Indian Journal of Forensic Medicine and Pathology
Volume 14 Number 2, April - June 2021 (Special Isuue)
DOI: http://dx.doi.org/10.21088/ijfmp.0974.3383.14221.53

REVIEW RATICLE

African Y-STR Haplotyping and Y-Chromosome Profiling: A Review

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ABSTRACT

Forensic genetics is an indispensable tool in forensic analysis that uses genetic evidence in crime investigation and/or identification of missing individuals or victims of mass disaster. It is highly reliable and can be used to substantiate evidence to prove the guilt or innocence of a suspect in question. There is paucity of data on African forensic DNA profiling. This is partly due to lack of funding and expertise. Moreover, there are very limited forensic genetic commercial kits that incorporate markers that are specific for African populations, markers that will provide highly specific information on the African Y-STR markers. Therefore, the purpose of this study is to consolidate the published Y-STR data of African population for forensic and population genetic reference. The review presents the Y-haplotype and genetic diversity of African male population. The review dissects the data into different regions of the African continent, viz., the Northern, Southern, Eastern, Western and Central African regions.

KEYWORDS | forensic genetics, dna profiling, y-str, y-haplotype, africa

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INTRODUCTION

The use of DNA profiling in criminal cases was first used a little above 30 years ago. The pioneer of this work was Professor Sir Alec Jeffreys, whose groundbreaking forensic work was able to link the assault and murder of two young girls to Colin Pitchfork in 1983 and 1986. The case served as the landmark criminal case that gave birth to the use of DNA fingerprinting in the criminal justice system.[1]

The Y-chromosome is male-specific in humans and follows a strict mode of paternal inheritance. It comprises of a major non-recombining region (NRY) that makes it suitable to providing one of the highest resolution tools for studying human population genetics.[2] This high resolution provides it with high discrimination power between individuals suitable for forensic investigations involving male victims or suspects.

The number of multiple alleles that are remarkably differentiated between individuals by the number of repeat units on Y-Chromosome is referred to as Y-Chromosomal Short Tandem Repeats (Y-STRs).[3] The forensic use of Y-STR genotyping has become instrumental in the identification of males involved in sexual assault, paternity and ancestral determination, missing and disaster victims investigations.[4] High mutation rates in Y-STR markers referred to as rapidly mutating Y-STRs or RM Y-STRs have been reported recently.[3] Some commercially available forensic analysis kits, for example, Y-Filer plus amplification kit of Thermo Fisher Scientific, USA, have introduced the RM Y-STRs with anticipation that they will assist in discriminating close male

How to cite this article
Ibrahim El-Ladan Shehu. African Y-STR Haplotyping and Y Chromosome Profiling: A Review. Indian J Forensic Med Pathol. 2021;14(3 Special):379-385.

The African continent is inhabited by people with enormous linguistic, cultural and genetic diversity of more than 2,000 different languages and ethnic populations. The demographic timeline of the continent has recorded oscillations in population size, admixture, long and short-term migrations leading to rich and diverse variations and in modern populations. It can be said that the most genetically diverse region of the world is Africa.[5] Africa by size and population is the second-largest continent, comprising numerous countries and diverse populations. However, the information available on the Y-STR haplotype and allele frequencies in these populations is very little.[6]

There are several databases that the scientific community use to compare their data with already published data, forensic laboratories and other security agencies also use the databases, the most common databases include: YHRD and with Relia-Gene database and PowerPlex Y Haplotype Database.[7] The data provided in this review will help in consolidating the valuable information on the haplotype and allele frequencies of African Y-STR profile for population genetics and forensic reference.

