MS1, MS31 AND MS43A SINGLE LOCUS PROBES: A PRELIMINARY STUDY IN THE BASQUE POPULATION AND ITS APPLICATION IN PATERNITY TESTING

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INTRODUCTION

Traditionally, phenotype markers have been used to establish identity and biological paternity. At the present time polymorphisms in minisatellite regions, such as those revealed by single locus probes, may solve all filliation matters with a much higher liability (Jeffreys et al. 1985a, 1985b; Rose et al. 1988; Valentin 1980).

In this work the results obtained from the study of loci D1S7, D7S21 and D12S11 in a small sample of Basque population are shown in order to set a data base with the frequency of the alleles detected on these loci with the probes MS1, MS31 and MS43A going, which will enable us to establish biological paternity using these DNA polymorphisms in our population. Using these probes we also studied five mother-child-alleged father's selected among those we have been requested to solve till now.

MATERIAL AND METHODS

Four micrograms from each individual were digested with Hinf I and the fragments obtained, fractionated by electrophoresis in 0.7% agarose gels. Single locus probes were provided already labeled with the NICE system (Cellmark Diagnostics). Allele sizes for fragments detected with SLPs, were performed taking as a reference the NICE DNA analysis ladder (from BRL) in combination with probe MW100, and using Elder and Southern's reciprocal method. K562 cell line was used as a control. The probability of paternity for each case was calculated using Jeffreys' method.

RESULTS AND DISCUSSION

The frequency distributions for the alleles detected with single locus probes MS1, MS31, and MS43A are shown in Fig. 1. The size ranges of the fragments (Table 1) are very similar to those found by Smith et al. (1990). The allele number obtained in this sample is lower than that reported in the literature. It might be argued, as Balazs et al. suggest (1989), that these polymorphic loci in our population contain alleles that are smaller than those retained by gels used here. The occurrence of such alleles would result in the detection of an excess number of homozygous individuals relative to those predicted by the frequency of alleles. However, the calculated heterozygosity does not differ statistically from that observed; therefore it seems more probable that this might reflect some differential features of the Basque population. This population has been shown to have gene frequency distributions different from the European ones in several number of studied polymorphic systems (García-Orad et al., 1990; Aguirre et al., 1991). A more extensive population sample will allow us to solve this point.

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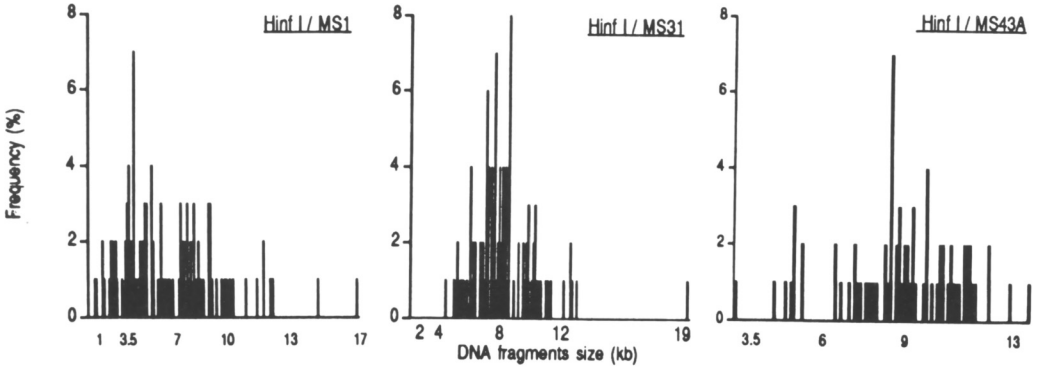

Fig. 1. Distribution of MS1, MS31 and MS43A alleles

Table 1. Observed (Ho) and expected (He) heterocigosities, allele sizes and mean frequencies for three loci

PROBE	Ho	He	Size-range (kb)	Most frequent allele (kb)	q
MS1	0.945	0.965	0.9 - 17	3.8 ± 0.14	0.035
MS31	0.833	0.891	1.9 - 19	8.0 ± 0,28	0.109
MS43A	0.892	0.920	3.4 - 14	8.8 ± 0.31	0.080

Table 2. Discriminatory capabilities of MS1, MS31 and MS43A for identity and paternity pourposes

PROBE	Alleles	$2q\text{-}q^2$ [(a)]	$q^2\ (2\text{-}q)$ [(b)]	Pex [(c)]
MS1	42	0.0688	0.0024	0.952
MS31	19	0.2061	0.0224	0.893
MS43A	18	0.1536	0.0123	0.887

(a) Band sharing probability
(b) Inclusion probability
(c) Exclusion probability of paternity

The inclusion probability and the exclusion probability of paternity estimated from the above results are showed in Table2. These parameters confirm the discrimination power of single locus probes MS1,MS31 and MS43A in the Basque Country. In order to test this, five mother-child-alleged father trios were analyzed; the results obtained are shown in table 3. In all the cases, the pattern of inclusion or exclusion of the alleged father, matched that observed using the conventional systems.

The results obtained with the application of these probes, points their power of exclusion up, and confirm the possibility of obtaining very high probabilities of paternity. Thus, we continue elaborating a more complete data base which will enable us to use these probes for identity and paternity purposes in our population.

Table 3. Results on five cases tested with MS1, MS31 and MS43A probes and conventional systems

Case	Exclusion			PP	Exclusion with conventional systems
	MS1	MS31	MS43A		
#1	-	-	-	0.995	
#2	+	+	+	-	Gc, ACP, PGM
#3	-	-	-	0.948	
#4	+	+	-	-	Rh, ADA, GLO
#5	-	-	-	0.989	

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