THE ALLELIC DISTRIBUTION OF 5 STR SYSTEMS IN A NORTH ITALIAN POPULATION.

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Systems and loci: HUMFES/FPS (15q25-qter); HUMVWA (12p12-pter); HUMF13B (1q31-q32.1); SE33 (ACTBP2); HUMD21S11.

Population sample size: North Italy (Milano residents). HUMFES/FPS: N=115; HUMVWA: N=118; HUMF13B: N=119; HUMACTBP2: N=118; HUMD21S11: N=119.

Methods: Primers: HUMFES/FPS (Polymeropoulos et al., 1991), HUMVWA (Kimpton et al., 1992), HUMF13B (Nishimura and Murray, 1992), HUMACTBP2 (Polymeropoulos et al., 1992), HUMD21S11(Sharma and Litt, 1992).

PCR and electrophoretic conditions: HUMFES/FPS, HUMVWA, HUMD21S11 (Moeller et al., 1994); HUMF13B (Alper et al., 1995a); HUMACTBP2 (Wiegand et al., 1993).

Statistical analyses: the statistical evaluations were carried out using the programme HWE Analysis ver. 3 provided by C. Puers (Muenster, Germany). The programme checks the Hardy-Weinberg equilibrium by the Chi-Squared test, the logarithmic likelihood ratio (G) test, and the exact test by randomly shuffling the observed alleles 5000 times, as well as other statistical parameters. The frequency profile comparison between Italians, Germans and Turks was performed using a dedicated software for genetic heterogeneity (RxC contingency table; G. Carmody, Ottawa - Canada).

Results and discussion

The allele frequency distributions for the 5 systems investigated in the Italian population were compared to German (B.Brinkmann personal communication) and Turkish data (Alper et al,1995a; Alper et al., 1995 b). Relevant statistical data for each system are summarised in Table 1. No deviation from Hardy-Weinberg equilibrium was found for each locus studied in the Italian population.

The distribution patterns were similar in Italians, Germans and Turks. However, some statistical significant differences exist in some systems (HUMFES/FPS: Germans-Turks Chi-squared P value = 0.002 ±0.0014 Standard Error (SE); F13B: Italians-Turks Chi-squared P value = 0.000, German-Turks = 0.001 ±0.0010 SE; HUMACTBP2: Italians-Germans Chi-squared P value = 0.004 ±0.002 SE, Italians-Turks = 0.005 ±0.0022 SE, Germans-

Turks 0.001 ±0.001 SE; HUMD21S11: Italians-Turks Chi-squared P value = 0.003 ±0.0017 SE, Germans-Turks = 0.000).
For medium polymorphic systems (HUMFES/FPS, HUMF13B, HUMD21S11)the main differences seem to be a higher frequency for one allele in one population (e.g. allele 12 in Turks for HUMFES/FPS, allele 10 in Italians for HUMF13B, allele 32.2 in Turks for HUMD21S11). Remarkably, the results of HUMVWA typing showed no significant differences among the populations. For the most polymorphic system HUMACTBP2 the differences seem to lie at the extremes of the allelic ladder, even though the lower molecular weight gaussian peak of the frequency distribution seems to show significant differences in the German population when compared to the Italian and Turkish ones.

Conclusions

The allele frequency distributions of 5 STR systems in an Italian population are presented and compared with 2 other Caucasian populations (Germans and Turks) pointing out some statistical differences between them. These differences may be caused first of all by the size of the populations studied or could be due to actual interpopulation differences, related to one allele for the medium polymorphic systems (HUMFES/FPS, HUMF13B, HUMD21S11). It is not surprising for the system HUMACTBP2 to show statistically significant differences: this can be due to its higher degree of polymorphism.
These data strongly suggest that in the European populations some differences do exist and therefore local population databases are needed to perform biostatistical calculations in routine forensic casework.

