Announcement of population data

Frequency assessment of 25 SNPs in five different populations

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ABSTRACT
Allele and genotype frequencies of 25 SNPs previously selected and validated for forensic purposes were assessed in 250 unrelated individuals originating from five different countries of Europe (Spain, Croatia, Bulgaria, Turkey and Serbia). All the SNPs generated extremely low Fst values confirming our previous results on Italian, African (Benin) and Asian (Mongolian) populations. As a consequence of such Fst values we observed similar values of random match probability across the populations: 2.26 \times 10^{-10} in the Spanish population, 2.13 \times 10^{-10} in the Croatian population, 4.21 \times 10^{-10} in the Bulgarian population, 2.52 \times 10^{-10} in the Serbian population and 1.46 \times 10^{-10} in the Turkish population.

1. Population
Two hundred and fifty unrelated individuals from five different populations: Spanish (n = 50), Croatian (n = 50), Bulgarian (n = 50), Serbian (n = 50), and Turkish (n = 50).

2. Extraction
Genomic DNA was extracted from whole blood by the QIAamp DNA Blood Mini Kit (QIAGEN Inc., Valencia, CA).

3. SNPs
A number of 25 SNPs were previously selected on the basis of a number of selection criteria reported and validated elsewhere [1,2]. The 25 SNPs are: rs1779866, rs1922807, rs2278741, rs905213, rs11242909, rs3130315, rs1075665, rs774023, rs10866988, rs585070, rs1506981, rs1533800, rs1981752, rs478347, rs11242909, rs3130315, rs1075665, rs774023, rs10866988, rs585070, rs1506981, rs1533800, rs1981752, rs478347, rs9562080, rs911621, rs999842, rs8033863, rs886528, rs154659, rs2317225, rs873289, rs11881170, rs380011 and rs2267628.

4. SNP typing
DNA typing was performed with 10 ng of target DNA using Pre-design TaqMan® Genotyping assays (Applied Biosystems, Foster City, CA). Fluorescence was detected using an ABI 7500 Sequence Detection System and genotypes were manually scored using Sequence Detection Software 2.0 (Applied Biosystems).

5. Genotyping confirmation and statistical analysis
Allele frequencies were calculated by direct counting. Genotypes of 50 random samples were confirmed by direct sequencing. All statistical and forensic parameters were calculated [3] using DNAVIEW™ 27.19. Statistical independence of selected markers was assessed by calculating linkage disequilibrium (LD) as $r^2$ [4] using LD plotter software (available at https://www.pharmgat.org/Tools/pbtoldplotform). Divergence from Hardy–Weinberg equilibrium (HWE) was examined using the on-line calculator (http://ihg2.helmholtz-muenchen.de/cgi-bin/hw/hwa1.pl). Inter-population genetic distance was assessed by calculating Fst for each marker (http://genepop.curtin.edu.au/genepop_op6.html).

6. Results
No departure from the Hardy–Weinberg equilibrium was detected. To exclude the dependence of markers from each other we calculated the pairwise LD values reported as $r^2$. All selected SNPs showed $r^2$ values near to zero (complete independence).

The frequencies of the minor allele (MAF) of the SNPs are reported in Table 2.

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The genetic distance $F_{ST}$ coefficients among the 5 populations ranged between 0.0001 and 0.0608, while the mean value observed for all SNPs was $0.0187 \pm 0.05$ (Table 2).

The random match probability for each population were: $2.26 \times 10^{-10}$ in the Spanish population, $2.13 \times 10^{-10}$ in the Croatian population, $4.21 \times 10^{-10}$ in the Bulgarian population, $2.52 \times 10^{-10}$ in the Serbian population and $1.46 \times 10^{-10}$ in the Turkish population.

7. Other remarks

Genetic data resulting from the typing of 250 unrelated individuals originating from 5 different European populations confirmed the high information content of the selected SNPs. The mean heterozygosity values calculated for the panel of 25 SNPs in the five populations considered in this study are 0.45 for Spanish population, 0.44 for Croatian, Bulgarian and Turkish populations and 0.42 for Serbian population. These values are quite similar to those reported in a previous work [2] for Italian populations and 0.42 for Serbian population. These values are almost identical to those reported in a previous work [2] for Italian populations and 0.42 for Serbian population. Finally the random match probability of a panel of 25 SNPs for each population analyzed in this work is quite similar to the RMP obtained for Italian population ($4.96 \times 10^{-10}$), Benin Gulf population ($5.30 \times 10^{-11}$) and for the Mongolian population ($3.11 \times 10^{-11}$).

This paper has strictly followed the requirements of FSI: Genetics guidelines and the ISFG recommendations [5-7].

Access to the data: Data is available on http://www.nacbo.net.

Table 1
Name, chromosomal localization, nucleotide position, assays ID and context sequence including FAM/VIC probes of all SNPs selected.

<table>
<thead>
<tr>
<th>SNPs</th>
<th>chr</th>
<th>Nucleotide position</th>
<th>Assay ID</th>
<th>Context sequence including FAM/VIC probe</th>
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<td>rs1779866</td>
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References


