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Y-chromosomal haplotype diversity for 27 STR loci in the Tigray population (Northern Ethiopia)

K. Haddish[a], H.R.S. Kumar[a], S. Raddi[b], E. Chierto[b], G. Di Vella[b], A.L. Bogale[c], E. Kidane[c], A. Yizengaw[c], Y. Getaneh[c], C. Robino[b,*]

[a] Department of Forensic Medicine, University of Mekelle, Mekelle, Ethiopia
[b] Department of Public Health Sciences and Pediatrics, University of Turin, Turin, Italy
[c] Ethiopian Public Health Institute, Addis Ababa, Ethiopia

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ABSTRACT

The Horn of Africa is among the main areas of origin of migrants trying to reach Europe through the so-called central Mediterranean route (from Libya to Sicily). Migration-related accidents in the Straits of Sicily are commonplace. In such circumstances, Y-STR analysis can effectively complement autosomal STR data in the identification of shipwreck victims and help reuniting families separated during the crossing.

To expand currently available Y-STR haplotype reference data for Eastern Africa, the AmpF*l*STR YFiler Plus PCR Amplification kit (Thermo Fisher Scientific) was used to analyze samples from 247 Ethiopian Tigray volunteer donors. The Tigray ethno-linguistic group represents over 95% of the population in the Regional state of Tigray (Northern Ethiopia), and accounts for ~50% of the population in neighboring Eritrea.

The results obtained were compared with those available for other Eastern African ethno-linguistic groups and neighbor populations from Northern Africa and the Middle East.

1. Introduction

Following the migration crisis that affected Southern Europe in the last 10–15 years, the number of DNA tests involving subjects of Eastern African ancestry performed by Italian forensic laboratories has dramatically increased. The Horn of Africa is among the main areas of origin of migrants trying to reach Europe through the so-called central Mediterranean route from Libya to Sicily. For instance, in 2018, 15% of total arrivals to Italy (19% of unaccompanied and separated minors) were from Eritrea [1]. Migration-related accidents in the Straits of Sicily are frequent and, in such cases, Y-STR analysis can effectively complement autosomal STR data in the identification of shipwreck victims and help reuniting families separated during the crossing and lacking identity documents.

The aim of this study was to expand the currently available Y-STR haplotype reference database for Eastern Africa, focusing on the Tigray population. The Semitic-speaking Tigray people are the fourth largest ethnic group in Ethiopia, reaching up to 4.5 million, and represent over 95% of the population in the regional state of Tigray (Northern Ethiopia) (Fig. 1a). Tigray is also the major ethnic group (~50%) of neighboring Eritrea.

2. Materials and methods

Buccal swabs were collected from 247 consenting adult donors (students and staff of Mekelle University, Mekelle, Ethiopia) self-reported as unrelated and having four grandparents of Tigray origin. The study was authorized by Mekelle University Research Ethics Review Committee (ERC 0841/2016).

DNA was isolated from buccal swabs with the ChargeSwitch gDNA Normalized Buccal Cell kit (Invitrogen) and 1 µl of each DNA extract (1–3 ng) was amplified with the AmpF*l*STR Yfiler Plus kit (Thermo Fisher Scientific). Detection and separation of PCR products were carried out using the ABI Prism 3500 Genetic Analyzer and GeneMapper ID-X software (Thermo Fisher Scientific). Statistical analysis (AMOVA, F_{ST} pairwise genetic distance) was performed with ARLEQUIN software version 3.5, excluding the duplicated loci DYS385 and DYF387S1 from calculations.

3. Results

All AmpF*l*STR Yfiler Plus (YFP) haplotypes resulted unique in the Ethiopian Tigray population sample, leading to haplotype diversity (h) and discrimination capacity (DC) values of almost 1.00 and 100%,

* Corresponding author.
E-mail address: carlo.robino@unito.it (C. Robino).

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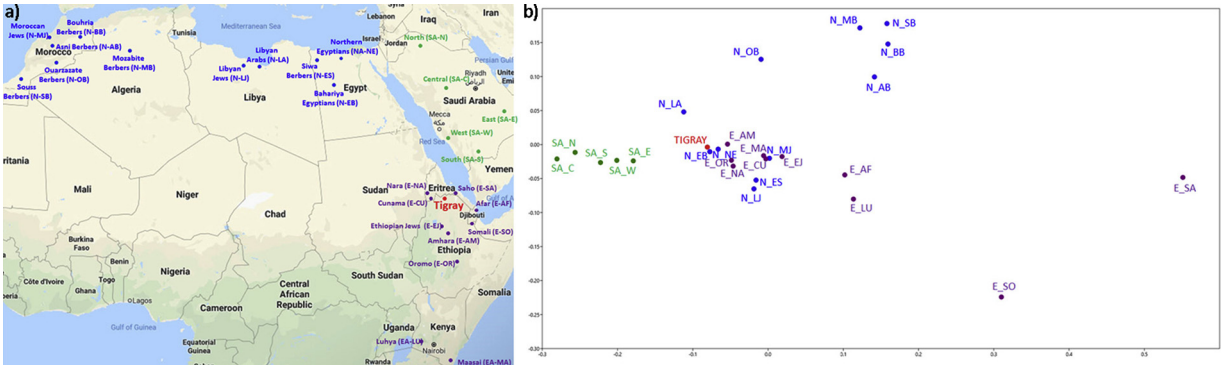

