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Announcement of Population Data

Population data on 11 Y-chromosome STRs from Guiné-Bissau

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Abstract

The forensic value of Y-STR markers in Guiné-Bissau was accessed by typing of 215 males. Allele and haplotype frequencies, determined for loci DYS19, DYS389-I, DYS389-II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439 and the duplicated locus DYS385, are within the limits of variation found in other populations south of the Sahara. The level of discrimination achieved is Guineans is higher than for European or other African populations with comparable data. The haplotype diversity of 0.9995 is reduced to 0.9981 when the minimal haplotype is considered thus revealing the importance of increasing the number of typed loci.
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Keywords: Y-chromosome; Short tandem repeats; Powerplex® Y-System; Guiné-Bissau

Population: A total of 215 unrelated healthy males from Guiné-Bissau population whose ancestors were known to inhabit the same region for the last three generations.

DNA extraction: Chelex method [1] from leukocitary blood fraction.

PCR: A multiplex reaction for 11 markers was performed with Powerplex® Y-System (Promega) following the manufacturer's instructions. For the samples with individually typed Y-STRs (GB155 to GB207) published primers and conditions were used (DYS19, DYS389I/II, DYS390, DYS391, DYS392, DYS393 [1,2]; DYS385 [3]; DYS439 [4]).

Typing: Amplified PCR fragments were analyzed in ABI PRISM™ 310 Genetic Analyser along with Genescan 2.1 analysis software (AB Applied Biosystems). Typing followed the ISFG guidelines for Y-STR analysis [5]. The allele nomenclature system used is the proposed in [6,7] with the exception of the DYS389 locus [8]. Guidelines for the presentation of population data, specified by Lincoln and Carracedo [9], have been considered.

Results: Described in Tables 1a–2. To note that the sample size is not the same for all markers, varying from $N = 163$ to 215 (Table 1).

Quality control: Proficiency testing of the GEP-ISFG.

Data analysis: Frequency and diversity indexes [10] were calculated with Arlequin ver. 2.000 [11] for both loci (D) and haplotypes (H). The same software performed AMOVA tests for selected populations and locus-by-locus and an exact test of population differentiation (not considering DYS385). The YHRD database (www.yhrd.org) was consulted in the search for exact matches (both extended and minimal haplotypes).

Other remarks: The allele frequencies and range of the studied loci in Guiné-Bissau population (Table 1a and b) fit into the determined by other studies on sub-Saharan African populations [12–18]. The most outstanding differences are found when comparing with Non-Africans [13,14,19–25] or even North-Africans [26,27]. To note is the high prevalence in Guineans of alleles 15 for DYS19 (42%), 21 for DYS390 (67%), 11 for DYS392 (88%), 14 to DYS 437 (72%) and 11

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Table 1a
Allele frequencies and gene diversity for ten Y-STR markers in Guiné-Bissau population

Allele	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS437	DYS438	DYS439
8									0.0667	
9					0.0279					
10					0.7767	0.0736			0.2364	0.0421
11		0.014			0.1907	0.8773			0.6485	0.2804
12		0.1907			0.0047	0.0368	0.0093		0.0485	0.4533
13	0.092	0.5628				0.0086	0.3535	0.0361		0.2009
14	0.0491	0.2279					0.586	0.7169		0.0234
15	0.4172	0.0047					0.0512	0.1205		
16	0.2638							0.012		
17	0.1779							0.1145		
20				0.0186						
21				0.6744						
22				0.214						
23				0.0419						
24				0.0512						
28			0.0143							
29			0.1667							
30			0.3714							
31			0.3095							
32			0.1333							
33			0.0048							
N	163	215	210	215	215	163	215	166	165	214
D	0.7182	0.5975	0.7239	0.497	0.3612	0.2248	0.5314	0.4598	0.52	0.6764
S.E.	0.0199	0.0249	0.0139	0.0339	0.0349	0.0422	0.0212	0.0431	0.0359	0.0178

N, sample size; *D*, gene diversity; S.E., standard error of *D*.