Y-haplotype and Genetic Diversity in Central Africans

Studies on Central African population conducted by Arroyo-Pardo *et al.,* (2005) studied 16 Y-STR loci in 101 male samples of Equatorial Guinea origin who live in Madrid, Spain. Of the 101 studied individuals, 94 different haplotypes were obtained in the study. Another study conducted on 873 samples from Gabon and Cameroon from Central Africa by typing 18 Y-STRs found a total of 728 different haplotypes indicating high discrimination between the populations. They also observe high frequency of modal Bantu haplotype and its one-step neighbors as described by other literature in all the 24 Bantu populations in the study.[8] They also observed modal Bantu haplotype in two pygmy samples from Gabon and one of its one-step neighbors in one pygmy sample from Cameroon. Multi-Dimensional Scale Plot (MDS) showed all the Bantu population clustering together obviously separated from the Pygmies, indicating population homogeneity among the Bantus and some population admixture between the two populations.

Another study on Y STR among 165 Bantu population living on Bangui, Central African Republic, was conducted by Lecerf et al., (2007) who reported 88 different haplotypes, of which 83 were unique. The authors observed DYS385 and DYS392 to have the highest (0.9305) and lowest (0.1685) gene diversity (GD), respectively.

Data of Y-haplotype in Fang and Bubi populations from Bioko (Equatorial Guinea) were studied by Barrot et al., (2007), of the 133 samples studied in Bubi population, 102 and 87 different and unique haplotypes were reported respectively. Gene diversity in the study revealed DYS385 as the most polymorphic system.

The data generated by the researchers on the Y-haplotype diversity among Central Africans revealed that the populations are ideal for forensic casework due to their unique haplotype profile. It has also been established that DYS385 is the most polymorphic marker in the Central African population. It has also been revealed that the Central African population has intermediate allele 13.2 at DYS385 locus.

Y-Haplotype and Genetic Diversity in East Africans

Eighteen Y-STR profile of the population living in Maputo from Mozambique was characterized by Alves et al., 2003 who reported 101 defined haplotype out of a total of 112 studied samples, two individuals with seven shared haplotypes, while the most frequent was shared by five individuals. The most diverse and less polymorphic loci were DYS385 and DYS392 respectively.[11]

Twelve Y-STR of 40 Karimojong males from Karamoja, Uganda revealed 32 different haplotypes with high discrimination power. Comparison with the Y-STR data of Uganda, Mozambique, Cabinda and Equatorial Guinea revealed a large genetic distance between the populations.[12] Another study of 17 Y-STR haplotypes involving 118 males from the Nilotes population of Karamoja region in Uganda by Gomes et al., (2010) reported 94 different haplotypes, a total of 19 shared, 14 and 5 in two and three individuals respectively.[13]

Another study employing 27 Y-STR haplotypes among the Tigray populations of Northern Ethiopia by Haddish et al., (2019) revealed that the recent expansion of Yfiler to

study 27 loci produced a haplotype diversity and high discrimination capacity of 100%. Seventeen Y-chromosomal STR haplotypes in 69 Rwanda-Hutu unrelated male individuals from East Central Africa revealed a total of 62 unique haplotypes out of the 69 individuals.[6] The authors reported the lowest and highest gene diversity at locus DYS392 and DYS385 respectively.

Based on the data generated by the researchers, it is revealed that the highly discriminating or rather highly polymorphic allele in the East African population is DYS385 making it highly relevant in discriminating East African populations using the allele in forensic casework. It has also been established that DYS392 is at least a polymorphic marker in East African populations. The data presented by the researchers have demonstrated the uniqueness of the East African population with very few shared haplotypes among the populations which are of high forensic relevance.

Y-haplotype and Genetic Diversity in North Africans

A study on 185 individual Y-STR haplotype among four different populations: Southern Moroccan Berbers, Mozabites, Moroccan Arabs and Saharawis from North West Africa. The most informative markers in the populations were DYS390, DYS389II, DYS389I and DYS391 in the respective order of magnitude, the highest and lowest haplotype diversity were observed in Moroccan Berbers and Mozabites respectively.[14]

The first study on Y-STR of the Tunisian population was conducted by El Khil et al., (2001) who studied six Y-STR loci among 135 males from different ethnic groups: Berbers, Blacks of Jerba Island and Arabs. There was no significant difference between the Arabs and the Berbers except on locus DYS390. Contrastingly, a significant difference between Blacks and the other two islander groups was observed except for the locus DYS39I.[15]

In another study of 135 Jerban males, 67 different haplotypes were reported: 33 haplotypes out of 42 Jerban of Sub-Saharan Africa, 27 haplotypes out of 46 Arabs and 18 haplotypes out of 47 Berbers.[16] The study population had a haplotype diversity ranging from 0.987 to 0.827 where the Jerbans of Sub-saharan origin had the uppermost value, whereas the Berbers had the lowest value.

