



Letter to the Editor

Allele frequencies of 15 STR loci in Azerbaijan population**Keywords:**

Short tandem repeats (STRs)
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Dear Editor,

The biological basis of contemporary forensic DNA profiling is linked to the processes of cell and human reproduction. From the many variations that subsequently exist on the human genome, short tandem repeats (STRs) have emerged as the most suitable markers for current forensic identification. The variation of short tandem repeats or microsatellites dispersed through the whole human genome, is actively investigated in forensic labs for personal identification and determination of genetic relationships between individuals. Population genetics and forensic biology are inextricably linked disciplines. The relationships among groups of populations and intra-population characteristics complement each other in phylogenetic and forensic studies. In order to perform a reliable statistical analysis, forensic population database should be established [1,2].

Buccal cell samples were collected by oral swabs (Sterile Omni Swab or Sterile Foam Tipped Swabs, Whatman International Ltd.) from 285 unrelated healthy female and male Azerbaijani donors from central and southern Azerbaijan currently living in capital Baku and age of the individuals ranged between 24 and 53 years old. DNA was extracted using QIAmp DNA Mini Kit Buccal swab protocol (QIAGEN) according to manufacturer's instruction. Approximately 1 ng target DNA was amplified using the commercial typing kit, AmpFISTR® Identifiler™ PCR Amplification Kit (Applied Biosystems) [3]. Cycling conditions: 95 °C for 11 min; then 28 cycles of 94 °C for 1 min, 59 °C for 1 min and 72 °C for 1 min; then 60 °C for 60 min and 4 °C for an indefinite time, in a GeneAmp PCR System 9700 Thermal cycler (Applied Biosystems). The amplified products were separated by capillary electrophoresis on ABI PRISM 3130 Genetic Analyzers (Applied Biosystems) according to the manufacturer's recommended protocols. Data collection was performed with Data Collection v. 2.0. Software (Applied Biosystems) and the sample run data were analyzed together with an allelic ladder and positive and negative controls using GeneMapper IDX Software Version 3.2. Allelic frequencies, the power of discrimination (PD), the probability of paternity exclusion (PE), the polymorphic information content (PIC), the typical paternity index (TPI), the match probability (PM) and the

observed and expected heterozygosity (H_o , H_e) were calculated using the PowerStats V12 (<http://www.promega.com>) [4]. p -Value of exact test for Hardy–Weinberg equilibrium and exact test of population differentiation were calculated by Arlequin ver. 3.5 [5]. Allele frequency distribution and statistical parameters regarding the 15 STR loci of Azerbaijan population are shown in Table 1 and no deviation from Hardy–Weinberg equilibrium was observed ($p > 0.05$). Allelic frequencies for the 15 STRs were compared to previously published population data [6–9]. According to the results of exact test differentiation (Table 2) no differences were observed with the population of Iran [6]. After Bonferroni's correction ($p < 0.0033$), population differentiation tests showed that the population of Azerbaijan had statistically significant differences with Turkey [7] in 1 out of 15 loci (TPOX), with Iraq [8] in 2 out of 15 loci (D19S433 and vWA), with Russia [9] in 1 out of 15 loci (THO1).

Laboratory internal control standards and kit control were employed. This paper follows the guidelines for publication of population data requested by the journal [10]. Population data for the 15 STR loci in Azerbaijan are available for the forensic testing.

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.2013.03.004>.

References

- [1] P.J. Collins, L.K. Hennessy, C.S. Leibelt, R.K. Roby, D.J. Reeder, P.A. Foxhall, Developmental validation of a singletube amplification of the 13 CODIS STR loci, D2S1338, D19S433 and amelogenin: the AmpFISTR Identifiler PCR Amplification kit, *J. Forensic Sci.* 49 (6) (2004) 1265–1277.
- [2] S. Rand, M. Schurenkamp, C. Hohoff, B. Brinkmann, The GEDNAP blind trial concept. Part II. Trends and developments, *Int. J. Legal Med.* 118 (2) (2004) 83–89.
- [3] AmpFISTR1 Identifiler™ PCR Amplification Kit User's Manual. Applied Biosystem, Foster City, CA, USA, 2001.
- [4] Promega Powerstats download page: <http://www.promega.com/geneticidtools/powerstats/>.
- [5] L. Excoffier, H.E. Lischer, Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows, *Mol. Ecol. Resour.* 10 (2010) 564–567.
- [6] E.M. Shepard, R.J. Herrera, Iranian STR variation at the fringes of biogeographical demarcation, *Forensic Sci. Int.* 158 (2006) 140–148.
- [7] I. Yavuz, A.T. Sarikaya, Turkish population data for 15 STR loci by multiplex PCR, *J. Forensic Sci.* 50 (2005) 737–738.
- [8] F. Barni, A. Berti, A. Pianese, A. Boccellino, M.P. Miller, A. Caperna, G. Lago, Allele frequencies of 15 autosomal STR loci in the Iraq population with comparisons to other populations from the middle-eastern region, *Forensic Sci. Int.* 167 (2007) 87–92.
- [9] B.A. Malyarchuk, M. Wozniak, J. Czarny, M.V. Derenko, T. Grzybowski, D. Miscicka-Sliwka, Variation of 15 autosomal microsatellite DNA loci in the Russian population, *Mol. Biol.* 41 (1) (2007) 1–4.
- [10] A. Carracedo, J.M. Butler, L. Gusmao, W. Parson, L. Roewer, P.M. Schneider, Publication of population data for forensic purposes, *Forensic Sci. Int. Genet.* 4 (2010) 145–147.

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