for DYS438 (65%) which in other populations are marginal or, if the most common allele, retain a lower fraction of the variation. For DYS393 a percentage of 59% of allele 14 is so far the highest reported, even for a West African population. A broader range for DYS389I (11–15 versus 12–14 for Europe) or a more limited one, as for DYS438 (10–12 versus 9–13 in Europe) are examples of other distinct features. The haplotype distribution of DYS385 ranges from alleles 13 to 21 where the most frequent haplotypes 15–16, 16–16 and 16–17 (~16%) are either absent or weakly represented outside of Africa. All loci show a unimodal distribution, including DYS392, which is bimodal in most non-Africans. As for the diversity indexes (*D*), DYS19 and DYS389II exhibit the highest diversity in this study ($D = 0.7182$ and 0.7239), not to consider DYS385 ($H = 0.9031$). Together with DYS393 these loci held higher gene/haplotype diversity than most Europeans, thus more informative for African populations. On the other hand, DYS391 seems to have a lower *D* than Europeans (but still higher than Asians) while DYS392 exhibits the lowest diversity. Data of both loci supports a limited utility in forensic casework in several sub-Saharan populations as previously suggested [18].

The eleven Y-STRs are fully typed for 161 individuals resulting in 154 distinct haplotypes ($H = 0.9995 \pm 0.0008$), with the highest frequency of two individuals (Table 2). GB155 to GB207 were not taken into account for the calculation, as their 11 Y-STR pattern might be similar to the previous. The discriminatory power achieved is higher

Table 1b
Haplotype frequency and diversity for DYS385 in Guiné-Bissau population

Haplotype	DYS385
13,14	0.0049
13,15	0.0049
13,16	0.0099
13,17	0.0049
14,14	0.0345
14,15	0.0148
14,16	0.0099
14,17	0.0345
15,15	0.0443
15,16	0.1576
15,17	0.0493
15,18	0.0197
16,16	0.1675
16,17	0.1478
16,18	0.0591
16,19	0.0197
16,20	0.0049
17,17	0.0985
17,18	0.069
17,20	0.0049
18,18	0.0197
18,19	0.0049
18,20	0.0099
20,21	0.0049
N	203
H	0.9031
S.E.	0.0084

N, sample size; *H*, haplotype diversity; S.E., standard error of *H*.

