

ALLELE FREQUENCY DISTRIBUTION OF THREE STRs LOCI: HUMARA, HUMPLA2 AND VS17T IN THE SPANISH POPULATION

C. Cabrero, A. Díez, E. Valverde and J. Alemany
 Depart. Biología Molecular, PharmaGen, Madrid, SPAIN

INTRODUCTION

The use of short tandem repeat loci for population genetic studies, genetic analysis of inherited diseases and individual identification purposes requires the establishment of databases for each reference population. Some groups have reported a number of STR's loci amenable to Polymerase Chain Reaction (PCR) analysis, as Edwards et al. (HUMTH01, HUMARA), Polymeropoulos et al. (HUMPLA2A), Kimpton (vWF) or Sharma (D21S11 or VS17T).

In the present study we have analysed the variability at three STRs loci (HUMARA, HUMPLA2A and VS17T), in a representative sample of the Spanish population.

METHODS

SAMPLES: Blood samples were obtained from 180 volunteer donors belonging to the Spanish population. DNA was extracted following the perchlorate protocol. The geographical distribution of the donors is similar to that given in Valverde et al.

PCR REAGENTS: All amplifications were performed in a final volume of 50 μ l in a Perkin Elmer thermocycler. Each reaction contained 2-200 ng of genomic DNA, 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1,5 mM MgCl₂ and 1.25 U AmpliTaq Polymerase. One of each pair of primers was end-labelled with ³²P- γ -ATP.

PRIMER SEQUENCES:

HUMPLA2A:

5'CTAGGTTGTAAGCTCCATGA3'

5'TTGAGCACTTACTCTGTGCC3'

VS17T:

5'GTGAGTCAATCCCCAAG3'

5'GTTGTATTAGTCAATGTTCTCC3'

HUMARA:

5'GCTGTGAAGGTTGCTGTTCCATCAT3'

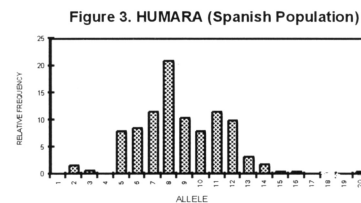
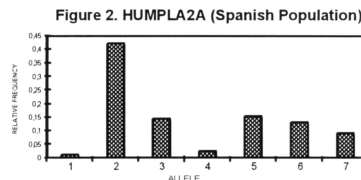
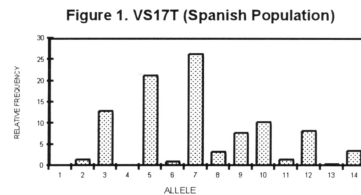
5'TCCAGAATCTGTTCCAGAGCGTGC3'

CYCLE TEMPERATURES: 95 °C (1 min), 54 °C (1 min) and 72 °C (1 min), 28 cycles. Prior to the first cycle the DNA was denatured at 95 °C for 10 min, and after the last cycle an additional extension at 72 °C for 10 min was performed.

RESULTS

Figures 1, 2 and 3 represent the allele frequency distribution of 180 unrelated Spanish individuals for the VS17T, HUMPLA2A and HUMARA loci respectively, and the table gives some statistical parameters.

	Heterozygosity	Chance of exclusion
HUMARA	0.744	0.506
HUMPLA2	0.743	0.504
VS17T	0.859	0.714



REFERENCES

- 1.- Edwards, A. et al. (1992). *Genomics* 12, 241-253
- 2.- Polymeropoulos, M.H. et al. (1991). *Nucl. Acids Res.* 19, 195
- 3.- Kimpton, C. et al. (1992). *Hum. Mol. Genet.* 1, 287
- 4.- Kimpton, C.P. et al. (1993). *PCR Methods and Applications* 3, 13-22.
- 5.- Valverde, E. et al. *Advances in Forensic Haemogenetics*, Vol. 4, Springer-Verlag, Berlin, 1992, pp. 187-189.
- 6.- Díez, A. et al. *Sangre*, 37, (1992) 275-278.
- 7.- Valverde, E. et al. *Int. J. Leg. Med.*, 105 (1993) 251-256