

## Four STRs in 300 Norwegians

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### INTRODUCTION

The tetrameric short tandem repeat loci HUMTH01, HUMFES/FPS, HUMVWA31 AND HUMF13A1 were studied. Amplification was performed according to EDNAP recommendation in a Perkin Elmer 9600, and fragments analysed in an ABI Model 373 Sequencing System using Genescan 672 software.

### MATERIAL

DNA was prepared from whole blood. Blood samples were obtained from 300 unrelated Norwegians (150 males, 150 females) involved in paternity cases. Alternating male/female individuals were chosen from consecutive cases, and ascertainment of nationality was based on typical Norwegian names.

### METHODS

HUMTH01/HUMFES/FPS and HUMVWA31/HUMF13A1 were amplified in two separate duplex PCR reactions. The STR-PCR products from both reactions were loaded in one single lane on a 24 cm denaturing 6% polyacrylamide gel. The internal standard ROX2500 was included in each sample for size determination.

Hardy-Weinberg was tested using the Chi-square test. Groups with expected values below 5 were excluded.

The polymorphic information content, PIC, was calculated using the formula of Botstein et al. (1980).

The Matching Probability, pM, was calculated from the allele frequency data using the formula of Jones (1972).

### RESULTS AND DISCUSSION

The genotype distributions are in accordance with Hardy-Weinberg expectations, ( $P > 0.6$  for all loci).

Allele distributions, PIC, and pM values are similar to those found in other Caucasian population materials (Colin P Kimpton 1993).

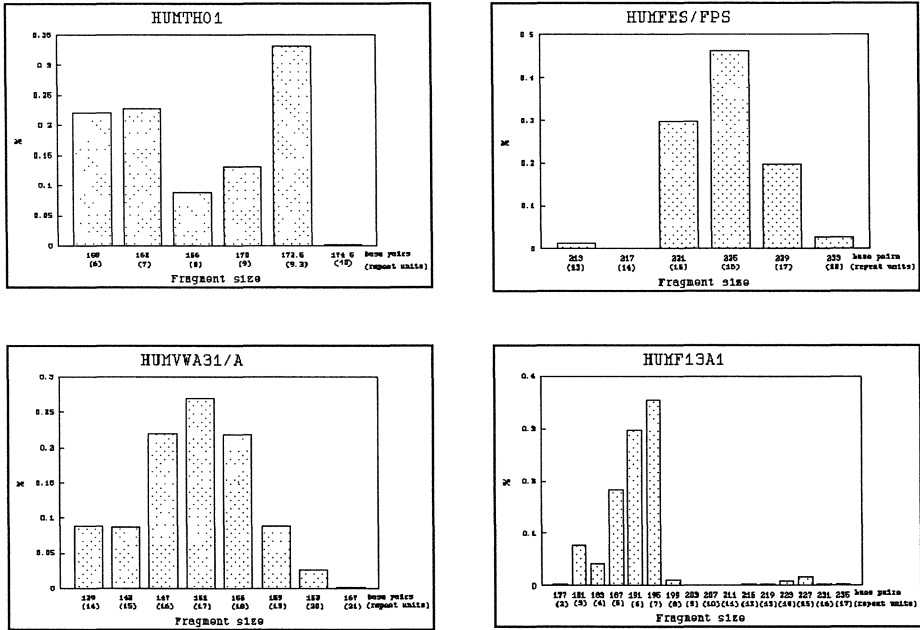


FIGURE 1 Allele frequency histograms.

TH01	tot. obs.	Allele freq.	FES	tot. obs.	Allele freq.
158	132	0.220	213	8	0.013
162	137	0.228	217	1	0.002
166	53	0.088	221	179	0.298
170	78	0.130	225	277	0.462
173.5	199	0.332	229	118	0.197
174.5	1	0.002	233	17	0.028
VWA			F13		
139	53	0.088	177	1	0.002
143	52	0.087	181	46	0.077
147	132	0.220	183	25	0.042
151	162	0.270	187	110	0.184
155	131	0.218	191	178	0.297
159	53	0.088	195	212	0.354
163	16	0.027	199	6	0.010
167	1	0.002	215	2	0.003
			219	2	0.003
			223	5	0.008
			227	10	0.017
			231	2	0.003
			235	1	0.002

TABLE 1 Allele frequency data.

TABLE 2 Number of alleles (K), gene diversity (gene D), and PIC of the STR loci studied in various Caucasian populations.

Locus	Norwegians (N=300)			Caucasians <sup>1</sup> (N=55)			North <sup>2</sup> Europeans	Whites <sup>3</sup>
	K	gene D	PIC	K	gene D	PIC	gene D	gene D
HUMTH01	6	0.76	0.75	5	0.77	0.76		0.76
HUMFES/FPS	6	0.66	0.60	5	0.67	0.62		
HUMVWA31	8	0.81	0.78	7	0.81	0.79		
HUMF13A1	13	0.74	0.70	7	0.72	0.68	0.73	

1 Colin P. Kimpton(1993). 2 Wilson J. Wall(1993). 3 Al Edwards(1991)

TABLE 3 Matching Probability (pM) of STR Loci

Locus	Norwegians	Caucasians <sup>1</sup>
HUMTH01	0.09	0.09
HUMFES/FPS	0.18	0.19
HUMVWA31	0.07	0.07
HUMF13A1	0.10	0.13

1 Colin P. Kimpton (1993)

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