POPULATION GENETIC DATA FOR F13A01, FES/FPS, F13B AND LPL IN THE SOUTH PORTUGUES E POPULATION

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Introduction

➢DNA parentage testing are currently performed using several highly polymorphic short tandem repeats.

➢ In our routine casework, we apply two validated STR kit, in order to have results in the 13 CODIS loci plus D2S1338,D19S433, PENTA E, PENTA D and Amelogenin.

➢ In complex paternity cases, in order to obtain conclusive likelihood ratios, it is often necessary to increment the number of STRs.

➢For this reason, we introduced in our laboratory GenePrint® FFFL Multiplex kit (Promega, USA) which can provide results in F13A1, FES/FPS, F13B and LPL loci.

➢It is our aim, establish an FFFL allele frequencies dataset for further use in biological kinship testing.

Material and Methods

➢ In this work, samples from 150 unrelated and healthy individuals collected from south Portugal population were studied.

➢ PCR amplifications were performed with GenePrint®FFFL multiplex kit (Promega, UK) according to manual.

➢Amplified products were detected in an ABI PRISM® 3130 *xl Genetic Analyser (Applied Biosystems,USA). DNA fragments were typed* with GeneMapper®*ID* v.3.2.1 *(Applied Biosystems, UK).*

➢Allele Frequencies and Statistical parameters were estimated with Arlequin 3.5.1.2.

➢Forensic and Paternity Statistics, were calculated with PowerStats v12 (Promega).

RESULTS

Figure 1 represents Allele frequencies distribution for F13A1, FES/FPS, F13B and LPL loci and in table 1 are represented all forensic and statistical parameteres estimated.

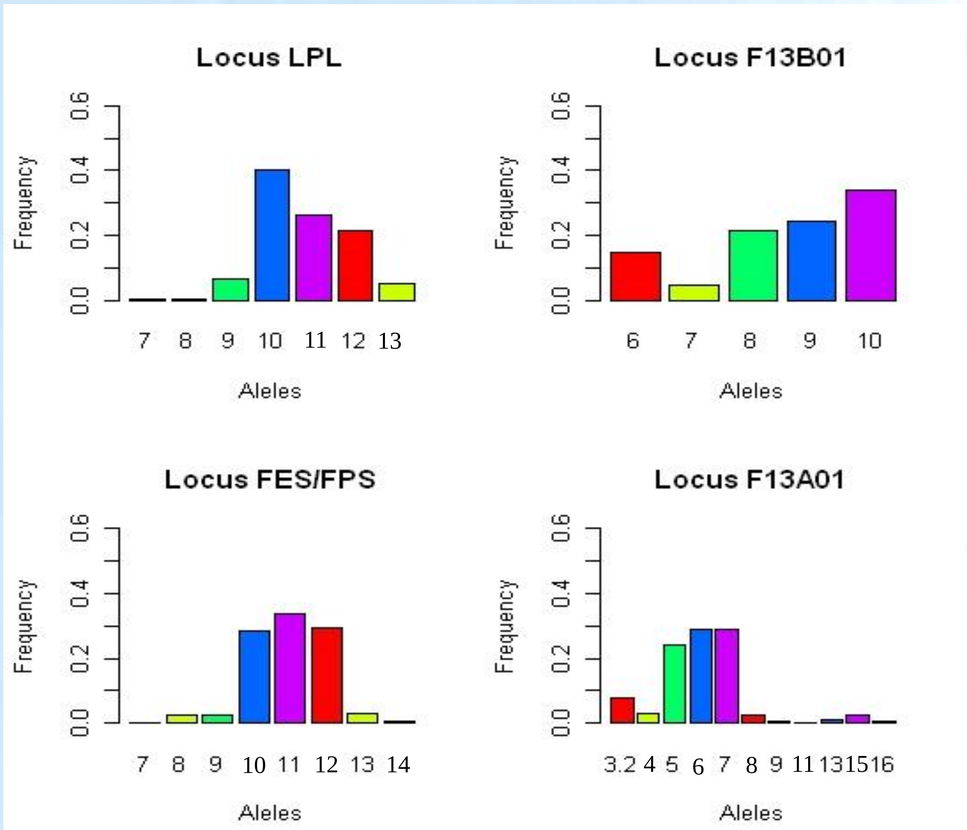

Figure 1-Allele Distributions in loci F13A1, FES/FPS, F13B and LPL in South Portuguese Population.

Table 1- Population statistics and forensic parameteres for the loci F13A1, FES/FPS, F13B and LPL in South Portuguese Population

	F13A01	FES/FPS	F13B01	LPL
PE	0.5238	0.8639	0.5611	0.4038
Ho	0.7613	0.6839	0.7806	0.6968
He	0.7690	0.7209	0.7543	0.7193
PIC	0.7233	0.6593	0.7066	0.6649
PD	0.9003	0.8639	0.8868	0.8693
TIP	2.0676	1.6630	2.2647	1.5816
P	0.5140	0.4441	0.5253	0.4585

MF-Minimal Frequency. PE-Power of exclusion. Ho- Observed Heterozigoty. He-expected heterozygoty, PIC-Polymorphic Information Content. PD-Discriminating Power, TIP-Tipical Paternity Index, *P*-Hardy Weinberg exact test *p* value with 10000 iterations.

✓**For *locus LPL*, 7 alleles were observed, and the most comon are alleles 10 (*f*=0.4032), 11 (*f=0.2613*) and 12 (*f=0.2129*).**

✓**For *locus F13B01*, 5 alleles were observed, and the most comon is allele 10 (*f*=0.3419)**

✓**For *locus FES\FPS*, 8 alleles were detected, and the most comon are alleles 10 *(f=0.2839),* 11(f=0.2355) and 12 (f=0.2935)**

✓**For *locus F13A01, 11 alleles were detected, and the most comon are alleles 5 (f=0.2419),6 (f=0.2871) and 7(f=0.2903). 3.2 (f=0.0774)* Microvariant**

✓**No deviations from Hardy-Weinberg expectations were found(p>0.05).**

✓ **F13A01 is the most polymorphic locus, with the highest Discrimination Power and Polymorfic Information Content values.**

conclusions

✓The forensic efficiency values sugested that loci **F13A01, FES/FPS, F13B01 and LPL** are discriminative and very useful to solve complex forensic casework, and should be added to the set of STRs loci routinely used in Forensic laboratories.

✓In conclusion a 4 loci dataset has been established for the south portuguese population, which can be used for both forensic casework and in complex kinship testing.

Bibliography

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