Another study on 13 Y-STR of 105 Southern Tunisian population by Ayadi et al., (2006) identified 81 different haplotypes, out of which 67 were unique, the most frequent haplotype was shared by five individuals in the study population.[17] The loci with the highest and lowest polymorphism are DYS385a/b and DYS436 respectively. In another study by Onofri et al., (2008) in Northern African populations: 52 Tunisian and 51 Moroccan samples, a lower haplotype diversity of 29 unique haplotypes out of 39 different haplotypes were observed in the Tunisian population, while higher haplotype diversity of 44 unique out of 47 different haplotypes in Moroccan population were reported.[16]

A study on a total of 267 Moroccan ethnic populations (Sahrawi, n=68, Berber-speaking, n=69 and Arab-speaking, n=130) revealed a total of 257 (96.25%) different haplotypes, out of which 10 alleles were found in two individuals each, 237 unique haplotypes were observed.[19] Highest Gene Diversity was recorded on alleles DYS385 (0.887) and DYS458 (0.820), the discrimination capacity (DC) and Haplotype Diversity (HD) were 0.963 and 0.9991 respectively.[19] Another study by Palet et al., (2010) on the Moroccan population from Figuig Oasis revealed 52 different haplotypes, and 36 unique in an overall total population of 96. The loci with the highest and lowest respective diversity were DSY458 and DYS392.

Another study on Berber and Arab-speaking populations in Morocco by[20] reported 74 different haplotypes out of the total 85 individuals. A non-significant difference in gene diversity between the Arab-speaking samples having higher (0.566) than the Berbers (0.472) was reported by the authors. The high polymorphic alleles in Arab-speaking and Berbers were DYS385 and DYS458 respectively, while the lowest polymorphic marker was DYS392 in both the populations. Two new alleles of DYS458 locus were observed in one Berber and one Arab.[20]

A study on 17 Y-STR of 208 individuals from South(Upper) Egypt reported 204 different haplotypes, of which 200 were unique and 4 alleles were found twice each.[21] The most polymorphic allele was DYS385a/b followed by DYS458. Another study on Y-STR of 238 Benghazi

population, East Libya revealed a total of 238 different haplotypes, out of which 214 were unique, and 24 shared haplotypes.[22] The most polymorphic loci were DYS385a/b and DYS458 with haplotype diversity of 0.82 and 0.73 respectively.[22] Another study on Libyan population by Triki-Fendri *et al.,* (2013) revealed 142 different haplotypes out which 124 were unique in a total population of 176 individuals.[23]

D'Atanasio *et al.,* (2019) studied the discrimination power of the Y-Filer Plus multiplex kit in 11 North African populations from Egypt, Libya, Algeria and Morocco. The authors observed null alleles at three different loci (FYF387S1, DYS448 and DYS389II). They determined the genetic diversity (GD) with the exclusion of the null alleles and observed DYS385 and DYS481 with the highest values of 0.86 and 0.85 respectively. DYF387S1 showed the fourth highest value comparable to the GD values of RM Y-STRs which the authors attributed to an observed low GD value in the Algerian population under study.[24]

The most polymorphic loci in North African populations are DYS385 and DYS458, while the least polymorphic locus in all the North African populations was DYS392. Some Tunisian populations revealed DYS710 as the most polymorphic marker. Intermediate alleles were observed in some of the North African populations. The North African populations also exhibited unique haplotype diversity even after search and comparison on Y-STR databases which makes them suitable for forensic casework.

