Correspondence

Genetic polymorphism of 22 autosomal STR markers in a Han population of Southern China

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Population genetic data and forensic statistics of 22 autosomal short tandem repeat (STR) loci (D1S1656, D2S1338, D3S3045, D4S2366, D5S2500, D6S477, D7S3048, D8S1132, D9S925, D10S1435, D11S2368, D12S391, D13S325, D14S608, D15S659, D16S539, D17S1290, D18S510, D19S253, D20S470, D21S1270 and GATA198B05) were determined for a sample of 515 unrelated individuals from Han population in Southern China. The expected heterozygosity and the discrimination power varied from 0.7358 to 0.8733 and 0.8915 to 0.9702, respectively. The probability of excluding an unrelated man as the true father (assuming no background relatedness in the population) for trios and for duos ranged from 0.5126 to 0.7415 and 0.3331 to 0.5864, respectively. The studied STRs appear to provide a significant improvement in the statistical power of kinship analysis.

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Dear Editor,

In recent years, extended short tandem repeat (STR) markers from the European standard set (ESS) or Combined DNA Index System (CODIS) have been introduced into the forensic community to increase the discrimination power [1,2] and standardize the analysed markers used in different countries. However, supplementary STRs are required to significantly evaluate pairwise, distant and/or complex relationships [3–5]. Additionally, additional STRs may be needed to confirm paternity in cases in which genetic mutations occur between the parents and progeny [6], null alleles are present [7] or a relative of an alleged father is involved [8–10].

The requirement of additional STRs has resulted in the development of a few new forensic autosomal multiplex STR systems in China, such as the Microreader™23sp ID System (Suzhou Microread Genetics Co., Ltd., Suzhou, Jiangsu Province, China). This kit was used to simultaneously amplify 22 STR loci (D3S3045, D4S2366, D6S477, D7S3048, D8S1132, D9S925, D10S1435, D11S2368, D13S325, D14S608, D15S659, D17S1290, D18S510, D19S253, D20S470, D21S1270, GATA198B05, D15S659, D25S1338, D5S2500, D12S391 and D16S539) and the amelogenin gender marker. Most of these loci have not been widely applied in the forensic community. We obtained genetic data for the reference samples from a Chinese Han population in southern China.

After obtaining informed consent, oral swab samples were collected from 515 unrelated individuals whose forefathers have resided in the Guangdong Province (405 samples) or Guangxi Province (110 samples) in southern China for at least 3 generations. DNA extraction was carried out using the Chelex-100 method [11] or DNA IQ system (Promega Corporation, Madison, WI, USA).

All DNA samples were amplified using the Microreader™23sp ID System following the manufacturer’s protocol. PCR reactions were performed in a GeneAmp 9700 PCR system Thermal Cycler (Applied Biosystems). Amplified products were analysed and detected using capillary electrophoresis in a 3500xl Genetic analyser (Applied Biosystems, Foster City, CA), and allele calling was obtained using the GeneMapper ID-X 1.2 software (Applied Biosystems). Allele assignment was determined by comparison with referenced ladders that were provided with the kit. Quality control was performed according to the laboratory internal control standards and kit controls.

Arlequin software v 3.5 [12] was used to calculate the allele frequencies, observed heterozygosity (H_o) and expected heterozygosity (H_e) as well as to assess departures from the Hardy–Weinberg equilibrium (HWE), linkage disequilibrium (LD) and population differentiation. The Power of Discrimination (PD) and polymorphic information content (PIC) were computed as previously described [13]. Probabilities of excluding the relatives of the true father from paternity for trios (TPF_e) and for duos (DPF_e) were calculated as previously described [9], assuming no background relatedness in the population (θ = 0) and considering only non-inbred alleged father and child. The parameter k0 is the probability of the alleged father and the child not sharing any identity by descent alleles: k0 = 1 for unrelated individuals, k0 = 3/4 for third degree relatives (first cousins, great grandparent–grandparent-offspring, half-avuncular or grand–avuncular), k0 = 1/2 for second degree relatives (half-sibs, grandparent–grandchild, etc.).
Conflict of interest

The authors declare no conflicts of interest.

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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.jsigen.2016.06.017.

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