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FOR THE RECORD

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Population Data of Three X-Chromosomal STRs: DXS7132, DXS7133 and GATA172D05 in North Italy

POPULATION: We have analyzed the distribution of allele frequencies at three X-chromosomal short tandem repeat (STR) loci (DXS7132, DXS7133, and GATA172D05) among individuals ($n = 175$) living and born in North Italy.

KEYWORDS: forensic science, X-chromosome, DNA typing, population genetics, DXS7132, DXS7133, GATA172D05, North Italy

The samples for database studies were obtained from 175 unrelated healthy individuals (85 women and 90 men) living and born in North Italy. The DNA from blood samples was extracted using a GenomicPrep Blood DNA Isolation Kit (APB, Milano, Italy), according to the manufacturer's instructions. The quantity of human DNA was determined by spectrophotometry. Aliquots of 2–5 ng of target DNA were amplified in singlepex with the primers reported by Edelmann (1) for DXS7133, GATA172D05 and newly designed forward primer for DXS7132. The primers for DXS7132 annealing more closely to the repeat units of the X-STR which resulted in a 19 bp shorter amplicon length compared with the previously published primer sequences. The primer sequences for DXS7132 were:

Primer forward: 5′-CCCTCTCATCTATCTGACTG-3′

Primer reverse: 5′-GCCAAACTCTATTAGTCAAC-3′

Primer forward for each locus was Cy5-labeled. PCR was carried out in a 25 μL of reaction volume containing 2–5 ng DNA, 0.4 μM of each primer, 0.2 mM of each dNTP, 2 mM $MgCl_2$, 1.5 U AmpliTaq DNA polymerase, 2.5 μL AmpliTaq buffer II.

The amplification conditions were the same for the three X-STRs markers and consisted of initial denaturation at 94°C for 5 min, followed by 28 cycles at 94°C for 60 s, 58°C for 45 s, 72°C for 60 s, and final extention step at 72°C for 10 min, in a GeneAmp PCR System 9700 Thermal Cycler (Applied Biosystems, Foster City, CA).

Typing of the amplified products was carried out using the Automated Laser Fluorescent DNA sequencer (ALF-Express, APB). Fragment size was typed by comparison with sequenced allelic ladders. Statistical analysis was performed by a computer program from the authors using Excel spread sheets.

Allele and genotype frequencies for each X-STR locus were determined by counting. Hardy-Wienberg equilibrium (HWE) and possible deviations from it were tested following the Chi-square testing method using the female genotypes only. The polymorphism information content PIC was calculated as suggested by Bostein (2), while observed heterozygosity (HET), power of discrimination in females (PD^F) and males (PD^M), and mean exclusion chance (MEC) were determined as proposed by Desmarais (3).

The complete dataset is available to any interested researcher upon request to the corresponding author, Prof. Domenico De Leo.

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TABLE 1—*Allele frequencies and forensic efficiency of DXS7132, DXS7133, GATA172D05 markers in identification and paternity analysis in a North Italy population sample (*n *= 175).*

	DXS7132		DXS7133		GATA172D05	
Allele	Female (n = 85)	Male (n = 90)	Female (n = 85)	Male (n = 90)	Female (n = 85)	Male (n = 90)
6					0.218	0.218
7					…	…
8					0.167	0.180
9			0.446	0.517	0.034	0.045
10			0.163	0.090	0.293	0.270
11	0.006	…	0.331	0.314	0.195	0.213
12	0.128	0.124	0.042	0.056	0.092	0.090
13	0.302	0.314	0.012	0.022		
14	0.337	0.314	0.006	…		
15	0.186	0.180				
16	0.041	0.045				
17		0.022				
HET	0.691		0.596		0.749	
PIC	0.710		0.646		0.781	
MEC	0.574		0.414		0.656	
PD^F	0.844		0.721		0.901	
PD^M	0.752		0.622		0.807	

HET: observed heterozygosity; PIC: polymorphism information content; MEC: mean exclusion chance for chrX markers in father/daughter duos, PD^F: power of discrimination in female sample; PD^M: power of discrimination in male sample.