.0058
11 19 32.1	1	0.0019	14 15 21	6	0.0116	13 29.2 19	3	0.0058	14 38 30	1	0.0019
11 19 40	1	0.0019	14 16 15	2	0.0039	13 29.2 22	1	0.0019	14 38 32	3	0.0058
11 19.1 16.3	1	0.0019	14 16 16	1	0.0019	13 30 16	3	0.0058	14 38 33	1	0.0019
11 19.1 17	3	0.0058	14 16 17	2	0.0039	13 30 17	2	0.0039	14 38 36.2	5	0.0097
11 19.1 18	2	0.0039	14 16 18	6	0.0116	13 30 18	3	0.0058	14 38 38	1	0.0019
11 20 13.3	1	0.0019	14 16 19	13	0.0251	13 30 19	5	0.0097	14 38 40.3	1	0.0019
11 20 24	1	0.0019	14 16 20	8	0.0155	13 30.2 17	2	0.0039	14 38 45.2	1	0.0019
11 20 24.1	2	0.0039	14 16 21	4	0.0077	13 30.2 18	5	0.0097	14 38.3 33	1	0.0019
11 20 25.1	1	0.0019	14 16 22	1	0.0019	13 30.2 19	6	0.0116	14 38.3 42.2	1	0.0019
11 20 27.1	1	0.0019	14 16 23	1	0.0019	13 30.2 20	2	0.0039	14 38.3 44.2	1	0.0019
11 20 28.1	2	0.0039	14 16 24	1	0.0019	13 30.2 21	1	0.0019	14 39 26	3	0.0058
11 20 29.1	2	0.0039	14 17 17	3	0.0058	13 31 16	8	0.0155	14 39 28	1	0.0019
11 20 30	1	0.0019	14 17 18	5	0.0097	13 31 17	5	0.0097	14 39 29	1	0.0019
11 20 32	1	0.0019	14 17 19	10	0.0193	13 31 18	4	0.0077	14 39 31	1	0.0019
11 20.1 16	1	0.0019	14 17 20	10	0.0193	13 31 19	5	0.0097	14 39 32	1	0.0019
11 20.1 19	1	0.0019	14 17 21	6	0.0116	13 31 20	4	0.0077	14 39 34	1	0.0019
11 20.1 25	1	0.0019	14 17 22	1	0.0019	13 31.2 16	1	0.0019	14 39 36.2	3	0.0058
11 20.1 29.2	1	0.0019	14 17 23	1	0.0019	13 31.2 17	1	0.0019	14 40 26	1	0.0019
11 20.1 32	1	0.0019	14 18 15	2	0.0039	13 31.2 18	4	0.0077	14 40 27	1	0.0019

