



Announcement of Population Data

Population data for 15 autosomal STRs loci and 12 Y chromosome STRs loci in a population sample from the Sardinia island (Italy)

Andrea Verzeletti^{a,*}, Nicoletta Cerri^a, Fausta Gasparini^a, Anna Poglio^a, Elena Mazzeo^b,
 Francesco De Ferrari^a

^a Department of Forensic Medicine, University of Brescia, Brescia, Italy

^b Department of Forensic Medicine, University of Sassari, Sassari, Italy

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ABSTRACT

One hundred twenty-five unrelated individuals (69 females and 56 males) from Sassari (Northern Sardinia) and Orgosolo (Central Sardinia) were typed for 15 STRs loci. The 56 males were typed for 12 Y chromosome STRs loci too. Frequency distribution is described.

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Introduction: Sardinia island is located in the middle of the Mediterranean sea. Due to geographical and historical reasons, that long-time isolated the island, Sardinia has been considered genetically different from other regions of the Mediterranean basin and from continental Italy in particular [1–3]. In consideration to the few available data for forensic markers regarding this population, a genetic study was performed.

Population: Fifty-six unrelated males and 69 unrelated females from Sassari and Orgosolo (Northern and Central Sardinia).

DNA extraction: Genomic DNA was extracted using Chelex®-100 procedure from buccal swabs.

PCR amplification: DNA was amplified using the commercial kit AmpFLSTR® Identifiler™ (Applied Biosystems, Foster City, CA, USA) and, for males' DNA, PowerPlex® Y System (Promega Corporation, Madison, WI, USA) according to manufacturers' recommendations.

Typing: Typing was performed by capillary electrophoresis (ABI Prism 310 Genetic Analyzer, ABI). Allele scoring for each marker was obtained by comparison to AmpFLSTR® Identifiler™ allelic ladder (Applied Biosystems, Foster City, CA, USA) and to PowerPlex® Y System allelic ladder (Promega Corporation, Madison, WI, USA) through the software GeneMapper ID® V3.2 (Applied Biosystems, Foster City, CA, USA).

Results: All data are shown in Tables 1–3 (Tables 4–6 as supplementary material).

Other remarks: A high degree polymorphism was observed among the analysed 15 autosomal loci. D21S11 and FGA loci exhibited the highest polymorphism (12 alleles). Least polymorphism was shown by CSF1P0, D3S1358 and TPOX loci (6 alleles). D21S11, D2S1338 and vWA loci showed significant deviations from Hardy–Weinberg expectations although after the Bonferroni's correction. The reasons for the observed deviations include inbreeding, population substructure, selection or “silent” alleles. Given the structure of the population from the Sardinia island, with contributions from both Caucasians and Africans to the genepool, population substructure might be likely.

Regarding the Y-chromosome haplotypes, 39 different haplotypes were found (Table 4, supplementary material). A search in the YHRD database [4] for the most frequent 11 loci “minimal haplotype + SWGDAM core set” found no matches for H₁, H₃, H₄ and H₅ in a population sample of 23979 haplotypes. For H₂, only 16 matches were found (4 from Spain, 2 from Northern Portugal and 10 from South America).

Our data were compared to those regarding other geographically related populations of the Mediterranean basin by exact tests as implemented in the Arlequin software [5].

Significant differences ($p < 0.05$) were found between our data and those regarding all the other considered populations (Tables 5 and 6, supplementary material) [6–16] both at autosomal and at Y-chromosome loci.

* Corresponding author. Tel.: +39 030 3995838; fax: +39 030 3995839.

E-mail address: verzelet@med.unibs.it (A. Verzeletti).

