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Y-chromosome STRs DYS385, DYS19, DYS389-I and II, DYS390, DYS391, DYS392 and DYS393 in five African populations

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Abstract

Background: The Y chromosome has been used to compare the relationship between populations, representing a rich source of potential information to trace paternal lineages and providing a record of our relatedness. Among different population groups, African populations seem to be very interesting to study, considering the theory of the origin of modern humans and the ethnic variability usually existing. *Methods*: Five male populations from Angola ($n = 48$), Cap Verde ($n = 47$), Guinea-Bissau ($n = 32$), Mozambique ($n = 36$) and S. Tome and Prince ($n = 30$) were studied for Y-chromosome Short Tandem Repeats (STRs) DYS385, in addition to DYS19, DYS389-I and II, DYS390, DYS391, DYS392 and DYS393 previously searched. *Results*: The high DYS385 polymorphism confers a considerable variability to the Y-chromosome haplotype. *Conclusions*: The comparisons between the African populations and other data, namely from a Portuguese population, showed an interesting location of insular populations, with an intermediate position between Caucasoid and African continental populations, probably due to the European presence in the colonization of those islands.

Keywords: Y-chromosome haplotype; Y-chromosome STRs; African populations; Population genetics

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1. Introduction

The aim of this work is to extend the study of Y-chromosome haplotypes of five African populations to the STR DYS385 in addition to the DYS19, DYS389-I and II, DYS390, DYS391, DYS392 and DYS393 previously searched [1] in order to point out their relative position along with a Caucasian population (Central Portugal) [2].

2. Material and methods

DNA was extracted from air-dried bloodstains from unrelated males, using the Chelex 100 extraction method [3]. Amplification conditions: singleplex DYS385 according to Schneider et al. [4]; multiplex DYS19/DYS389 I and II/DYS390/DYS393 according to Gusmão et al. [5]; multiplex DYS391/DYS392/DYS393 as described by Kloosterman et al. [6]. The detection was carried on ABI 377 DNA sequencers.

The haplotype diversity and the correspondent standard error were calculated according to Nei [7] ($1 - \Sigma f_i$ where f_i is the relative frequency of each haplotype in the population). The mean number of pairwise differences between all pairs of haplotypes for one population was performed according to Tajima ($\Sigma\Sigma p_i p_j d_{ij}$; $j < i$ where p_i is the frequency of the ith haplotype and d_{ij} is an estimate of the number of mutations occurred since the divergence of haplotypes i and j) [8].

The probability of obtaining different haplotypes when sampling two individuals from two different populations (differentiation probability) was calculated according to Nei [7]

Table 1
Haplotype diversity (Hapl. Div.) and correspondent standard error, and the mean number of pairwise differences calculated for the five African populations

Population	*N*	Nb. Hapl.	Hapl. Div. (%)	Mean Nb. pairwise differences
Angola	48	42	97.40 ± 0.18	4.24
Cap Verde	47	40	97.06 ± 0.31	5.69
Guinea-Bissau	32	29	96.09 ± 0.48	3.59
Mozambique	36	34	96.91 ± 0.21	5.63
S. Tome and Prince	30	29	96.44 ± 0.21	5.41

N is the total of individuals and Nb. Hapl. is the number of different haplotypes found in each population.

Table 2
Shared haplotypes between all the six populations

	Angola	Cap Verde	Guinea-Bissau	Mozambique	S. Tome and Prince	Portugal (central)
Angola	–	1	1	4	2	0
Cap Verde	1	–	0	0	2	3
Guinea-Bissau	1	0	–	0	0	0
Mozambique	4	0	0	–	0	0
S. Tome and Prince	2	2	0	0	–	2
Portugal (central)	0	3	0	0	2	–

Table 3
Matrix of differentiation probability

	Angola	Cap Verde	Guinea-Bissau	Mozambique	S. Tome and Prince	Portugal (central)
Angola	–	0.9991	0.9987	0.9971	0.9979	1.0000
Cap Verde	0.9991	–	1.0000	1.0000	0.9950	0.9965
Guinea-Bissau	0.9987	1.0000	–	1.0000	1.0000	1.0000
Mozambique	0.9971	1.0000	1.0000	–	1.0000	1.0000
S. Tome and Prince	0.9979	0.9950	1.0000	1.0000	–	0.9962
Portugal (central)	1.0000	0.9965	1.0000	1.0000	0.9962	–

Table 4
Matrix of genetic distances

	Angola	Cap Verde	Guinea-Bissau	Mozambique	S. Tome and Prince	Portugal (central)
Angola	–	0.1584	0.0793	0.1687	0.1158	0.4485
Cap Verde	0.1584	–	0.1500	0.1141	0.0421	0.1148
Guinea-Bissau	0.0793	0.1500	–	0.1343	0.1304	0.4566
Mozambique	0.1687	0.1141	0.1343	–	0.1297	0.2868
S. Tome and Prince	0.1158	0.0421	0.1304	0.1297	–	0.1451
Portugal (central)	0.4485	0.1148	0.4566	0.2868	0.1451	–

$(1 - \Sigma X_i Y_i$ where X_i and Y_i are the frequencies of the ith haplotype in X and Y populations, for each shared haplotypes). Nei's genetic distances were determined with Phylip software (version 3.5c) and the corresponding phylogenetic tree was obtained from the software TreeView (version 1.5.2), neighbor-joining method.

3. Results

Table 1 shows the haplotypic diversity (and corresponding standard error) and also the mean number of pairwise differences for each one of the five African populations studied

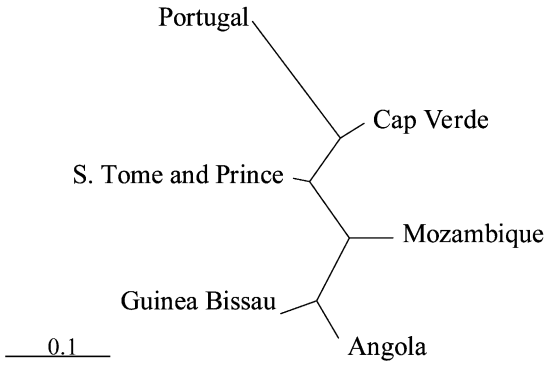

Fig. 1. Phylogenetic tree between the 5 African populations and Central Portugal population.

as well as the number of different haplotypes found. The numbers of shared haplotypes in the six populations are shown in Table 2. Table 3 contains the values of differentiation probability for each pair of populations. These values reflect the values presented in Table 2. The geneic distances calculated from the haplotypic frequencies according to Nei are presented in Table 4 and the corresponding phylogenetic tree is shown in Fig. 1.

4. Discussion

From Table 4 and Fig. 1, we can observe that Angola and Guinea-Bissau are more closely related to each other than with the other African populations as well as Cap Verde and S. Tome and Prince. Mozambique has an intermediate position between those two population groups.

The comparison of Central Portugal along with the five African populations shows that the more closely linked group is the one formed by Cap Verde and S. Tome and Prince, perhaps because their colonisation was made as a result of an admixture between a great number of Portuguese males (and other Caucasoid groups) and African females.

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