LG1			LG2			LG3			LG4		
DXS8378-DXS10135-DXS10148			DXS7132-DXS10074-DXS10079			HPRTB-DXS10101-DXS10103			DXS7423-DXS10134-DXS10146		
Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency
11 21 18	1	0.0019	14 18 17	3	0.0058	13 31.2 19	4	0.0077	14 40 31	1	0.0019
11 21 23	1	0.0019	14 18 18	3	0.0058	13 31.2 20	1	0.0019	14 40 38.2	1	0.0019
11 21 25.1	1	0.0019	14 18 19	5	0.0097	13 31.2 21	1	0.0019	14 40.3 30	1	0.0019
11 21 26.1	2	0.0039	14 18 20	3	0.0058	13 31.3 16	1	0.0019	14 40.3 31	1	0.0019
11 21 28.1	1	0.0019	14 18 21	5	0.0097	13 32 15	1	0.0019	14 41.3 27	1	0.0019
11 21 31	1	0.0019	14 18 22	1	0.0019	13 32 16	7	0.0135	14 41.3 31	1	0.0019
11 21 31.1	1	0.0019	14 19 18	1	0.0019	13 32 17	4	0.0077	14 42.3 30	1	0.0019
11 21.1 20.1	2	0.0039	14 19 19	3	0.0058	13 32 18	6	0.0116	15 26.1 24	1	0.0019
11 21.1 29	1	0.0019	14 19 20	3	0.0058	13 32 19	3	0.0058	15 30 43.2	1	0.0019
11 21.1 31	1	0.0019	14 19 21	1	0.0019	13 32 20	4	0.0077	15 30.1 30	1	0.0019
11 21.1 41.1	1	0.0019	14 19 22	1	0.0019	13 32.2 19	3	0.0058	15 31 42.2	1	0.0019
11 21.1 42.1	1	0.0019	14 7 18	3	0.0058	13 32.2 20	1	0.0019	15 32 29	1	0.0019
11 22 18	1	0.0019	14 7 20	4	0.0077	13 33 16	2	0.0039	15 32 30	1	0.0019
11 22 19	2	0.0039	14 8 16	1	0.0019	13 33 17	7	0.0135	15 32 33.2	1	0.0019
11 22 24.1	2	0.0039	14 8 17	4	0.0077	13 33 18	3	0.0058	15 33 24	1	0.0019
11 22 25.1	4	0.0077	14 8 18	1	0.0019	13 33 19	1	0.0019	15 33 26	1	0.0019
11 22 26.1	2	0.0039	14 8 19	2	0.0039	13 33 20	3	0.0058	15 33 26.2	1	0.0019
11 22 29	1	0.0019	14 8 20	3	0.0058	13 33 21	1	0.0019	15 33 27	1	0.0019
11 22 29.1	1	0.0019	14 8 21	1	0.0019	13 33.1 20	1	0.0019	15 33 29	1	0.0019
11 22 41.1	1	0.0019	14 9 16	1	0.0019	13 33.2 18	2	0.0039	15 33 30	3	0.0058
11 22.1 18	2	0.0039	14 9 19	1	0.0019	13 33.2 19	1	0.0019	15 33 31	2	0.0039
11 22.1 19	1	0.0019	15 11 19	2	0.0039	13 34 15	1	0.0019	15 33 32	1	0.0019
11 22.1 22.1	1	0.0019	15 12 21	1	0.0019	13 34 19	1	0.0019	15 33 36.2	1	0.0019
11 22.1 24.1	3	0.0058	15 12 24	1	0.0019	14 24.2 19	1	0.0019	15 33 44.2	2	0.0039
11 23 18	1	0.0019	15 13 19	1	0.0019	14 27 17	1	0.0019	15 33.3 31	1	0.0019
11 23 18.2	1	0.0019	15 13 20	3	0.0058	14 27 18	1	0.0019	15 34 21	1	0.0019
11 23 19	2	0.0039	15 13 21	1	0.0019	14 27.2 19	1	0.0019	15 34 26	2	0.0039

