



Mitochondrial genetic profile of the Yoruba population from Nigeria

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ABSTRACT

Nigeria is located in the Gulf of Guinea, also known as the “giant of Africa”, being the seventh most populated country in the world. The territory has a high genetic and cultural diversity. Yoruba is the second major ethnic group (and the most spoken language), and its population is concentrated in the southern region of the country. Aiming the elaboration of an accurate forensic mitochondrial DNA database for this region, the mtDNA control region was analysed from 71 Yoruba individuals. 65 unique haplotypes was found resulting in a haplotype diversity of 0.9976 ± 0.0028 . F_{ST} genetic distances were calculated, including previously published data from North, East, West Central and Southwest African populations. No significant differences were observed between Yoruba and the Nigerian population from the 1000 Genome project database ($F_{ST} = -0.00148$, $p = 0.5598$) and with the geographically close population of Ghana ($F_{ST} = 0.0124$, $p = 0.01386$). The Yoruba population reported in this study have a mitochondrial genetic profile similar to populations of the West Africa region, probably due to continuous gene flow and ethnic affinities with these neighbouring countries.

1. Introduction

More than 500 ethnic/linguistic groups inhabit the territory of present-day Nigeria. Yoruba (speaking a language that belongs to Niger-Congo linguistic family) is the second major ethnic group and occupy the southern region of Nigeria [1]. In the present day, after numerous divisions and political influences, the Yoruba is the main ethnic group in the states of Ekiti, Lagos, Ogun, Ondo, Osun and Oyo among others. They spread out to other African countries such as Egypt, Ghana, Togo, Sierra Leone, Burkina Faso, Ivory Coast and Liberia [2]. Because of the high genetic diversity found in Africa, it is common to find populations in the same country that are very genetically distant from each other. Thus, it is important to establish forensic databases that accurately represent all regions from each country. To evaluate and increase the maternal genetic knowledge of populations from sub-Saharan Africa, we analysed the genetic profile of mitochondrial DNA in the Yoruba from Nigeria.

2. Materials and methods

Bloodstains from 71 individuals belonging to the Yoruba ethnic

group (Nigeria) were collected under informed consent. These samples were previously typed for Y chromosome STRs [3]. The mtDNA control region segment was amplified in a single reaction and the amplification products were incubated with ExoProStar reagent for purification. Sequencing was achieved with BigDye Terminator v3.1 cycle Sequencing kit (AB) using the primers described in [4]. Post-sequencing purification was performed with Sephadex columns. Fragments separation and detection were obtained by capillary electrophoresis on an ABI 3500. The sequences were analyzed on Sequencing Analysis v.5.2 software and compared with rCRS on SeqScape v.2.7 (AB) software, following the ISFG recommendations for haplotype classification [5]. Haplogroups were assign on EMPOP database v4/R12 and confirmed manually on PhyloTree Build 17. Haplogroup frequencies were calculated by direct counting. Haplotype diversity values, pairwise genetic distances and non-differentiation probabilities were calculated using the Arlequin software [6].

3. Results and discussion

From the 71 Yoruba samples analysed, 65 unique haplotypes were found resulting in a haplotype diversity of 0.9976 ± 0.0028 . The

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Table 1
Pairwise F_{ST} genetic distances (below diagonal) and p -values (above diagonal) between Yoruba (Nigeria) samples and other nine African samples. $p \geq 0.001$.