Table 2
Y-chromosome STR haplotypes detected in Guiné-Bissau population

Haplotype	*N*	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS437	DYS438	DYS439	DYS385
GB001	1	13	12	30	22	9	11	13	14	10	13	14,17
GB002	1	13	13	29	24	11	11	14	14	10	13	14,16
GB003	1	13	13	30	21	10	11	14	14	11	14	15,16
GB004	1	13	13	30	22	9	12	12	14	10	12	16,17
GB005	1	13	13	30	22	10	11	14	14	10	12	14,17
GB006	1	13	13	30	23	10	13	13	14	11	12	16,16
GB007	1	13	13	30	24	10	10	13	14	10	13	15,16
GB008	1	13	13	30	24	10	11	13	14	10	12	16,17
GB009	1	13	13	30	24	10	11	13	14	10	12	17,17
GB010	1	13	13	30	24	10	11	14	14	10	13	16,16
GB011	1	13	13	30	24	10	12	13	15	10	12	15,15
GB012	1	13	13	31	23	10	11	13	14	10	11	16,17
GB013	1	13	13	31	24	10	11	14	14	10	12	16,17
GB014	1	13	13	31	24	10	12	14	15	10	13	16,16
GB015	1	13	14	31	21	10	11	14	15	10	11	16,17
GB016	1	14	12	30	23	10	11	14	14	8	12	15,16
GB017	1	14	13	30	21	10	11	14	15	11	13	18,18
GB018	1	14	13	30	21	10	13	14	14	11	11	16,19
GB019	1	14	13	30	23	10	11	14	14	10	10	13,14
GB020	1	14	13	30	23	11	11	14	14	8	13	16,16
GB021	1	14	13	31	22	11	11	14	14	8	12	17,17
GB022	1	14	13	31	22	11	11	14	14	8	14	17,19
GB023	1	14	14	32	21	10	10	14	14	10	11	17,17
GB024	1	15	12	29	21	10	11	13	13	11	12	15,16
GB025	1	15	12	29	22	10	11	13	17	10	12	14,15
GB026	1	15	12	29	22	10	11	13	17	10	13	13,17
GB027	1	15	12	29	22	10	11	13	17	10	13	15,17
GB028	1	15	12	29	22	11	10	13	16	8	11	15,15
GB029	1	15	12	29	22	11	10	13	17	10	11	15,16
GB030	1	15	12	29	22	11	11	13	17	10	11	15,15
GB031	2	15	12	29	22	11	11	13	17	10	12	14,14
GB032	1	15	12	30	21	10	10	13	17	10	13	14,15
GB033	1	15	12	30	21	10	11	13	17	10	12	15,16
GB034	1	15	12	30	21	10	11	14	13	11	11	15,16
GB035	2	15	12	30	21	10	11	14	13	11	12	15,16
GB036	1	15	12	30	21	10	11	14	13	11	13	15,16
GB037	1	15	12	30	21	10	11	14	13	11	13	16,16
GB038	1	15	12	31	21	10	11	13	14	11	11	15,18
GB039	1	15	13	29	21	10	11	14	14	11	12	16,17
GB040	1	15	13	29	21	10	11	14	14	11	12	16,18
GB041	1	15	13	29	22	10	11	14	14	11	11	16,17
GB042	1	15	13	29	22	11	11	14	17	10	12	14,14
GB043	1	15	13	30	21	10	10	14	14	11	11	16,16
GB044	1	15	13	30	21	10	11	13	14	11	11	16,17
GB045	1	15	13	30	21	10	11	13	14	11	12	15,16
GB046	1	15	13	30	21	10	11	13	14	11	12	16,16
GB047	1	15	13	30	21	10	11	13	17	10	11	14,15
GB048	1	15	13	30	21	10	11	14	14	10	12	14,14
GB049	1	15	13	30	21	10	11	14	14	11	11	16,17
GB050	1	15	13	30	21	10	11	14	14	11	14	16,17
GB051	1	15	13	30	21	10	11	14	14	12	12	17,17
GB052	1	15	13	30	21	10	11	14	15	11	12	17,18
GB053	1	15	13	30	21	10	11	15	14	11	12	15,16
GB054	1	15	13	30	21	11	11	13	14	11	11	16,19
GB055	1	15	13	30	21	11	11	14	14	11	11	16,17
GB056	1	15	13	30	22	10	11	14	14	10	11	13,15
GB057	1	15	13	30	22	10	11	14	15	11	12	15,16

Table 2 (*Continued*)