LG1			LG2			LG3			LG4		
DXS8378-DXS10135-DXS10148			DXS7132-DXS10074-DXS10079			HPRTB-DXS10101-DXS10103			DXS7423-DXS10134-DXS10146		
Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency
11 23 21	1	0.0019	15 13 22	1	0.0019	14 28.2 19	1	0.0019	15 34 27	3	0.0058
11 23 24	1	0.0019	15 14 17	1	0.0019	14 29 19	5	0.0097	15 34 28	1	0.0019
11 23 25.1	1	0.0019	15 14 18	1	0.0019	14 29 20	1	0.0019	15 34 29	2	0.0039
11 23 28.2	1	0.0019	15 14 19	1	0.0019	14 29.2 16	1	0.0019	15 34 31	4	0.0077
11 23 30	1	0.0019	15 14 20	1	0.0019	14 29.2 17	1	0.0019	15 34 32	3	0.0058
11 23 31	1	0.0019	15 14 21	2	0.0039	14 29.2 18	2	0.0039	15 34 33	1	0.0019
11 23 32	1	0.0019	15 14 22	1	0.0019	14 29.2 19	1	0.0019	15 34 42.2	3	0.0058
11 23.1 24.1	1	0.0019	15 14.2 19	1	0.0019	14 30 17	1	0.0019	15 34.2 24	1	0.0019
11 23.1 41.1	1	0.0019	15 15 15	2	0.0039	14 30 18	1	0.0019	15 34.2 26	1	0.0019
11 24 18	5	0.0097	15 15 17	1	0.0019	14 30 19	2	0.0039	15 34.2 28	1	0.0019
11 24 20	1	0.0019	15 15 18	4	0.0077	14 30.2 16	1	0.0019	15 34.2 30	1	0.0019
11 24 21	1	0.0019	15 15 19	1	0.0019	14 30.2 18	5	0.0097	15 34.3 32	1	0.0019
11 24 24	1	0.0019	15 15 20	3	0.0058	14 30.2 19	6	0.0116	15 34.3 33	2	0.0039
11 24 25.1	1	0.0019	15 15 21	10	0.0193	14 30.2 20	2	0.0039	1534.3362	1	0.0019
11 24 27.1	2	0.0039	15 15 22	2	0.0039	14 31 16	3	0.0058	15 35 25	3	0.0058
11 24 28.1	2	0.0039	15 16 17	2	0.0039	14 31 17	5	0.0097	15 35 26	2	0.0039
11 24 32	1	0.0019	15 16 18	4	0.0077	14 31 18	5	0.0097	15 35 27	4	0.0077
11 25 18	3	0.0058	15 16 19	5	0.0097	14 31 19	7	0.0135	15 35 28	5	0.0097
11 25 21	1	0.0019	15 16 20	6	0.0116	14 31 20	3	0.0058	15 35 29	4	0.0077
11 25 24.1	3	0.0058	15 16 21	5	0.0097	14 31.2 18	2	0.0039	15 35 30	3	0.0058
11 25 25	1	0.0019	15 16 22	1	0.0019	14 31.2 19	4	0.0077	15 35 31	1	0.0019
11 25 25.1	1	0.0019	15 17 14	1	0.0019	14 32 16	5	0.0097	15 35 32	2	0.0039
11 25 26.1	1	0.0019	15 17 15	3	0.0058	14 32 17	1	0.0019	15 35 34.2	1	0.0019
11 25 27.1	2	0.0039	15 17 17	1	0.0019	14 32 18	2	0.0039	15 35 38.2	1	0.0019
11 25 30.1	1	0.0019	15 17 18	2	0.0039	14 32 19	5	0.0097	15 35 45.2	1	0.0019
11 25.1 25.1	1	0.0019	15 17 19	3	0.0058	14 32 20	2	0.0039	15 35.1 27	1	0.0019
11 26 18	1	0.0019	15 17 20	7	0.0135	14 32.2 18	3	0.0058	15 36 25	4	0.0077

LG1			LG2			LG3			LG4		
DXS8378-DXS10135-DXS10148			DXS7132-DXS10074-DXS10079			HPRTB-DXS10101-DXS10103			DXS7423-DXS10134-DXS10146		
Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency
11 26 23.1	2	0.0039	15 17 21	3	0.0058	14 32.2 19	1	0.0019	15 36 26	2	0.0039
11 26 24.1	2	0.0039	15 17 21.2	1	0.0019	14 33 16	6	0.0116	15 36 27	3	0.0058
11 26 25.1	2	0.0039	15 17 22	1	0.0019	14 33 17	1	0.0019	15 36 28	6	0.0116
11 26 26.1	1	0.0019	15 17 24	1	0.0019	14 33 18	2	0.0039	15 36 29	4	0.0077
11 26.3 13.3	1	0.0019	15 18 15	2	0.0039	14 33 19	3	0.0058	15 36 30	4	0.0077
11 26.3 28	1	0.0019	15 18 18	1	0.0019	14 34 16	1	0.0019	15 36 31	6	0.0116
11 27 18	3	0.0058	15 18 19	2	0.0039	14 34 20	2	0.0039	15 36 32	1	0.0019
11 27 23.1	1	0.0019	15 18 20	6	0.0116	14.2 35 15	1	0.0019	15 36 32.2	1	0.0019
11 27 24	2	0.0039	15 18 21	4	0.0077	15 27 18	1	0.0019	15 36 39.2	1	0.0019
11 27 25.1	1	0.0019	15 18 22	2	0.0039	15 28.2 16	1	0.0019	15 36 40.2	3	0.0058
11 27 26.1	2	0.0039	15 19 18	2	0.0039	15 29 18	2	0.0039	15 36 41.2	1	0.0019
11 27 27	1	0.0019	15 19 19	1	0.0019	15 29 20	1	0.0019	15 36 44.2	1	0.0019
11 27 27.1	2	0.0039	15 19 21	5	0.0097	15 29 21	1	0.0019	15 36 45.2	1	0.0019
11 27 29	1	0.0019	15 20 18	1	0.0019	15 29.2 19	1	0.0019	15 36.3 26	1	0.0019
11 27 32.1	1	0.0019	15 7 22	1	0.0019	15 30 16	1	0.0019	15 36.3 27	1	0.0019
11 27.1 13.3	2	0.0039	15 8 17	1	0.0019	15 30 18	1	0.0019	15 37 0	1	0.0019
11 27.3 27	1	0.0019	15 8 18	3	0.0058	15 30.2 16	2	0.0039	15 37 23	1	0.0019
11 28 21	1	0.0019	15 8 19	3	0.0058	15 31 16	1	0.0019	15 37 24	2	0.0039
11 28 23	1	0.0019	15 8 20	4	0.0077	15 31 17	1	0.0019	15 37 25	1	0.0019
11 28 24.1	4	0.0077	15 9 20	1	0.0019	15 31 19	1	0.0019	15 37 26	1	0.0019
11 28 25.1	2	0.0039	16 12 22	1	0.0019	15 31.2 20	1	0.0019	15 37 27	1	0.0019
11 28 26	1	0.0019	16 13 18	1	0.0019	15 32 16	1	0.0019	15 37 28	2	0.0039
11 28 26.1	1	0.0019	16 13 20	1	0.0019	15 32 18	1	0.0019	15 37 29	4	0.0077
11 28 27.1	1	0.0019	16 15 16	2	0.0039	15 32 19	4	0.0077	15 37 30	3	0.0058
11 28 28.1	2	0.0039	16 15 18	1	0.0019	15 32.2 20	1	0.0019	15 37 31	5	0.0097
11 28.1 26.1	1	0.0019	16 15 22	1	0.0019	15 33 16	1	0.0019	15 37 34.2	1	0.0019
11 28.3 19	1	0.0019	16 16 18	1	0.0019	15 33 17	1	0.0019	15 37 38.2	1	0.0019