	Yoruba	Marrocos	Kenya	Uganda	Guinea Bissau	Ghana	Khoesan Angola	Mozambique	Nigeria 1000g	Gambia
Yoruba	–	< 5E-06	< 5E-06	< 5E-06	< 5E-06	0.01386 ± 0.0013	< 5E-06	< 5E-06	0,55985 ± 0.0047	0.00099 + -0.0003
Marrocos	0.07498	–	< 5E-06	< 5E-06	< 5E-06	< 5E-06	< 5E-06	< 5E-06	< 5E-06	< 5E-06
Kenya	0.06518	0.12018	–	< 5E-06	< 5E-06	< 5E-06	< 5E-06	< 5E-06	< 5E-06	< 5E-06
Uganda	0.03719	0.09567	0.02678	–	< 5E-06	< 5E-06	< 5E-06	< 5E-06	< 5E-06	< 5E-06
Guinea Bissau	0.04366	0.12153	0.07533	0.05960	–	< 5E-06	< 5E-06	< 5E-06	< 5E-06	< 5E-06
Ghana	0.01235	0.11377	0.09668	0.06212	0.03814	–	< 5E-06	0.00010 ± 0.0001	< 5E-06	< 5E-06
Khoesan Angola	0.33087	0.40403	0.29766	0.25342	0.34078	0.31302	–	< 5E-06	< 5E-06	< 5E-06
Mozambique	0.08054	0.17539	0.05889	0.03673	0.08437	0.09022	0.24161	–	< 5E-06	< 5E-06
Nigeria 1000g	0.08055	0.09722	0.06167	0.03189	0.03838	0.01352	0.29108	0.05823	–	< 5E-06
Gambia	0.02083	0.10216	0.10690	0.07003	0.03240	0.02152	0.34865	0.12059	0.02828	–

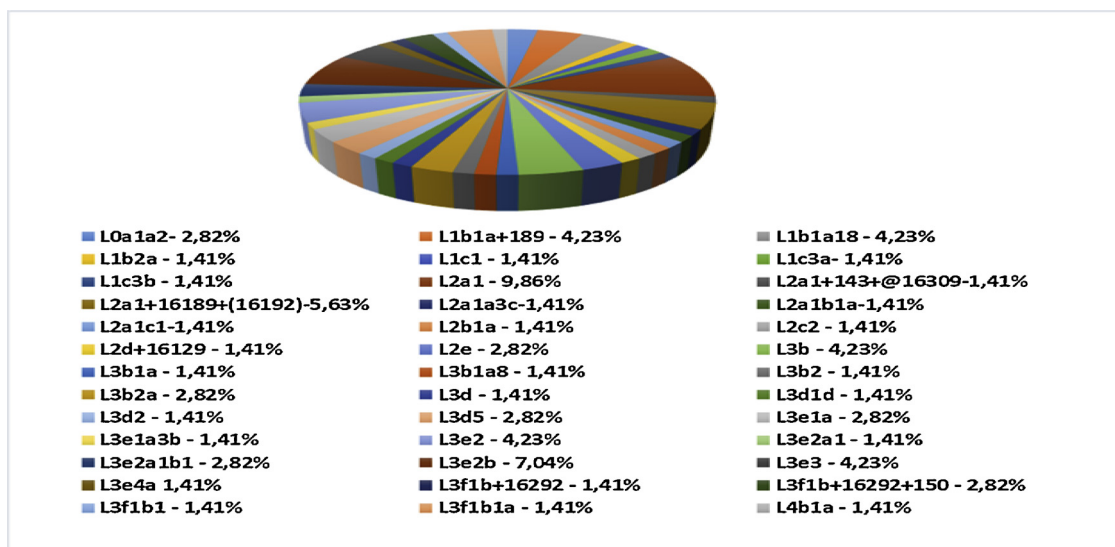


Fig. 1. mtDNA haplogroups frequencies in Yoruba sample.

haplotype mismatch distribution showed a unimodal representation with a high mean number of pairwise differences (13.86) representing the presence of distantly related haplotypes. Published mtDNA control region from samples from North, East, West Central and Southwest African populations [7–14] were used for comparative purposes. The F_{ST} pairwise genetic distances calculated (disregarding indel positions 16193.xC, 309.xC, 315.xC, 523-524del, 524.xC and 573.xC) showed no significant differences between the Yoruba sample from this study and the Nigerian samples from the 1000 Genome project database ($F_{ST} = -0.00148, p = 0.5598$), which also belong to the Yoruba ethnic group [12]. Furthermore, both Yoruba samples had low F_{ST} genetic distances and high probability of non-differentiation with the population from Ghana, a close geographic country (see Table 1). As expected, all haplotypes belong to African haplogroups, distributed among branches L0 to L4 as described in Fig. 1.

