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Letter to the Editor

Allele frequencies of the new European Standard Set (ESS) loci in a population of Apulia (Southern Italy)

Dear Editor,

Allele frequencies of five miniSTRs loci (D1S1656, D2S441, D12S391, D10S1248 and D22S1045) included in the new European Standard Set (ESS) were calculated in Apulian population (Southern Italy), using two different kits for each samples: Investigator ESSplex SE Kit PCR Assay (Qiagen) and AmpFISTR NGM SElect PCR Amplification Kit (Applied Biosystems), in order to evaluate the concordance of the genotypes. This paper follows the guidelines for publication of population data requested by the journal [1].

Blood samples were collected from 150 unrelated individuals following informed consent.

Genomic DNA was extracted from peripheral blood by Blood genomicPrep Mini Spin Kit (GE Healthcare) and quantified by the Investigator Quantiplex Kit (Qiagen) using a Rotor-Gene Q. PCR Amplifications were performed by the Investigator ESSplex SE Kit PCR Assay (Qiagen) and AmpFISTR NGM SElect PCR Amplification Kit (Applied Biosystems). Both PCR kits simultaneously coamplifies the previous well established loci (D3S1358, vWA, D16S539, D2S1338, D8S1179, D21S11, D18S51, D19S433, TH01, FGA, Amelogenin) together with the additional new ones recommended by the European Network of Forensic Science Institutes (ENFSI) and by the European DNA Profiling Group (EDNAP) (D1S1656, D12S391, D10S1248, D22S1045 and D2S441), plus the highly polymorphic locus, SE33 [ACTBP2] [2–6].

Separation and detection of PCR products amplified by the multiplex assays were performed on the ABI Prism 310 Genetic Analyzer (Applied Biosystems). Genotyping of each samples was carried out automatically using the allelic ladders included in each kit as a reference and using GeneMapper[®] ID software v3.2 (Applied Biosystems).

Matching probability (MP), power of discrimination (PD), polymorphic information content (PIC), power of exclusion (PE) and typical paternity index (TPI) were calculated using PowerStat version 1.2 software package [7]. Hardy–Weinberg equilibrium (HWE) was assessed with GENEPOP software version 4.0 [8].

Allele frequencies and forensic indices are summarized in Table 1, available as an e-component.

The concordance study, performed by comparing the results obtained with the two PCR Amplification Kits, showed no differences in all genotype profiles.

No deviation from Hardy–Weinberg expectations was detected at either locus (p -value >0.05). Moreover genetic analysis using F_{st} estimation showed no evidence for differentiation at the five new

loci between Apulia and Italian populations (F_{st} values ranged from 0.01 to 0.10) [9–12].

The combined power of discrimination (PD) for the five studied loci is 0.999998793; this means that when two individuals are chosen at random from an Apulian population, they will show different genetic profiles with a probability of 99.9998793%. The combined power of exclusion (PE) is 0.996834296, higher than power of exclusion if these markers are used one by one.

All five loci showed an observed heterozygosity greater than 0.71, with the highest value for D1S1656 and D12S391. These loci have also the highest value of polymorphism information content (PIC), so they may be considered as the most informative markers. The high levels of polymorphisms of the analyzed loci in the Apulian population allow to confirm that these markers are useful tools in paternity and forensic analysis from degraded DNA samples [13–20].

Conflict of interest statement

None.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.fsigen.2012.10.007>.