Y-haplotype and Genetic Diversity in West Africans

A study on the population of Guinea Bissau was conducted by.[25] The authors studied Y-STR population data of 215 unrelated healthy males whose ancestors were known to have lived in Guinea Bissau for three generations. The authors observed that the range of the studied loci and the allele frequencies are similar to the ones observed in other Sub-saharan Africa. The authors noted high prevalence of alleles 11 for DYS392 (88%), 14 for DYS437 (72%), 11 for DYS438 (65%), 21 for DYS390 (67%), and 15 for DYS19 (42%). The highest genetic diversity was observed in DYS19 and DYS389II (0.7182 and 0.7239) respectively, while the highest haplotype diversity was observed in DYS385 (0.9031). One hundred and fifty-four distinct haplotypes were observed in 161 fully typed individuals.

Benin and Ivory Coast ethnic populations were studied by Fortes-Lima et al., (2015). The Authors studied 288 individuals. The data from the research showed 30 minimum haplotypes and a total of 45 Y-filer in Yoruba as well as 34 minimum haplotypes and 44 Y-filer in Bariba population. The Yoruba and the Bariba exhibited high genetic diversity values of 0.9937 and 0.9929 respectively.[26]

A study was conducted at the Institute of Legal Medicine, Cologne, Germany. Individuals from different countries of West Africa (Nigeria, Gambia, Niger, Senegal, Benin, Togo, Sierra Leone, Ghana, Ivory Coast and Liberia) were selected for the study.[5] High values of haplotype diversity (1.0000 ± 0.0018) were observed in 86 samples under study, the values obtained were similar to what was reported by other studies.[5]

Y-STR profile of 142 individuals from the three largest ethnic groups in Nigeria (Yoruba, Hausa and Igbo) was studied by Martinez et al., (2017). 140 different haplotypes were observed, comprising of two individuals with two shared haplotypes. The authors reported an increase in the number of shared haplotypes when Y-filer kit was used: four and one haplotypes shared by two and three individuals respectively.[27]

The data presented on the genetic profile of West African populations revealed low genetic diversity with very few shared haplotypes among the individuals which translates to population homogeneity. Upon comparison with other populations on YHRD, very few matches were obtained. DYS385 was found to be the most polymorphic allele in some West African populations.

Y-haplotype and Genetic Diversity in Southern Africans

A study was conducted by Sánchez-Diz P *et al.,* [28] on African population groups from Mozambique. The authors studied a sample of 308 unrelated healthy individuals from the following groups: Nguni, Rongas, Senas, Changanes, Nhungwes, Tswas, Macondes, Chopes, Yao, Bitongas, Chuabos, Shonas, Lomwe, Ndaus, Makuas and

Nyanjas. Lower gene diversity was observed on DYS391 and DYS392 in all the populations under study. Of the total 308 samples studied, only 126 different haplotypes were observed, with the most frequent haplotype present in 22 samples. The observed average haplotype diversity was 97%.

Study on individuals living in KwaZulu-Natal and Western Cape provinces in South Africa was conducted by Lea N *et al.*[29] Three subpopulations (88 Xhosa, 101 English Speaking Caucasian and 77 Asian Indian males) were recruited for the study. Of the total population, 77, 101 and 73 different haplotypes were observed in Xhosa, Caucasian and Asian Indian populations. The number of alleles ranges from three (DYS391 and DYS392) to 21 in DYS710, while the average gene diversity ranged from 0.32 in DYS391 to 0.89 in DYS711 loci. The authors reported DYS710, DYS711, DYS712, DYS713, DYS7114 as novel markers and among the most variable markers.[29]

In another study conducted by D'Amato et al., (2008) on 99 indigenous Xhosa, 100 Caucasian English, 86 Asian Indian, 114 mixed "colored" and 107 Caucasian Afrikaan populations. Of the 506 individuals, 394 different haplotypes were observed, shared haplotypes were observed in 33 individuals. The allele frequency and haplotype diversity in 54 Ovambo male population in Namibia were carried out.[30] The study was conducted on 28 Y-STRs, where a total of 51 different haplotypes and 48 unique haplotypes were observed. Three shared haplotypes were also observed in two individuals. DYS385 and DYS392 had the highest (0.9000) and lowest (0.036) respective diversity values.

