CHARACTERIZATION OF YNZ 22 LOCUS FOR FORENSIC PURPOSES . ALLELE AND GENOTYPES FREQUENCIES IN A NORTHERN ITALIAN POPULATION .

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INTRODUCTION

PCR amplification discriminates several polymorphic VNTR regions also in forensic situations, where limited amounts of DNA are available .
One of the most highly polymorphic region is YNZ 22 (HGM locus D17S30)(1). This genomic locus contains 70 base pair sequence tandemly repeated a variable number of times.
The allele frequencies distribution of this VNTR system was investigated in order to create an own database for pratical applications in paternity testing and identification of stains.

MATERIALS AND METHODS

100 samples of unrelated subjects living in Brescia (Northern Italy) were considered . DNA was extracted from EDTA blood using proteinase K, phenol-chloroform isoamylalcohol and ethanol precipitation. DNA concentration was extimated by agarose minigel (0,8%) electrophoresis .
PCR amplification was performed according to the following conditions :

Denaturation	95°C	3 min.
Annealing	55°C	1 min.
Extention	72°C	1 min.

The amplification products were separated in agarose electrophoresis gel (2%).
The bands were visualized by ethidium bromide staining at the concentration of 1 mg/ml .
The fenotypes were identified by comparision with 123 BRL ladder.

RESULTS AND DISCUSSION

Table 1 shows the calculated allele frequencies while the Table 2 reports the observed genotypes and their frequencies.
A total of 22 different genotypes corresponding to 9 alleles, were found for YNZ 22 in 100 blood samples examined. The most frequent genotypes were the homozygotes 2 and 4, followed by the heterozygotes 3-4 and 2-4.
This distribution is different from that found in previous studies on Italian groups (Central Italy) (2-5). In fact, with regard to the allele frequencies, we observed that the frequencies of the allele 2 exceeded the allele 4 frequency.(Figure 1)
We propose to continue compiling a more complete and wide database to have a better and more precise valuation of these results, with special regard to the great number of homozygotes 2. This could depend on real higher value of the frequency or a selective amplification of the low WM allele.

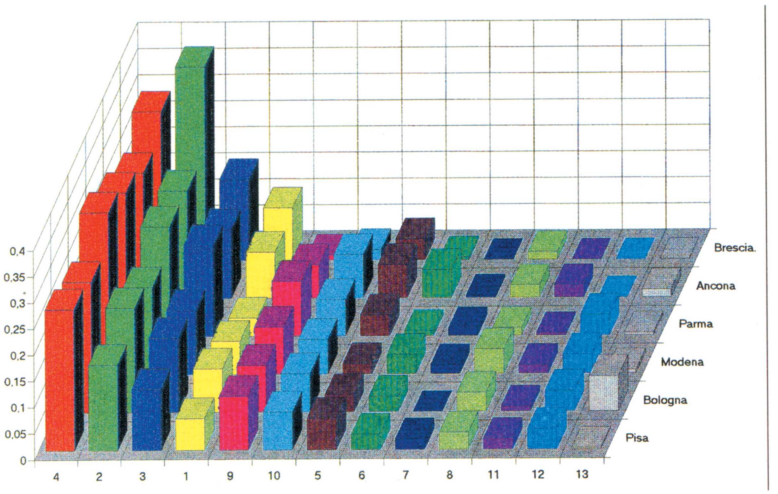

Figure 1: Distribution of YNZ22 alleles in Italy

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TABLE 1

ALLELE FREQUENCIES		OBSERVED
YNZ 22 1	0,1	20
YNZ 22 2	0,37	74
YNZ 22 3	0,155	31
YNZ 22 4	0,285	57
YNZ 22 5	0,04	8
YNZ 22 6	0,005	1
YNZ 22 8	0,015	3
YNZ 22 9	0,01	2
YNZ 22 10	0,02	4

TABLE 2

GENOTYPE	OBSERVED	FREQUENCY	EXPECTED
1-1	3	0.03	1.0
1-2	4	0.04	7.4
1-3	2	0.02	3.1
1-4	7	0.07	5.7
1-5	1	0.01	0.8
2-2	27	0.27	13.69
2-3	7	0.07	11.47
2-4	8	0.08	21.09
2-9	1	0.01	0.74
3-3	5	0.05	2.4025
3-4	11	0.11	8.835
3-5	1	0.01	1.24
4-4	14	0.14	8.1225
4-5	1	0,01	2.28
4-8	1	0.01	0.855
4-10	1	0.01	1.14
5-5	1	0.01	0.16
5-6	1	0.01	0.04
5-8	1	0.01	0.12
5-10	1	0.01	0.16
8-9	1	0.01	0.03
10-10	1	0.01	0.04

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System and locus: YNZ 22 (HGM D17S30)

Population and sample size: Brescia (Northern Italy). 100 unrelated blood donors

Methods: - DNA extracted from EDTA blood using proteinase K, phenol-chloroform · isoamylalcohol and ethanol precipitation.
- PCR amplification : Denaturation 95°C 3 min., Annealing 55°C 1 min., Extention 72°C 1 min.
- Electrophoretic method: agarose gel (2%) at 80 V. with ethidium bromide
- The fenotypes were identified by comparision with 123 BRL ladder.

Results:

ALLELE FREQUENCIES		OBSERVED
YNZ 22 1	0,1	20
YNZ 22 2	0,37	74
YNZ 22 3	0,155	31
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YNZ 22 10	0,02	4

Comments:

The allele distribution is different from that found in other Italian population. We propose to continue compiling a more complete and wide database to have a better and more precise valuation of these results, with special regard to the great number of homozygotes 2. This could depend on real higher value of the frequency or a selective amplification of the low WM allele.