Haplotype	*N*	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS437	DYS438	DYS439	DYS385
GB058	1	15	13	31	21	10	11	13	14	11	13	16,18
GB059	1	15	13	31	21	10	11	13	14	11	12	17,18
GB060	1	15	13	31	21	10	11	14	14	10	13	15,16
GB061	1	15	13	31	21	10	11	14	14	11	11	16,16
GB062	1	15	13	31	21	10	11	14	14	11	11	16,17
GB063	2	15	13	31	21	10	11	14	14	11	12	15,16
GB064	1	15	13	31	21	10	11	14	14	11	12	16,16
GB065	1	15	13	31	21	10	11	14	14	11	12	17,18
GB066	1	15	13	31	21	10	11	15	14	11	12	15,15
GB067	1	15	13	31	21	11	11	13	14	11	11	16,18
GB068	1	15	13	31	22	11	11	14	14	11	12	18,18
GB069	1	15	13	31	24	10	10	14	17	10	12	16,17
GB070	1	15	13	32	21	10	11	13	14	11	11	16,16
GB071	1	15	13	32	21	10	11	13	14	11	12	17,18
GB072	1	15	13	32	21	10	11	14	14	10	13	15,16
GB073	1	15	13	32	23	11	11	13	14	8	12	17,17
GB074	1	15	13	32	24	11	11	14	14	8	12	17,17
GB075	1	15	14	29	22	10	10	14	17	10	12	14,17
GB076	1	15	14	30	21	10	11	14	14	11	13	16,18
GB077	2	15	14	31	21	10	11	14	14	11	12	14,14
GB078	1	15	14	31	21	10	11	14	14	11	12	16,17
GB079	1	15	14	31	21	11	11	13	14	11	12	16,18
GB080	1	15	14	31	22	10	11	13	14	11	12	15,16
GB081	1	15	14	31	22	10	11	13	17	10	13	14,17
GB082	1	15	14	31	22	10	11	13	17	11	13	14,17
GB083	1	15	14	31	22	10	11	14	17	10	13	14,16
GB084	1	15	14	31	23	11	11	14	14	8	12	15,17
GB085	1	15	14	32	21	10	11	13	14	11	11	16,17
GB086	1	15	14	32	21	10	11	13	14	11	12	16,17
GB087	1	15	14	32	21	10	11	14	14	11	12	16,16
GB088	1	16	11	28	21	10	11	13	14	11	12	16,17
GB089	1	16	12	28	21	10	11	14	14	11	12	16,16
GB090	1	16	12	29	22	10	11	13	17	8	11	15,15
GB091	1	16	12	30	21	10	11	14	14	11	13	15,16
GB092	1	16	12	30	21	10	11	14	14	11	13	16,16
GB093	1	16	12	30	21	11	11	14	14	11	12	17,17
GB094	1	16	12	30	22	9	11	14	16	10	13	16,16
GB095	1	16	13	29	21	10	11	14	14	11	11	15,18
GB096	1	16	13	29	21	10	11	14	14	11	11	16,18
GB097	1	16	13	29	21	10	11	14	14	11	12	15,18
GB098	1	16	13	29	21	10	11	14	14	11	12	16,16
GB099	1	16	13	30	21	10	11	14	14	12	12	16,16
GB100	1	16	13	30	21	11	11	14	14	11	11	17,17
GB101	1	16	13	30	21	11	11	14	14	11	12	17,18
GB102	1	16	13	30	22	10	11	14	14	12	12	16,16
GB103	1	16	13	30	22	10	11	14	15	11	11	15,17
GB104	1	16	13	31	21	10	11	14	14	10	12	16,16
GB105	1	16	13	31	21	10	11	14	14	11	10	16,16
GB106	1	16	13	31	21	10	11	14	14	12	11	16,16
GB107	1	16	13	31	21	10	11	15	14	10	12	16,17
GB108	1	16	13	31	22	10	11	14	14	11	12	14,17
GB109	1	16	13	32	21	10	11	13	14	11	12	17,17
GB110	1	16	13	32	21	10	11	14	14	11	10	16,16
GB111	1	16	13	32	21	11	11	13	14	11	11	17,18
GB112	1	16	13	32	21	12	11	14	14	11	13	15,17
GB113	1	16	14	29	23	11	10	13	17	10	12	15,16
GB114	1	16	14	31	21	10	11	13	14	11	12	15,17
GB115	1	16	14	31	21	10	11	13	14	11	13	17,17
GB116	1	16	14	31	21	10	11	14	14	10	12	16,18

Table 2 (*Continued*)