Analysis of 17 Y-STR loci in 105 healthy, unrelated Muslim populations of Cape Town, South Africa was conducted.[31] Eighty-three, 102 and 89 Asian-Indian, European-English and native Xhosa respectively were used for the comparison. The most polymorphic (0.958) and least polymorphic (0.449) loci based on GD values reported were DYS385 and DYS391 respectively. Ninety-one unique haplotypes and DC values of 0.866 were observed when considering the nine minimal haplotype Y-STRs, while in the case of the remaining eight loci.

The Y-STR haplotypes in three ethnic groups of Angola were studied by Melo *et al.* (2011). The authors studied 11 Y-STR haplotypes from a total of 166 individuals of three main ethnolinguistic groups of Angola: 53 Ovimbundo, 57 Bakongo and 56 Kimbundo populations. The Ovimbundo ethno-linguistic group showed 39 and 46 different and unique haplotypes respectively with two shared haplotypes that appear twice and one shared haplotype that appeared three times. Fifty-three and 49 different and unique haplotypes were observed respectively in the Bakongo group, four shared haplotypes were observed twice in the Bakongo group. In the Kimbundo group, 53 and 50 different and unique haplotypes were reported, while three shared haplotypes were observed twice. The most polymorphic locus was DYS385. Of the total of 166 individuals, 138 and 120 different and unique haplotypes were observed respectively.

The first study on Y-STR in Botswana population was conducted by Tau *et al.,* (2015), the authors studied 17 Y-STR profiles of 252 individuals among Botswana population: The authors clustered the samples into two regions: Northern [North and North-Western (1 San, 1 Sobea, 1 Herero, 6 Yeyi, 3 Mbukushu) n=12] and Southern Botswana [South and South East(1 Pedi, 2 Ndebele, 5 Tswapong, 11 Birwa, 8 Kgalagadi, 24 Kalanga, and 189 Tswana) n= 240]. The authors observed Haplotype Diversity and Discrimination capacity of 0.9990 and 0.9444 respectively and 238 unique haplotypes. The most common haplotype was observed five times in the populations except in the Tswana and Mbukushu that had four and one most frequent haplotypes.

D'Amato & Kasu, (2017) designed a highly discriminating Y-STR kit to preferentially target and amplify African samples, this genetic tool has been developed to a commercial prototype called UniQTyper Y-10. It was made up of 10 Y-STR loci markers including four RM Y-STRs. The authors studied 957 individuals from native and immigrant South African ethnic populations: English, Afrikaan, Indian, Admixed and native Bantu groups such as Venda, Pedi, Xhosa and Zulu. Of the total 957 studied samples, 870 unique haplotypes were observed with an overall Discrimination Capacity of 0.909. Another study conducted by Lesaoana et al., (2019) also used UniQTyper Y-10 to type the Y-STR profile of 938

individuals in five Bantu ethnic groups living in 10 Lesotho districts composed of South, North and Central regions. The authors reported 698 and 588 different and unique haplotypes respectively. A total of 350 individuals shared 110 haplotypes, the most frequent haplotype was shared by 28 individuals. The same haplotype was also reported to have been observed in 17 unrelated samples in Northern South Africa.

