Allelic Frequency Distribution of Four STR Loci (FGA, D7S820, D1S533, D9S304) in the Argentinean Population

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Introduction: DNA typing by means of STRs is a very useful tool in forensic casework and paternity testing. When a match between two forensic samples exists, the analyst must by able to determine the probability that a man, randomly chosen from the population where the crime has occurred, has the same genetic pattern as the analyzed evidence. In a similar way, in cases of disputed paternity, the analyst must be able to report how much more probability a man that shares alleles with a child has of being the biological father of that child than a randomly chosen man from the population that the alleged father belongs to. Knowing the allelic frequency distribution of each analyzed locus is necessary to give weight to both, a match between forensic samples and non-exclusion paternity cases. Since the frequency distribution differs among different populations for each locus, it is important for the laboratory to have its own databases with allelic frequencies for the local population of different loci. We previously reported (2nd European Symposium on Human Identification, Innsbruck, June 1998) the frequency distribution of three STR loci (D12S1090, D3S1744, D18S849) in the Buenos Aires population. Data presented here correspond to the frequency distribution of four STR loci located in four different chromosomes in the Buenos Aires population.

Materials and Methods: 178 chromosomes belonging to unrelated individuals from the metropolitan area of the city of Buenos Aires were studied. DNA was extracted from whole blood by a non-organic procedure. DNA amplification was performed in multiplex reactions using a GeneAmp 9600 PCR system (Perkin Elmer) for FGA, D7S820, D1S533, D9S304 loci. Amplification products were separated by electrophoresis in 4% acrylamide denaturing gels in 0.5X TBE buffer and the detection was accomplished through silver staining. Alleles were determined by directly comparing with an allelic ladder. Frequency distribution and % of heterozygosity of each locus were calculated.

Results:

Locus FGA   Heterozygosity: 89%

AL	*16*	*17*	*18*	*19*	*20*	*21*	*22*	*23*
FR	0.0056	0.0000	0.0112	0.0843	0.1292	0.1404	0.1629	0.0787

AL	*24*	*25*	*26*	*27*	*28*	*29*	*29.2*	*30*
FR	0.2247	0.0843	0.0674	0.0112	0.0000	0.0000	0.0000	0.0000

Locus D7S820   Heterozygosity: 77%

AL	7	8	9	10	11	12	13	14	15	16
FR	0.0000	0.1067	0.1180	0.3034	0.2584	0.1854	0.0281	0.0000	0.0000	0.0000

Locus D1S533   Heterozygosity: 79%

AL	7	8	9	10	11	12	13	14	15	16