LG1			LG2			LG3			LG4		
DXS8378-DXS10135-DXS10148			DXS7132-DXS10074-DXS10079			HPRTB-DXS10101-DXS10103			DXS7423-DXS10134-DXS10146		
Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency
11 28.3 24	1	0.0019	16 16 19	1	0.0019	16 29.2 19	1	0.0019	15 37 40.2	1	0.0019
11 29 18	1	0.0019	16 16 20	2	0.0039	16 32 19	1	0.0019	15 37 43.2	1	0.0019
11 29 23	1	0.0019	16 17 21	2	0.0039	16 33 19	1	0.0019	15 37 45.2	1	0.0019
11 29 23.1	1	0.0019	16 17 22	1	0.0019	16 34 16	1	0.0019	15 37.2 27	1	0.0019
11 29 24	1	0.0019	16 18 17	1	0.0019	9 30.2 18	1	0.0019	15 37.3 34.2	1	0.0019
11 29 24.1	1	0.0019	16 18 21	2	0.0039	9 31.2 18	1	0.0019	15 38 27	2	0.0039
11 29 25	1	0.0019	16 18 22	1	0.0019				15 38 27.3	1	0.0019
11 29 25.1	2	0.0039	16 19 18	2	0.0039				15 38 28	3	0.0058
11 29 28	1	0.0019	16 19 19	1	0.0019				15 38 29	2	0.0039
11 29 29	1	0.0019	16 20 18	1	0.0019				15 38 30	3	0.0058
11 29.3 27	1	0.0019	16 7 19	1	0.0019				15 38 31	1	0.0019
11 30 18	2	0.0039	16 8 18	2	0.0039				15 38 34.2	2	0.0039
11 30 23	1	0.0019	17 15 21	1	0.0019				15 38 35.2	1	0.0019
11 30 24.1	1	0.0019	17 16 18	1	0.0019				15 38 36.2	1	0.0019
11 30 26.1	3	0.0058	18 20 21	1	0.0019				15 38 44.2	1	0.0019
11 30 27.1	1	0.0019	18 7 21	1	0.0019				15 38.2 40.2	2	0.0039
11 30 28.1	1	0.0019							15 38.3 28	1	0.0019
11 30 29	1	0.0019							15 39 27	1	0.0019
11 30.1 24.1	1	0.0019							15 39 28	3	0.0058
11 31 18	1	0.0019							15 39 30	1	0.0019
11 31 25.1	1	0.0019							15 39 31	1	0.0019
11 31 40.1	1	0.0019							15 39.3 28	1	0.0019
11 31.2 27.1	1	0.0019							15 39.3 30	1	0.0019
11 32 24.1	1	0.0019							15 39.3 31	1	0.0019
11 32 25.1	1	0.0019							15 39.3 39.2	1	0.0019
11 32.1 14	1	0.0019							15 39.3 43.2	1	0.0019
11 32.1 18	1	0.0019							15 40 0	1	0.0019