Another study on 27 Y-STR profiles of 200 unrelated individuals of Shona ethnic group of Zimbabwe in Harare province was conducted by Shonhai et al., (2020a) using 5-dye SureID 27Y kit. The authors reported only 159 complete 27 loci profiles, in response to that, the authors downgraded the loci to 12 Y-STR of PowerPlex. A total of 154 unique haplotypes out of the 159 were observed, two and one haplotype appeared twice and four times respectively. With a high genetic diversity depicted by the haplotype diversity of 0.9994, the overall DC of the population was 0.9686 while haplotype match probability was computed as 0.0069. The authors performed a single locus analysis of the whole Y-STR profile where they reported several observations which included but were not limited to triallelic pattern for locus DYS387S1, microvariant allele markers at DYS387S1 and DYS385. The lowest GD values were observed at loci DYS392 (0.03748) and DYS437 (0.096702). Meanwhile, DYS449, DYS481, and DYS518 had the highest GD values of 0.867239, 0.85042, and 0.825179, respectively.

In another study by Shonhai et al., (2020b) on Zimbabwean Shona brother pairs using the same kit used by Shonhai et al., (2020a). Only four brother pairs out of the 18 pairs were distinguishable based on the variation of allele numbers on only one allele marker among the 27 loci studied in addition to RM Y-STR DYS518. The authors observed loci DYS481 and DYS518 to have the highest GD with values of 0.8252 and 0.8502 respectively. Although the authors described the loci DYS393 and DYS458 as mini Y-STRs, they could not clearly explain the reason why variation between the brothers was observed in the markers. It is clear that the kit is not suitable for discriminating between related individuals. However, it can be noted that the kit was discriminatory between unrelated male Shona population of South Africa.[36]

The studies conducted on the Southern African populations have revealed that the most polymorphic markers reported were DYS385 and DYS710 in some populations. DYS391 and DYS392 were reported with the lowest GD values in the South African populations. Analysis of molecular variance in the study population revealed variations within the study groups. Searches on YHRD and Applied Biosystem databases presented very few numbers of shared haplotypes with other African populations. Additionally, very few shared haplotypes were observed within the study samples. The high frequency of unique haplotypes in the populations has highlighted the suitability of Southern African populations for forensic casework.

CONCLUSION

It can be concluded based on the review that the African populations are unique populations with high discrimination haplotypes, thus making them unique for forensic reference. DYS385 is the most polymorphic allele, intermediate allele 13.2 at the same locus was observed in Central African populations. The most informative marker in East African is also DYS385, while DYS392 is the least polymorphic locus. The North African populations bear DYS385 as the most polymorphic marker in addition to DYS458, while DYS392 is also the least polymorphic marker. However, the Tunisian population has exhibited DYS710 as the most informative marker. DYS385 was also the most informative marker in West African populations. DYS385 is also the most informative marker in South African populations in addition to DYS710 in small populations as observed in Tunisian populations of Central Africa. DYS391 and DYS392 are as well the least polymorphic markers in the South African populations. However, based on the number of African populations and the number of countries where the studies were conducted, it can be said that the African genetic data for forensic reference is under-represented. There is also no dedicated African database for forensic reference.

It is recommended that African nations should embrace the use of DNA forensics to minimize the rate of crimes in their countries. The need for

African nations to embrace the use of Combined DNA Information System (CODIS) cannot be over-emphasized, as this will help in solving many mysterious criminal cases involving mass disaster victims, victims of rape, murder, and other criminal cases. Based on the data generated from the review, it is visible that there is a need to develop and validate Y-STR kits that will primarily target and amplify the unique African haplotypes.

RECOMMENDATIONS

It is recommended that Africans should embrace the DNA forensics to minimize the rate of crimes in Africa. The need for Africa to embrace the use of Combined DNA Information System (CODIS) cannot be over-emphasized, as this will help in solving many criminal cases involving mass disaster victims, victims of rape, murder, and other criminal cases. Based on the data generated from the review, it is visible that there is a need to develop and validate Y-STR kits that will primarily target the unique African haplotypes. IJFMP

Acknowledgement:
The authors have made no acknowledgment in this article.
Conflict of Interest:
The authors declare that there is no commercial or financial links that could be construed as conflict of interests.
Source of Funding:
The author declares that there is no funding for this project.

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