4. Conclusions

The results of this study showed a high diversity of mtDNA lineages in the Yoruba population from Nigeria, which showed a mitochondrial genetic profile similar to other populations belonging to West Africa region, probably due to continuous gene flow and ethnic affinities with these neighbouring populations. Future studies on other ethnic groups from Nigeria are required in order to disclose the genetic structure of the country, crucial for the implementation of forensic databases.

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Declaration of Competing Interest

None

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References

- [1] T. Falola, M.M. Heaton, A History of Nigeria, Cambridge University Press, 2008.
- [2] A.R. Mustapha, Ethnic Structure, Inequality and Governance of the Public Sector in Nigeria, United Nations Research Institute for Social Development, 2004.
- [3] B. Martínez, L. Catelli, M. Romero, V.O. Okolie, S.O. Keshinro, E.F. Carvalho, C. Vullo, L. Gusmão, Forensic evaluation of 27 y-str haplotypes in a population sample from Nigeria, Forensic Sci. Int. Genet. Suppl. Ser. 6 (2017) e289–e291.
- [4] Filipa Simão, Ana Paula Ferreira, Elizeu Fagundes de Carvalho, Walther Parson, Leonor Gusmão, Defining mtDNA origins and population stratification in Rio de Janeiro, Forensic Sci. Int. Genet. 34 (2018) 97–104.

- [5] W. Parson, L. Gusmao, D.R. Hares, J.A. Irwin, et al., DNA commission of the international society for forensic genetics: revised and extended guidelines for mitochondrial DNA typing, *Forensic Sci. Int. Genet.* 13 (2014) 134–142.
- [6] L. Excoffier, H.E.L. Lischer, Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows, *Mol. Ecol. Resour.* 10 (2010) 564–567.
- [7] Rachid Aboukhalid, Kimberly Sturk-Andreaggi, Mehdi Bouabdellah, Driss Squalli, Jodi A. Irwin, Saaïd Amzaz, Mitochondrial DNA control region variation from samples of the Moroccan population, *Int. J. Legal Med.* 127 (2013) 757–759.
- [8] Anita Brandstätter, Christine T. Peterson, Jodi A. Irwin, Solomon Mpoke, Davy K. Koech, Walther Parson, Thomas J. Parsons, Mitochondrial DNA control region sequences from Nairobi (Kenya): inferring phylogenetic parameters for the establishment of a forensic database, *Int. J. Legal Med.* 118 (2004) 294–306.
- [9] Verónica Gomes, Maria Pala, Antonio Salas, Álvarez-Iglesias Vanesa, António Amorim, et al., Mosaic maternal ancestry in the Great Lakes region of East Africa, *Hum. Genet.* 134 (2015) 1013–1027.
- [10] M. Carvalho, P. Brito, A.M. Bento, V. Gomes, H. Antunes, H.A. Costa, V. Lopes, A. Serra, F. Balsa, L. Andrade, M.J. Anjos, F. Corte-Real, L. Gusmão, Paternal and maternal lineages in Guinea-Bissau population, *Forensic Sci. Int. Genet.* 5 (2) (2011) 114–116.
- [11] L. Fendt, A. Röck, B. Zimmermann, M. Bodner, T. Thye, F. Tschentscher, E. Owusu-Dabo, T.M. Göbel, P.M. Schneider, W. Parson, MtDNA diversity of Ghana: a forensic and phylogeographic view, *Forensic Sci. Int. Genet.* 6 2 (2012) 244–249.
- [12] The 1000 Genomes Project Consortium, et al., A global reference for human genetic variation, *Nature* 526 (7571) (2015) 68–74.
- [13] Liane Fendt, Gabriela Huber, W. Alexander Röck, Bettina Zimmermann, Martin Bodner, Rhena Delpert, Konrad Schmidt, Walther Parson. Mitochondrial DNA control region data from indigenous Angolan khoe-san lineages, *Forensic Sci. Int. Genet.* 6 (2012) 662–663.
- [14] Maria Cerezo, Leonor Gusmao, Viktor Cerny, Nabeel Uddin, Denise Syndercombe-Court, Alberto Gomez-Carballea, Tanja Gobel, Peter M. Schneider, Antonio Salas, Comprehensive analysis of pan-african mitochondrial DNA variation provides new insights into continental variation and demography, *J. Genet. Genom.* 43 (2016) 133–143.