Fig. 1. a) Geographic position of Tigray (red) and relevant populations from Eastern Africa (purple), Northern Africa (blue) and Saudi Arabia (green) considered in Y-STR haplotype comparisons **b)** MDS plots obtained from Slatkin's linearized F_{ST}: populations compared with the Tigray sample (red) are identified by the same colors and abbreviations shown in a) (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

Table 1
Resolution of the modal YFiler haplotype in the Tigray population by additional YFP loci (indicated in bold in the first column). Rows corresponding to YPF markers leading to unique haplotypes are shaded in grey.

DYS576	18	17	17	17	18	16	19	18
DYS389I	13	13	13	13	13	13	13	13
DYS635	20	20	20	20	20	20	20	20
DYS389II	31	31	31	31	31	31	31	31
DYS627	22	21	21	21	21	21	18	21
DYS460	11	11	10	11	11	11	11	11
DYS458	16	16	16	16	16	16	16	16
DYS19	14	14	14	14	14	14	14	14
YGATAH4	11	11	11	11	11	11	11	11
DYS448	18	18	18	18	18	18	18	18
DYS391	10	10	10	10	10	10	10	10
DYS456	11	11	11	11	11	11	11	11
DYS390	23	23	23	23	23	23	23	23
DYS438	10	10	10	10	10	10	10	10
DYS392	11	11	11	11	11	11	11	11
DYS518	42	40	40	42	40	42	41	42
DYS570	20	20	20	20	19	19	19	20
DYS437	14	14	14	14	14	14	14	14
DYS385	16,16	16,16	16,16	16,16	16,16	16,16	16,16	16,16
DYS449	32	32	32	32	32	32	32	32
DYS393	14	14	14	14	14	14	14	14
DYS439	11	11	11	11	11	11	11	11
DYS481	24	24	24	24	24	24	24	24
DYF387S1	37,38	37,38	37,38	37,38	37,38	37,38	37,37	37,38
DYS533	12	12	12	12	12	12	12	12

respectively, compared to h = 0.9986 and DC = 92.31% obtained for markers included in its predecessor AmpF*l*STR Yfiler kit (Thermo Fisher Scientific). An example of the increased power of male individualization of YFP can be found in Table 1, showing how the modal YFiler haplotype observed in 8 (3.24%) of the Tigray samples was completely resolved through additional Y-STR loci included in YFP.

YFP haplotypes in the Ethiopian Tigray population were compared with those previously obtained from populations grouped in three macrogeographic areas: Eastern Africa [2], Northern Africa [3], and the Arabian peninsula (Saudi Arabia) [4] (Fig. 1a). No YFP haplotype observed in the Ethiopian Tigray population was shared with any individual from other populations. The Ethiopian Tigray sample was grouped with Eastern African populations for AMOVA analysis (only Eastern African populations from [2] with sample size ≥ 15 were considered). AMOVA showed significant differences ($p < 0.05$; 10,000 permutations) between macrogeographic areas (7.6% F_{ST}) and between populations within macrogeographic areas (11.2% F_{ST}).

Multidimensional scaling (MDS) plot obtained from Slatkin's linearized F_{ST} distances is shown in Fig. 1b. It could be seen that, while Saudi Arabians formed a compact cluster, Norther and Eastern African populations were more spread out. A clear West-East gradient was evident for Northern Africa [3]. Excluding the outlier position of the Saho and the Djibuti Somali, previously shown to display extremely low levels of Y-STR diversity [2], no clear pattern of differentiation (e.g. according to linguistic affiliation of the tested populations) was evidenced in Eastern Africa, based on YFP haplotypes. Actually, the lowest F_{ST} values between Ethiopian Tigray and other Eastern African populations ($F_{ST} < 001$) were observed in pairwise comparisons with the Nilo-Saharan-speaking Cunama and Nara of Eritrea, who were also the populations closest to Tigray in geographical terms.

4. Conclusions

The present study represents an upgrade of previous information regarding forensic Y-STR diversity in the Tigray population (currently limited to 28 haplotypes from Eritrea and 5 from Ethiopia described in [2]). In contrast to what previously observed for populations from the Horn of Africa organized in patrilinear and patrilocal clans, like the Saho and the Somali [2], by this enlarged dataset it was possible to appreciate the extremely high intra-population variation of YFP haplotypes in Tigray. The YFP marker set appears therefore a suitable instrument for male identification and kinship testing of migrants of Tigray descent involved in naval accidents in the Southern Mediterranean.

Declaration of Competing Interest

None.

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