Table 1

Allele frequencies and forensic parameters at 15 autosomal STRs loci in a population sample of 125 unrelated individuals from the Sardinia island

Allele	D8S1179	D21S11	D7S820	CSF1P0	D3S1358	TH01	D13S317	D16S539
5	/	/	/	/	/	0.004	/	/
6	/	/	0.004	/	/	0.227	/	/
7	/	/	0.068	/	/	0.175	/	/
8	/	/	0.086	/	/	0.134	0.163	0.038
9	0.012	/	0.100	0.015	/	0.191	0.025	0.126
9.3	/	/	/	/	/	0.260	/	/
10	0.096	/	0.227	0.197	/	0.008	0.041	0.130
11	0.124	/	0.227	0.368	/	/	0.272	0.307
12	0.084	/	0.245	0.335	/	/	0.374	0.185
13	0.300	/	0.037	0.078	/	/	0.093	0.176
13.2	/	/	/	/	/	/	/	/
14	0.147	/	0.009	0.005	0.025	/	0.033	0.034
14.2	/	/	/	/	/	/	/	/
15	0.144	/	/	/	0.215	/	/	0.004
15.2	/	/	/	/	/	/	/	/
16	0.060	/	/	/	0.275	/	/	/
16.2	/	/	/	/	/	/	/	/
17	0.036	/	/	/	0.210	/	/	/
17.2	/	/	/	/	/	/	/	/
18	/	/	/	/	0.235	/	/	/
19	/	/	/	/	0.035	/	/	/
20	/	/	/	/	/	/	/	/
21	/	/	/	/	/	/	/	/
22	/	/	/	/	/	/	/	/
23	/	/	/	/	/	/	/	/
24	/	/	/	/	/	/	/	/
24.2	/	0.018	/	/	/	/	/	/
25	/	/	/	/	/	/	/	/
26	/	0.005	/	/	/	/	/	/
27	/	0.022	/	/	/	/	/	/
28	/	0.107	/	/	/	/	/	/
29	/	0.233	/	/	/	/	/	/
30	/	0.241	/	/	/	/	/	/
30.2	/	0.005	/	/	/	/	/	/
31	/	0.063	/	/	/	/	/	/
31.2	/	0.210	/	/	/	/	/	/
32.2	/	0.063	/	/	/	/	/	/
33.2	/	0.014	/	/	/	/	/	/
35.2	/	0.005	/	/	/	/	/	/
H_{obs}	0.963	0.893	0.791	0.734	0.768	0.780	0.705	0.783
H_{exp}	0.836	0.807	0.817	0.709	0.779	0.801	0.749	0.810
p	0.473	0.002 ^a	0.025 ^a	0.157	0.302	0.491	0.243	0.086
PE	0.675	0.633	0.636	0.450	0.556	0.591	0.530	0.619
PI_C	0.811	0.801	0.787	0.655	0.741	0.763	0.7100	0.779
Allele	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA	
5	/	/	/	/	/	/	/	/
6	/	/	/	/	/	/	/	/
7	/	/	/	0.012	/	/	/	/
8	/	/	/	0.450	/	0.004	/	/
9	/	/	/	0.087	/	0.060	/	/
9.3	/	/	/	/	/	/	/	/
10	/	/	/	0.128	/	0.012	/	/
11	/	/	/	0.314	/	0.423	/	/
12	/	0.116	/	0.008	0.145	0.327	/	/
13	/	0.272	/	/	0.100	0.165	/	/
13.2	/	0.012	/	/	/	/	/	/
14	/	0.312	0.100	/	0.190	0.008	/	/
14.2	/	0.040	/	/	/	/	/	/
15	/	0.172	0.184	/	0.135	/	/	/
15.2	/	0.020	/	/	/	/	/	/
16	0.045	0.036	0.196	/	0.135	/	/	/
16.2	/	0.012	/	/	/	/	/	/
17	0.209	0.004	0.164	/	0.110	/	0.009	/
17.2	/	0.004	/	/	/	/	/	/
18	0.073	/	0.272	/	0.070	/	0.005	/
19	0.068	/	0.068	/	0.020	/	0.100	/
20	0.191	/	0.008	/	0.020	/	0.114	/
21	0.023	/	/	/	0.070	/	0.206	/
22	0.041	/	/	/	/	/	0.219	/
23	0.136	/	/	/	/	/	0.114	/
24	0.095	/	0.008	/	/	/	0.076	/
24.2	/	/	/	/	/	/	/	/
25	0.114	/	/	/	/	/	0.081	/
26	0.005	/	/	/	/	/	0.044	/

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