Haplotype	*N*	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS437	DYS438	DYS439	DYS385
GB117	1	16	14	31	21	10	11	14	14	11	11	17,18
GB118	1	16	14	31	21	10	11	14	14	11	12	16,16
GB119	1	16	14	31	21	10	12	14	15	12	11	18,19
GB120	1	16	14	31	22	10	11	13	14	11	13	16,16
GB121	1	16	14	31	22	10	11	13	14	11	14	16,17
GB122	1	16	14	31	22	10	11	13	15	11	12	16,17
GB123	1	16	14	31	22	10	11	14	14	11	11	15,17
GB124	1	16	14	31	22	10	11	14	15	11	11	16,18
GB125	1	16	14	32	21	10	11	13	14	11	12	15,15
GB126	1	16	14	32	21	10	11	14	14	11	11	15,17
GB127	1	16	14	32	21	10	11	14	15	11	12	17,20
GB128	1	16	14	32	21	10	11	14	15	11	13	20,21
GB129	2	17	12	29	21	10	11	14	14	11	13	17,17
GB130	1	17	12	30	21	10	11	14	15	11	13	15,16
GB131	1	17	12	32	22	11	11	13	17	8	11	15,15
GB132	1	17	13	29	21	10	11	14	14	11	12	15,18
GB133	1	17	13	30	21	10	11	13	14	11	12	17,18
GB134	1	17	13	30	21	10	11	13	14	11	13	17,18
GB135	2	17	13	30	21	10	11	14	14	11	11	17,17
GB136	1	17	13	30	21	10	11	14	15	11	11	16,17
GB137	1	17	13	30	21	10	12	14	14	11	13	18,18
GB138	1	17	13	30	21	11	11	13	14	11	11	17,17
GB139	1	17	13	31	20	11	11	15	14	11	11	16,16
GB140	1	17	13	31	21	10	11	13	14	11	10	15,16
GB141	1	17	13	31	21	10	11	14	14	11	10	16,16
GB142	1	17	13	31	21	10	11	14	14	11	12	17,17
GB143	2	17	13	32	20	10	11	14	14	11	11	15,16
GB144	1	17	13	32	21	10	11	13	14	11	10	16,17
GB145	1	17	13	32	21	10	11	15	14	11	11	15,16
GB146	1	17	13	32	22	10	11	13	15	11	13	16,17
GB147	1	17	14	31	21	10	11	13	14	11	12	16,16
GB148	1	17	14	31	21	10	11	14	15	11	12	18,20
GB149	1	17	14	31	21	10	11	15	15	11	12	18,20
GB150	1	17	14	31	21	11	10	14	14	11	12	16,18
GB151	1	17	14	31	21	11	11	14	15	11	12	18,18
GB152	1	17	14	31	22	10	11	13	14	11	12	15,17
GB153	1	17	14	32	21	10	11	14	14	11	11	17,17
GB154	1	17	15	31	22	10	12	13	15	11	13	17,17
GB155	1	–	11	30	21	10	–	14	–	–	11	16,17
GB156	1	16	11	–	21	10	–	13	14	–	–	–
GB157	1	–	12	29	21	11	–	14	14	–	13	16,17
GB158	1	–	12	29	21	11	–	14	–	–	12	17,18
GB159	1	–	12	29	21	10	–	14	–	–	14	16,17
GB160	1	–	12	29	21	10	–	14	–	–	12	16,19
GB161	1	–	12	29	22	10	10	14	–	12	11	15,16
GB162	1	–	12	29	22	11	–	13	–	–	11	15,16
GB163	1	–	12	29	22	11	–	13	–	–	11	15,16
GB164	1	–	12	29	22	11	–	13	–	–	12	14,14
GB165	1	–	12	30	21	10	–	14	–	–	12	16,16
GB166	1	–	12	30	21	10	–	14	–	–	13	14,17
GB167	1	–	12	30	21	10	–	14	–	–	13	15,16
GB168	1	–	12	30	22	11	–	13	–	–	12	13,16
GB169	1	–	13	28	21	10	–	13	–	–	12	16,17
GB170	1	–	13	29	21	10	–	13	–	–	12	16,16
GB171	1	–	13	29	21	10	–	14	–	–	12	16,18
GB172	1	–	13	29	21	10	–	14	–	–	12	–
GB173	1	–	13	30	20	10	–	14	–	–	11	15,16
GB174	1	–	13	30	21	9	–	13	–	–	13	15,15
GB175	1	–	13	30	21	9	–	13	–	–	13	15,16

Table 2 (*Continued*)

Haplotype	N	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS437	DYS438	DYS439	DYS385
GB176	1	–	13	30	21	10	–	13	–	–	12	16,16
GB177	1	–	13	30	21	10	–	14	–	–	12	14,14
GB178	1	–	13	30	21	10	–	14	–	–	12	15,16
GB179	1	–	13	30	21	10	–	14	–	–	12	17,17
GB180	1	–	13	30	21	10	–	14	–	–	12	17,18
GB181	1	–	13	30	21	10	–	14	–	–	13	16,18
GB182	1	–	13	30	21	10	–	15	–	–	11	16,19
GB183	1	–	13	30	21	10	–	15	–	–	12	15,15
GB184	1	–	13	30	21	10	–	15	–	–	12	16,16
GB185	1	–	13	30	21	11	–	12	–	–	11	17,17
GB186	1	–	13	30	21	11	–	13	–	–	11	16,17
GB187	1	–	13	30	21	11	–	13	–	–	11	16,20
GB188	1	–	13	30	21	11	–	14	–	–	11	17,17
GB189	1	–	13	30	21	11	–	14	–	–	11	17,18
GB190	1	–	13	30	22	10	–	13	–	–	12	13,16
GB191	2	–	13	31	21	10	–	14	–	–	10	16,16
GB192	1	–	13	31	21	10	–	14	–	–	11	15,16
GB193	1	–	13	31	21	10	–	14	–	–	12	17,18
GB194	1	–	13	31	22	10	–	14	15	12	13	16,17
GB195	1	–	13	31	23	10	–	13	–	–	11	16,18
GB196	1	–	13	32	21	11	–	13	–	–	12	17,17
GB197	1	–	13	–	24	10	–	13	–	–	12	16,16
GB198	1	–	14	31	21	9	–	13	–	–	12	15,16
GB199	1	–	14	31	21	10	–	15	–	–	11	16,16
GB200	1	–	14	31	22	10	–	13	–	–	13	15,17
GB201	1	–	14	32	21	10	–	14	–	–	10	16,16
GB202	1	–	14	32	21	10	–	14	–	–	11	16,17
GB203	1	–	14	32	21	10	–	14	–	–	12	14,14
GB204	1	–	14	33	21	11	–	14	–	–	12	15,16
GB205	1	16	14	–	21	10	10	14	14	8	13	–
GB206	1	–	14	–	21	10	–	15	14	12	11	–
GB207	1	–	14	–	22	10	–	13	–	–	13	15,17

