ALLELE FREQUENCY DISTRIBUTION OF D2S44, D12S11, D7S21, D7S22 AND D5S43 LOCI IN SOUTHERN SPAIN.

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INTRODUCTION

DNA analysis of restriction fragment length polymorphisms (RFLP's) has become one of the most powerful methods in forensic science casework and paternity testing. Nearly all laboratories working in the field of paternity testing and stain analysis prefer single locus probes (SLP's) because these probes have a better sensitivity than multilocus probes and offer the possibility of building a database for the allele frequency. We have implemented in routine case work in our laboratory the use of 5 single locus probes and the results of DNA analysis are reported as frequency data.

The forensic use of this technique is regarded as valid and reliable (NRC, 1992; Lander and Budowle, 1994). However, interpretation of test results is highly dependent on the population genetics of the markers, and a sufficiently large database of the relevant population must be established. The purpose of this study was to develop a frequency database for five hypervariable loci (D2S44, D12S11, D7S21, D7S22 and D5S43) of the population of our area (S Spain).

MATERIALS AND METHODS

DNA from blood samples of 110 unrelated individuals of southern Spain was extracted according to the method of Gill et al (1987, 1991) using phenol/chloroform. Complete restriction of DNA was carried out with the enzyme Hinf I. DNA was then quantified using a Hoefer TKO100 DNA fluorometer.

Size separation of restricted DNA and K562 / Hinf I digest genomic control DNA was achieved by electrophoresis in a 0.7% agarose gel running in TBE buffer for 18 hours (Gill et al, 1992). Following denaturation the DNA was transferred onto a nylon membrane and the DNA was fixed by ultraviolet irradiation. Alkaline phosphatase conjugated single locus probes MS31, MS43a, G3, MS8 and MS43a from Cellmark Diagnostics and YNH24 from Promega Corporation were used sequentially.

All autoradiographs were analysed using a computerized digital image analysis system (Bioimage, Millipore Corp.) which utilised the Elder and Southern method (1987) for band size calculation with reference to molecular weight markers (BRL/NICE). Data points were recorded at 0.01 kb intervals and binned to 0.1 kb for generation of the histograms.

RESULTS AND DISCUSSION

Our findings on VNTR allele frequency distribution in the population of Southern Spain are presented in Fig. 1. A summary of data is also presented in Table 1.

The histograms generated by our data show good correlation with previously published, caucasian data collections where loci and restriction enzyme are in common (Gill et al. 1991; Brinkman et al. 1991; Odelberg et al. 1989; Valverde et al., 1992).

Table 1: Allele size range, most frequent size range, frequency of the most common size range and heterozigosity of the five VNTR-loci studied on the population of Southern Spain (N=110).

Genetic locus	D2S44	D12S11	D7S21	D7S22	D5S43
DNA-probe	YNH24	MS43a	MS31	G3	MS8
Allele size range (Kbp)	1.86-9.61	2.90-14.78	2.46-9.97	1.66-14.78	2.33-9.16
Most frequent size range (Kbp)	2.65-2.75	9.05-9.15 9.15-9.25	5.45-5.55	3.15-3.25	6.65-6.75
Frequency of most common size range (%)	11.7	12.08	6.43	4.76	12.08
Heterozygosity (%)	95.75	95.10	95.05	83.33	85.0

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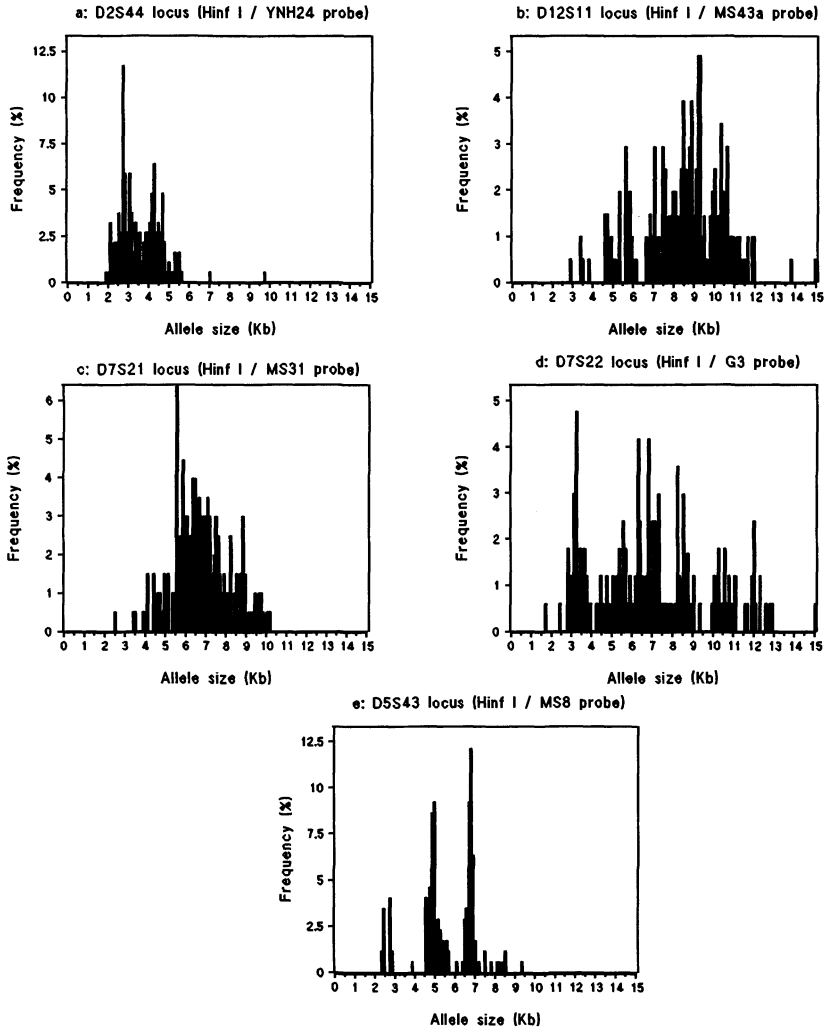

Figure 1: Distribution pattern of allele frequencies for D2S44 (a), D12S11 (b), D7S21 (c), D7S22 (d) and D5S43 (e) loci in the population of Southern Spain (N=110)