LG1			LG2			LG3			LG4		
DXS8378-DXS10135-DXS10148			DXS7132-DXS10074-DXS10079			HPRTB-DXS10101-DXS10103			DXS7423-DXS10134-DXS10146		
Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency
11 32.1 35.1	1	0.0019							15 40 26	1	0.0019
11 33 26.1	1	0.0019							15 40.3 27	1	0.0019
11 34 24	1	0.0019							15 40.3 28	1	0.0019
11 34.1 28	1	0.0019							15 40.3 39.2	1	0.0019
12 16 18	1	0.0019							15 40.3 43.2	1	0.0019
12 17 26.1	2	0.0039							15 41 32	1	0.0019
12 17.1 25	1	0.0019							15 41.3 27	1	0.0019
12 18 18	1	0.0019							15 41.3 44.2	1	0.0019
12 18 24.1	1	0.0019							15 42.3 28	1	0.0019
12 18 25.1	1	0.0019							15 42.3 29	1	0.0019
12 18 26	1	0.0019							15 43.3 43.2	1	0.0019
12 18 26.1	1	0.0019							16 32 27	1	0.0019
12 18 27	1	0.0019							16 32 29	3	0.0058
12 18 27.1	2	0.0039							16 32 32	1	0.0019
12 18.1 13.3	2	0.0039							16 32 37.2	1	0.0019
12 18.1 19	1	0.0019							16 34 26	1	0.0019
12 18.1 24	1	0.0019							16 34 27	1	0.0019
12 18.1 25.1	1	0.0019							16 34 29	6	0.0116
12 18.1 28.1	1	0.0019							16 34 31	1	0.0019
12 18.1 31	1	0.0019							16 34.3 32	1	0.0019
12 19 19	1	0.0019							16 35 0	1	0.0019
12 19 20	2	0.0039							16 35 26	1	0.0019
12 19 23.1	1	0.0019							16 35 27	2	0.0039
12 19 24	1	0.0019							16 35 29	1	0.0019
12 19 25.1	1	0.0019							16 35 30	1	0.0019
12 19 27.1	1	0.0019							16 35 32	1	0.0019
12 19 29	1	0.0019							16 35 35.2	1	0.0019

LG1			LG2			LG3			LG4		
DXS8378-DXS10135-DXS10148			DXS7132-DXS10074-DXS10079			HPRTB-DXS10101-DXS10103			DXS7423-DXS10134-DXS10146		
Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency
12 19.1 13.3	1	0.0019							16 35 40.2	1	0.0019
12 19.1 19	2	0.0039							16 35 41.2	1	0.0019
12 19.1 24.1	1	0.0019							16 35 45.2	1	0.0019
12 20 13.3	2	0.0039							16 36 22.1	1	0.0019
12 20 18	3	0.0058							16 36 25	1	0.0019
12 20 23	2	0.0039							16 36 28	4	0.0077
12 20 24.1	1	0.0019							16 36 29	1	0.0019
12 20 39.1	1	0.0019							16 36 30	1	0.0019
12 20.1 17	1	0.0019							16 36 32	2	0.0039
12 20.1 25	1	0.0019							16 37 26	1	0.0019
12 20.3 40.1	1	0.0019							16 37 28	3	0.0058
12 21 17	1	0.0019							16 37 30	2	0.0039
12 21 22	1	0.0019							16 37 32	1	0.0019
12 21 24.1	2	0.0039							16 37 43.2	1	0.0019
12 21 25.1	1	0.0019							16 37 46.2	1	0.0019
12 21 26	1	0.0019							16 37.3 30	1	0.0019
12 21 26.1	2	0.0039							16 38 26	1	0.0019
12 21 27	1	0.0019							16 38 27	1	0.0019
12 21 28.1	1	0.0019							16 38 28	2	0.0039
12 21 32.1	1	0.0019							16 38 39.2	1	0.0019
12 21.1 13.3	1	0.0019							16 39 35	1	0.0019
12 21.1 27.1	2	0.0039							16 39.3 28	1	0.0019
12 21.1 29	1	0.0019							16 40.3 39.2	2	0.0039
12 21.1 41.1	1	0.0019							16 40.3 40.2	2	0.0039
12 21.1 42.1	1	0.0019							16 41.3 40.2	1	0.0019
12 22 18	1	0.0019							16 43.3 28	1	0.0019
12 22 28.1	1	0.0019							17 33 28	2	0.0039