References

- [1] A. Carracedo, J.M. Butler, L. Gusmão, W. Parson, L. Roewer, P.M. Schneider, Publication of population data for forensic purposes, *Forensic Sci. Int. Genet.* 4 (2010) 145–147.
- [2] M.V. Lareu, C. Pestoni, M. Schürenkamp, S. Rand, B. Brinkmann, A. Carracedo, A highly variable STR at the D12S391 locus, *Int. J. Legal Med.* 109 (1996) 134–138.
- [3] M.V. Lareu, S. Barral, A. Salas, C. Pestoni, A. Carracedo, Sequence variation of a hypervariable short tandem repeat at the D1S1656 locus, *Int. J. Legal Med.* 111 (1998) 244–247.
- [4] M.D. Coble, J.M. Butler, Characterization of new miniSTR loci to aid analysis of degraded DNA, *J. Forensic Sci.* 50 (2005) 43–53.
- [5] T. Lederer, G. Braunschweiger, Commentary on: Coble MD, Butler JM. Characterization of new miniSTR loci to aid analysis of degraded DNA, *J. Forensic Sci.* 50 (2005) 43–53, *J. Forensic Sci.* 52 (2007) 493.
- [6] P. Gill, L. Fereday, N. Morling, P.M. Schneider, The evolution of DNA databases—recommendations for new European STR loci, *Forensic Sci. Int.* 156 (2006) 242–244.
- [7] A. Tereba, Tools for analysis of population statistics, *Profile in DNA*, 1999, pp. 14–16 (free software distributed at <http://www.promega.com/geneticidtools/>).
- [8] F. Rousset, Genepop'007: a complete reimplementation of the Genepop software for Windows and Linux, *Mol. Ecol. Resour.* 8 (2008) 103–106.
- [9] B.S. Weir, C.C. Cockerham, Estimating F -statistics for the analysis of population structure, *Evolution* 38 (1984) 1358–1370.
- [10] A. Berti, F. Brisighelli, A. Bosetti, E. Pilli, C. Trapani, V. Tullio, C. Franchi, G. Lago, C. Capelli, Allele frequencies of the new European Standard Set (ESS) loci in the Italian population, *Forensic Sci. Int. Genet.* 5 (2011) 548–549.

- [11] A. Barbaro, P. Cormaci, S. Votano, A. Agostino, Allele frequencies of the new European Standard Set (ESS) loci in a population of Southern Italy (Calabria), *Forensic Sci. Int. Genet.* 6 (2012) e37–e38.
- [12] V. Cortellini, N. Cerri, A. Verzeletti, Population data on 5 non-CODIS STR loci (D10S1248, D22S1045, D2S441, D1S1656, D12S391) in a population sample from Brescia county (Northern Italy), *Forensic Sci. Int. Genet.* 5 (2011) e97–e98.
- [13] P. Martín, O. García, C. Albarrán, P. García, I. Yurrebaso, A. Alonso, Allele frequencies of six miniSTR loci (D10S1248, D14S1434, D22S1045, D4S2364, D2S441 and D1S1677) in a Spanish population, *Forensic Sci. Int.* 169 (2007) 252–254.
- [14] T. Seider, R. Fimmers, P. Betz, T. Lederer, Allele frequencies of the five miniSTR loci D1S1656, D2S441, D10S1248, D12S391 and D22S1045 in a German population sample, *Forensic Sci. Int. Genet.* 4 (2010) e159–e160.
- [15] S. Sorçaburu Cigliero, F. Gerin, C. Previderè, P. Fattorini, Allele frequencies of three mini-STR loci (D22S1045, D14S1434 and D10S1248) in North-East Italy, *Forensic Sci. Int. Genet. Suppl. Ser. 2* (2009) 378–379.
- [16] A. Barbaro, P. Cormaci, A. La Marca, Genetic data for the locus SE33 in a Southern Italy population with AmpFISTR NGM Select™ PCR Amplification Kit, *Forensic Sci. Int. Genet. Suppl. Ser. 3* (2011) e101–e102.
- [17] C. Previderè, P. Grignani, S. Presciuttini, Italian population data for the new ENFSI/EDNAP loci D1S1656, D2S441, D10S1248, D12S391, D22S1045. The GeFI collaborative exercise and concordance study, *Forensic Sci. Int. Genet. Suppl. Ser. 3* (2011) e238–e239.
- [18] P.E. Raimann, A.P. de Oliveira, R. Rodenbusch, J.B. Picanço, T.C. Albuquerque, C.S. Alho, Genetic data for D1S1677, D2S441, D4S2364, D10S1248, D14S1434 and D22S1045 miniSTR loci from the state of Rio Grande do Sul, Southern Brazil, *Forensic Sci. Int. Genet.* 6 (2012) e42–e43.
- [19] R. Bai, M. Shi, X. Yu, J. Lv, Y. Tu, Allele frequencies for six miniSTR loci of two ethnic populations in China, *Forensic Sci. Int.* 168 (2007) e25–e28.
- [20] S. Turrina, G. Filippini, D. De Leo, Concordance study and allele frequencies for 5 new European Standard Set (ESS) loci in the North-East Italian population, *Forensic Sci. Int. Genet. Suppl. Ser. 3* (2011) e329–e330.

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