

FOR THE RECORD

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Allele Frequencies for Ten *Alu* Insertion Polymorphisms in Anatolian Population

POPULATION: Different regions of Turkey, mostly Central Anatolia ($n = 102$)

KEYWORDS: forensic science, DNA typing, *Alu* insertion polymorphisms, ACE, APO, A25, B65, D1, FXIII B, HS4.32, HS4.69, PV92, TPA25, Anatolian population, Turkey, population genetics

Ten biallelic, autosomal human-specific *Alu* insertion polymorphisms; ACE, APO, A25, B65, D1, FXIII B, HS4.32, HS4.69, PV92 and TPA25 were analyzed in Anatolian population. DNA extraction was performed from both blood and buccal samples. DNA extraction from whole blood was performed with the standard Phenol-Chloroform-Isoamylalcohol (25:24:1) Isolation Method (1). For DNA isolation from buccal samples; phenol-chloroform-isoamylalcohol (25:24:1) and chloroform-isoamylalcohol solution (24:1) extractions were performed, overnight incubation at -20°C with 3 M sodium acetate (NaAc) and 0.6 volumes of isopropanol was done and precipitation of DNA was done by 70% ethanol. Specific oligonucleotide primer sequences and the annealing temperatures for PCR amplification are reported in Arcot et al. (2,3) and Romualdi et al. (4) PCR products were visualized by agarose gel electrophoresis. The allele frequencies, observed and expected heterozygosities for each loci were calculated with the help of GENETIX 4.0 software (5). The assessment of the Hardy-Weinberg (HW) equilibrium was performed by the chi-square (χ^2) test statistic (6). It was observed that all the loci were in the HW equilibrium ($p > 0.05$). Results of all the population statistics calculations are presented in Table 1.

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The complete data are available to any interested researcher upon request.

References

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TABLE 1—Population statistics for 10 Alu insertion polymorphisms in Anatolian population.

Alu Insertion	N	Frequency of the Insertion	Genotype	Observed Number	Expected Number	χ^2	Observed Heterozygosity	Expected Heterozygosity
ACE	102	0.3333	+/+	15	11.33	2.670	0.3725	0.4444
			+/-	38	45.33			
			-/-	49	45.34			
APO	102	0.9510	+/+	92	92.25	0.266	0.0980	0.0932
			+/-	10	9.51			
			-/-	0	0.24			
A25	101	0.0693	+/+	0	0.48	0.555	0.1386	0.1290
			+/-	14	13.03			
			-/-	87	87.49			
B65	101	0.4851	+/+	26	23.77	0.786	0.4554	0.4996
			+/-	46	50.45			
			-/-	29	26.78			
D1	101	0.3713	+/+	17	13.93	1.716	0.4059	0.4669
			+/-	41	47.15			
			-/-	43	39.92			
FXIIIB	101	0.4604	+/+	26	21.41	3.380	0.4059	0.4969
			+/-	41	50.18			
			-/-	34	29.41			
HS4.32	95	0.6684	+/+	41	42.44	0.448	0.4737	0.4433
			+/-	45	42.11			
			-/-	9	10.45			
HS4.69	96	0.3021	+/+	7	8.76	0.726	0.4583	0.4217
			+/-	44	40.48			
			-/-	45	46.76			
PV92	102	0.1520	+/+	1	2.36	1.088	0.2843	0.2577
			+/-	29	26.29			
			-/-	72	73.35			
TPA25	101	0.4802	+/+	21	23.29	0.833	0.5446	0.4992
			+/-	55	50.42			
			-/-	25	27.29			
Average Heterozygosities							0.3637	0.3752