LG1			LG2			LG3			LG4		
DXS8378-DXS10135-DXS10148			DXS7132-DXS10074-DXS10079			HPRTB-DXS10101-DXS10103			DXS7423-DXS10134-DXS10146		
Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency
12 22 32.3	1	0.0019							17 33 31	1	0.0019
12 22.1 27	1	0.0019							17 34 40.2	1	0.0019
12 22.1 27.1	1	0.0019							17 36 31	1	0.0019
12 23 13.3	1	0.0019							17 37 27	2	0.0039
12 23 19	3	0.0058							17 37 29	1	0.0019
12 23 23.1	1	0.0019							17 39.3 30	1	0.0019
12 23 24	1	0.0019							17 42.3 38.2	1	0.0019
12 23 24.1	3	0.0058							8 35 37.2	1	0.0019
12 23 25.1	1	0.0019							8 39 24	1	0.0019
12 23 29.1	1	0.0019									
12 23 31.3	1	0.0019									
12 23.1 18	1	0.0019									
12 23.1 19	1	0.0019									
12 24 18	1	0.0019									
12 24 20.3	1	0.0019									
12 24 21	1	0.0019									
12 24 23.1	1	0.0019									
12 24 24	1	0.0019									
12 24 24.1	1	0.0019									
12 24 25.1	1	0.0019									
12 24 26	1	0.0019									
12 24 26.1	1	0.0019									
12 24 39.1	1	0.0019									
12 25 18	3	0.0058									
12 25 22.1	2	0.0039									
12 25 23.1	1	0.0019									
12 25 24.1	1	0.0019									

LG1			LG2			LG3			LG4		
DXS8378-DXS10135-DXS10148			DXS7132-DXS10074-DXS10079			HPRTB-DXS10101-DXS10103			DXS7423-DXS10134-DXS10146		
Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency
12 25 25.1	1	0.0019									
12 25 30.1	1	0.0019									
12 26 17	2	0.0039									
12 26 18	1	0.0019									
12 26 20.1	1	0.0019									
12 26 24.1	1	0.0019									
12 26 25.1	2	0.0039									
12 26 26.1	1	0.0019									
12 26 28.1	1	0.0019									
12 26 31	1	0.0019									
12 26 32.1	1	0.0019									
12 27 19	1	0.0019									
12 27 23.1	1	0.0019									
12 27 24	1	0.0019									
12 27 24.1	3	0.0058									
12 27 25	1	0.0019									
12 27 25.1	1	0.0019									
12 27 26.3	1	0.0019									
12 27 27.1	1	0.0019									
12 27 30	1	0.0019									
12 28 18	2	0.0039									
12 28 24.1	1	0.0019									
12 28 26.1	2	0.0039									
12 28 27.1	1	0.0019									
12 28 28.1	1	0.0019									
12 28.1 22.3	1	0.0019									
12 29 25.1	1	0.0019									

LG1			LG2			LG3			LG4		
DXS8378-DXS10135-DXS10148			DXS7132-DXS10074-DXS10079			HPRTB-DXS10101-DXS10103			DXS7423-DXS10134-DXS10146		
Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency
12 29 26	1	0.0019									
12 29 26.1	1	0.0019									
12 30 22.1	1	0.0019									
12 30 24	1	0.0019									
12 30 25.1	1	0.0019									
12 30 27.1	1	0.0019									
12 31 18	1	0.0019									
12 31 23	1	0.0019									
12 31 25.1	2	0.0039									
12 32 25.1	1	0.0019									
12 32 26	1	0.0019									
12 32 27	1	0.0019									
12 32 28.1	1	0.0019									
12 32 30.1	1	0.0019									
12 33 18	2	0.0039									
12 33 27	1	0.0019									
12 33.1 13.3	1	0.0019									
12 34 19	1	0.0019									
12 34 251	1	0.0019									
12 34 27	1	0.0019									
12 34 32	1	0.0019									
12 34.1 30	1	0.0019									
12 35 28	2	0.0039									
12 35.1 23.1	1	0.0019									
12 36 26	1	0.0019									
12 36 32	1	0.0019									
12 36.2 13.3	1	0.0019									