N, number of individuals; –, not determined.

than for other populations with similar or higher number of analysed loci—Europeans, 11 loci: 0.9983 [19], 14 loci: 0.9992 [20], 19 loci: 0.9988 [24]; Japanese, 14 loci: 0.9987 [22]; North Africans, 12 loci: 0.9605–0.9821 [27]. Most Y-STR data on African populations refers to the 9 Y-STR ‘‘minimal haplotype’’ or includes even less markers thus limiting comparisons with our data when diversity indexes are concerned. Haplotype diversity in Guineans decreases to 0.9981 ± 0.0010 (142 haplotypes) when the minimal set is considered, comparatively higher than data on Europeans (0.9972 [19]), Afro-Americans (0.998 [20]) and other sub-Saharians (0.989–0.9900 [15,16]). For DYS19, DYS389I, DYS389II, DYS390, DYS391 and DYS392 the haplotype combinations 15-13-30-21-10-11 and 15-13-31-21-10 are quite common in our data (GB044 to GB053, GB058 TO GB066). Moreover, DYS437 allele 17 appears to be associated to DYS438 10 and DYS19 15 (GB025) as DYS438 8 relates with DYS391 11 and DYS437 14 (GB020, with 3 exceptions).

Previously published haplotypic data were considered for an analysis of molecular variance (AMOVA) in selected populations (North Africa [28], Equatorial Guinea [29], Mozambique [30], North Portugal [21] and Spain [31]). In a three-group structure, defined by geographic criteria, the vast majority of variance is explained at a intrapopulational level (99.1%). The among group variance is of 0.34% ($P = 0.08504 \pm 0.00762$) while the intragroup component displayed 0.56%. A locus-by-locus AMOVA revealed significant differences ($P < 0.05$) in the among group variation of DYS19, DYS389II, DYS391, DYS437, DYS438 and DYS439. According to the exact test of population differentiation (10,000 steps of Markov chain) the six considered populations are distinct.

The YHRD database search resulted in 21 exact matches (10 markers, excluding DYS385): six Africans, eight Afro-descendents, six Europeans and one Indian, out of 6281 haplotypes). It is worth mentioning that there is a pattern of matching for the haplotypes order as shown in Table 2. The European similar haplotypes refer to data between GB008 and GB056 while the African ancestry ones are reported from GB044 on. Although increasing the total number of matches to 69 (44 Africans, 20 Europeans and five of other origin, some shared out of 27,773 haplotypes), a similar pattern is maintained when narrowing the analysis to an 8-

STRs set. For the African populations in the database, the highest number of matching lineages were with Angola, Mozambique and West Africa.

In order to evaluate the discriminatory power of an extended haplotype, H was determined for sets of ten markers (minimum haplotype plus one). The additional marker causes a variation in haplotype diversity as follows: DYS437 ($H = 0.9982 \pm 0.0010$, 143 haplotypes), DYS438 ($H = 0.9986 \pm 0.0009$, 146 haplotypes) and DYS439 ($H = 0.9994 \pm 0.0008$, 153 haplotypes). The level of discrimination obtained by additional typing of DYS439 confirms its usefulness for forensic purposes [12,24].

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