

Allele frequencies for CODIS loci in a Sicilian population sample

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Abstract. Data from an island population can be useful for understanding effects of forensic evaluations of DNA evidence. In this study, allele frequencies for the thirteen CODIS loci were generated from 220 unrelated volunteer donors from a Sicilian (Italy) population sample, as well as from casework using both the AmpFISTR™ Profiler and Co-Filer™ Amplification Kits (PE Applied Biosystems, Foster City, CA). All loci met Hardy–Weinberg expectations. The data were compared with population studies from individuals residing in other Italian geographic locations and found not be substantially different. The combined power of discrimination is high and comparable to other European population groups. © 2003 Elsevier B.V. All rights reserved.

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1. Introduction

Short tandem repeat (STR) polymorphisms are the genetic markers of choice for human identification and paternity testing. Moreover, STR loci are the genetic markers of national and international DNA databanks, such as CODIS (FBI, USA), based on a core of 13 STRs. In this preliminary study we investigated the 13 STR CODIS loci in a Sicilian sample (220 unrelated Sicilian donors). The results obtained were compared with previous studies on Italian populations and were found not to be substantially different [1,2].

2. Statistical analysis

Allele designations were determined by comparison of the sample fragments with those of the allelic ladders supplied with each kit. At each locus, the frequency of each allele was calculated from the numbers of each genotype in the sample set (i.e., the gene count method). Unbiased estimates of expected heterozygosity were computed as described by

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Edwards et al. [3]. Possible divergence from Hardy–Weinberg expectations (HWE) was tested by calculating the unbiased estimate of the expected homozygote/heterozygote frequencies and also by performing an exact test [4]. The probability of discrimination (PD) and probability of exclusion (PE) was calculated according to Fisher [5].

3. Results and discussion

The distribution of observed alleles for all 13 STR loci is shown in Table 1. All loci are highly polymorphic with the loci D18S51 (86.8%), D21S11 (85.5%) and FGA (84.5%) having the highest observed heterozygosities, and the locus TPOX showing the lowest observed heterozygosity (65.5%). The most polymorphic loci are the most discriminating loci: FGA (97%), D18S51 (96.5%) and D21S11 (95.1%). The TPOX locus is the least discriminating (80.3%). For all 13 STR loci the combined power of discrimination is greater than 0.99999999 and the combined probabilities of exclusion are 0.99998. There was no evidence for departures from HWE for any loci based on the exact test. The Sicilian population data for these 13 loci do not differ substantially from other Caucasian data for the loci (data not shown). In conclusion, a database for the 13 STR loci has been established for the Sicilian population. These data can be used for both forensic casework and paternity testing in Sicilian population. These data together with previous studies on Italian populations could be a useful tool to appreciating the diversity of some island populations. Future projects will attempt to increase the number of samples in the Sicilian dataset so that greater confidence can be obtained for statistical estimates of the rarity of a DNA profile.

References

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