LG1			LG2			LG3			LG4		
DXS8378-DXS10135-DXS10148			DXS7132-DXS10074-DXS10079			HPRTB-DXS10101-DXS10103			DXS7423-DXS10134-DXS10146		
Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency
12 36.2 23	1	0.0019									
12 37 25	1	0.0019									
12 37.1 23.1	1	0.0019									
12 37.2 13.3	2	0.0039									
12 38.2 13.3	1	0.0019									
12 39.2 40.1	1	0.0019									
13 17 20	1	0.0019									
13 17 25.1	1	0.0019									
13 18 26	1	0.0019									
13 18 27.1	2	0.0039									
13 18.1 19	1	0.0019									
13 19 27	1	0.0019									
13 19 27.1	1	0.0019									
13 20 13.3	1	0.0019									
13 21 22.1	1	0.0019									
13 21 23	1	0.0019									
13 21 24.1	1	0.0019									
13 21 25.1	3	0.0058									
13 24 24	1	0.0019									
13 24 42.1	1	0.0019									
13 25 18	1	0.0019									
13 25 24	1	0.0019									
13 25 25	1	0.0019									
13 25 25.1	1	0.0019									
13 25 40.1	1	0.0019									
13 25 41.1	1	0.0019									
13 26 18	1	0.0019									

LG1			LG2			LG3			LG4		
DXS8378-DXS10135-DXS10148			DXS7132-DXS10074-DXS10079			HPRTB-DXS10101-DXS10103			DXS7423-DXS10134-DXS10146		
Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency	Haplotype	Count	Frequency
13 26 25.1	1	0.0019									
13 26 27.1	1	0.0019									
13 27 27	1	0.0019									
13 30 17	1	0.0019									
13 33 27.1	1	0.0019									
13 37 33	1	0.0019									
14 19 18	1	0.0019									
14 31 26.1	1	0.0019									
8 28 26.1	1	0.0019									
9 17.1 24.3	1	0.0019									
9 18 18	1	0.0019									
9 18 27.1	1	0.0019									
9 19 35.1	1	0.0019									
9 20 23.1	1	0.0019									
9 21 23.1	1	0.0019									
9 22 18	2	0.0039									
9 23 19.3	1	0.0019									
9 24 23.1	1	0.0019									
9 28 27.1	1	0.0019									
9 31 20	1	0.0019									

Table H2 *Haplotype forensic parameters for 517 South African males.*

	LG1	LG2	LG3	LG4	Combined
	DXS8378-DXS10135-DXS10148	DXS7132-DXS10074-DXS10079	HPRTB-DXS10101-DXS10103	DXS7423-DXS10134-DXS10146	
Number of unique haplotypes	421	228	218	302	-
HD	0.999	0.994	0.994	0.996	-
PIC	0.997	0.992	0.992	0.994	-
PD_Male	0.997	0.992	0.992	0.994	0.999999998975966
PD_Female	1.000	1.000	1.000	1.000	1
MEC_Kruger	0.984	0.981	0.981	0.983	0.999999898770688
MEC_Kishida	0.987	0.989	0.989	0.988	0.999999980879369
MEC_Desmarais	0.997	0.992	0.992	0.994	0.99999999895124
MEC_Desmarais_duo	0.994	0.984	0.984	0.989	0.999999983927333

Abbreviations - LG: linkage group. HD: haplotype diversity. PD: power of discrimination. MEC: mean exclusion chance.