References

Alper B, Schuerenkamp M, Meyer E (1995a) HumFES/FPS and HumF13B: population genetic study on a Turkish and German population survey. Int J Legal Med - In press.
Alper B, Wiegand P, Brinkmann B (1995b) Population genetic study from a Turkish population survey using 3 STR systems. Int J Legal Med - In press.
Kimpton C, Walton A, Gill P (1992) A further tetranucleotide repeat polymorphism in the vWF gene. Hum Mol Genet 1: 287.
Moeller A, Meyer E, Brinkmann B (1994) Different types of structural variation in STRs: HumFES/FPS, HumVWA and HumD21S11. Int J Legal Med 106: 319-323.
Nishimura DY and Murray JC (1992) A tetranucleotide repeat for the F13B locus. Nucleic Acid Res 20: 1167.
Polymeropoulos MH, Rath DS, Xiao H, Merril RM (1991) Tetranucleotide repeat polymorphism at the human c-fes/fps proto-oncogene (FES). Nucleic Acids Res 19: 4018.
Polymeropoulos MH, Rath DS, Xiao H, Merril CR (1992) Tetranucleotide repeat polymorphism at the human beta-actin related pseudogene H-beta-Ac-psi-2 (ACTBP2). Nucleic Acids Res 20: 1432.
Sharma V, Litt M (1992) Tetranucleotide repeat polymorphism at the D21S11 locus. Hum Mol Genet 1: 67.
Wiegand P, Budowle B, Rand S, Brinkmann B (1993) Forensic validation of the STR systems SE33 and TC11. Int J Legal Med 105: 315-320.

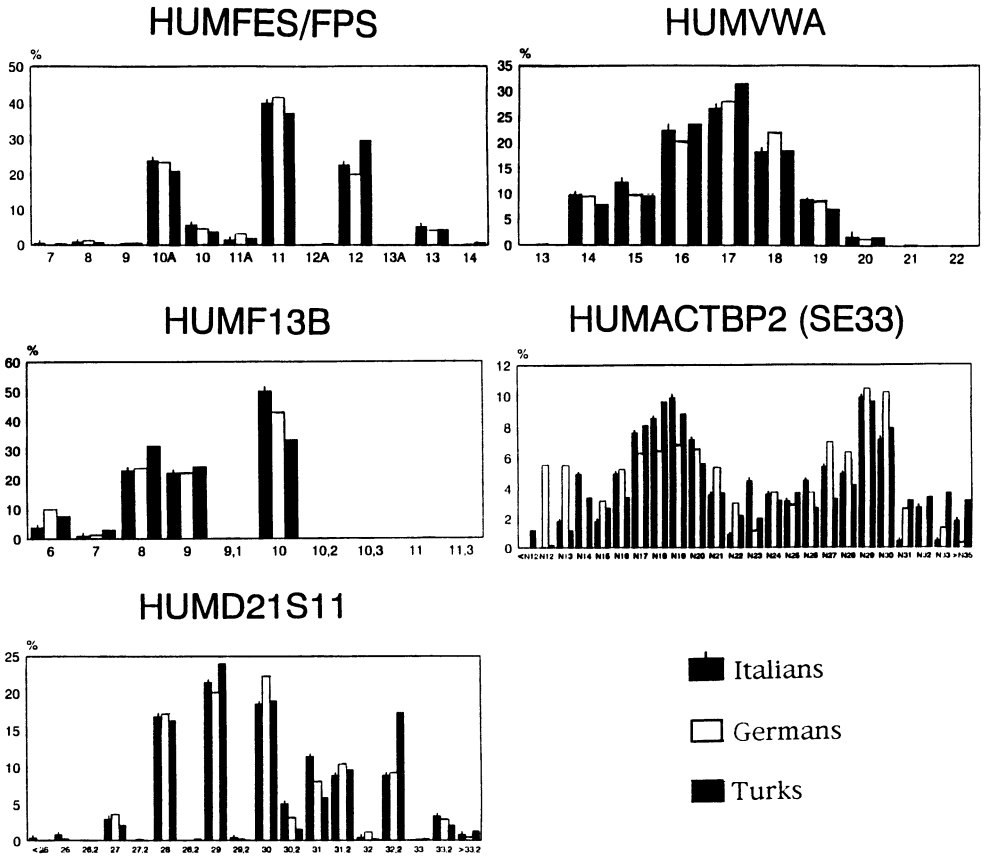

Fig. 1.
Comparative results of the allele frequency distribution for the 5 systems investigated in the Italian, German and Turkish populations.

System	Observed Heterozyg.	Mean Excl. Chance	Polym.info content	Prob. of match	Discrim. power
FES/FPS	0.6870	0.5024	0.6892	0.1155	0.8845
VWA	0.7966	0.6282	0.7862	0.0653	0.9346
F13B	0.5882	0.3842	0.5876	0.1787	0.8213
ACTBP2	0.9182	0.8564	0.9352	0.0165	0.9835
D21S11	0.8103	0.7074	0.8397	0.0427	0.9573

Table 1.
Statistical evaluations relevant to the STR systems studied in the Italian population.