Appendix I:

Table I1 *Linkage disequilibrium test p-values for all pairs of loci. For male samples (upper triangle) the Exact test using a Markov chain (Chain length = 10000) was used. For female samples (lower triangle) likelihood ratio test for linkage disequilibrium was used. Significant p-values are bolded. i.e., p < 0.0008.*

Linkage group (LG)		1			2			3			4		
	Locus	DXS8378	DXS10135	DXS10148	DXS7132	DXS10074	DXS10079	HPRTB	DXS10101	DXS10103	DXS7423	DXS10134	DXS10146
1	DXS8378	-	0.015	0.146	0.695	0.823	0.738	0.092	0.265	0.343	0.644	0.228	0.840
	DXS10135	0.44703	-	0.289	0.719	0.229	0.905	0.004	0.923	0.413	0.370	0.001	0.552
	DXS10148	0.09327	0.00267	-	0.857	0.480	0.421	0.630	**0.000**	0.549	0.127	0.416	0.379
2	DXS7132	0.80990	0.95772	0.73050	-	0.045	0.222	0.070	0.364	0.692	0.191	0.618	0.959
	DXS10074	0.58139	0.54713	**0.00020**	0.22218	-	0.147	0.040	0.380	0.226	0.120	0.160	0.080
	DXS10079	0.93881	0.96000	0.28475	0.51604	0.14614	-	0.384	0.214	0.583	0.513	0.362	0.782
3	HPRTB	0.37010	0.63327	0.47396	0.33554	0.20713	0.17040	-	**0.000**	0.026	0.810	0.946	0.013
	DXS10101	0.06396	0.69614	0.13802	0.99673	0.00733	0.51554	0.05327	-	**0.000**	0.048	**0.000**	0.655
	DXS10103	0.41347	0.52713	0.03366	0.93347	0.20050	0.44663	0.00366	**0.00000**	-	0.141	0.161	0.339
4	DXS7423	0.70020	0.96455	0.72604	0.63505	0.36178	0.01782	0.11891	0.09416	0.18891	-	0.426	0.236
	DXS10134	0.74267	0.43634	0.15139	0.04446	0.19416	0.38030	0.74723	0.53287	0.08416	0.15158	-	**0.000**
	DXS10146	0.57228	0.29960	0.03059	0.26228	0.18515	0.45802	0.56129	0.08158	0.46594	0.01396	**0.00010**	-

Appendix J:

Table J1 *List of off-ladder alleles observed within the South African population. Bolded alleles have previously been reported* [71,97,103,108,109,113,117,118,157].

Marker	Allele	Total number of observations	Number of observations			
			African ancestry	European ancestry	Mixed ancestry	Indian/Asian ancestry
DXS10148	16.3	1			1	
	19.3	1			1	
	20.3	1			1	
	22.3	1	1			
	24.3	1			1	
	26.3	1			1	
	28.3	1			1	
	29.2	2	2			
	31.3	1	1			
	32	7	3	1	3	
	32.1	10	8	1	1	
	32.3	1	1			
	33	3	2		1	
	35.1	4	3		1	
	36.1	1	1			
	37.1	1			1	
	39.1	9	3	2	4	
	40	1	1			
	40.1	7	6		1	
	41.1	12	8	1	3	
	42.1	7	4	1	2	
	43.1	1	1			
	44.1	1	1			
DXS10134	26.1	1	1			
	27.1	1			1	
	28.2	1	1			
	29.1	1			1	
	29.2	1			1	
	30.1	2	1		1	
	33.2	1	1			
	33.3	4	3		1	
	35.1	1		1		
	36.2	2			1	1
DXS10135	26.3	3	1		2	
	27.1	2			2	
	28.3	5			5	
	29.3	2	1		1	
	30.1	1	1			
	33.1	2	1			1
	37.1	2			2	

Marker	Allele	Total number of observations	Number of observations			
			African ancestry	European ancestry	Mixed ancestry	Indian/Asian ancestry
DXS10135	**38.2**	1	1			
	40.2	1	1			
DXS10146	22.1	2			1	1
	26.2	1	1			
	30.1	1				1
	31.2	4	3		1	
	36	2	2			
	36.2	20	15		5	
	38	1			1	
	40.3	1	1			
DXS10101	22.2	1	1			
	28.1	1			1	
	31.3	2	1			1
	33.1	1				1
DXS10074	**13.2**	2		2		
	14.2	1	1			
	16.3	5	3		2	
DXS10079	**13**	11	9		1	1
HPRTB	14.2	1				1
Total		**166**	**96**	**9**	**53**	**8**