# Population genetic data from El Salvador (Central America) using AmpFlSTR® Identifiler® PCR Amplification Kit

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**Abstract.** This study presents allele distribution data of the 13 core short tandem repeat (STR) loci standardized under the Combined DNA Index System (CODIS): CSF1PO, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D21S11, vWA, FGA, TH01, TPOX, and two additional tetranucleotide loci, D2S1338 and D19S433, using AmpFlSTR® Identifiler® PCR Amplification Kit, in an El Salvadoran sample population, consisting of 228 unrelated individuals. All PCR product separations were performed by capillary electrophoresis using an ABI PRISM® 310 Genetic Analyzer. GeneScan® v 3.7. and Genotyper® Software v 3.7 was used for automated STR analysis and allele designation. Allele frequencies for each locus, observed (Ho) and expected (He) heterozygosities, *p* values of chi square test (*p*-Chi) and Fisher test (*p*-Fish) for departures from Hardy–Weinberg expectations (HWE), power of discrimination (PD), probability of exclusion (PE) and Polymorphism Information Content (PIC) were calculated. The results demonstrate that the AmpFlSTR® Identifiler® PCR Amplification Kit is a highly discriminating test suitable for paternity and identity testing in El Salvadoran population. © 2003 Elsevier B.V. All rights reserved.

*Keywords:* STR; DNA polymorphism; El Salvadoran population database; Identifiler®

## 1. Introduction

Short tandem repeat (STR) polymorphisms are the standard genetic markers mainly used for paternity testing and human identification. In routine forensic casework, it is important to establish a population genetic database for further reliable statistical analyses. This study presents allele distribution data of the 13 core STR loci standardized under the Combined DNA Index System (CODIS): CSF1PO, D3S1358, D5S818, D7S820, D8S1179, D13S317,

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D16S539, D18S51, D21S11, vWA, FGA, TH01, TPOX, and two additional tetranucleotide loci, D2S1338 and D19S433, in an El Salvadoran sample population.

## 2. Materials and methods

Blood and/or buccal swab samples were obtained from 228 unrelated El Salvadoran individuals and DNA was extracted using the organic phenol–chloroform–isoamyl alcohol method.

Amplification was performed using the AmpFlSTR® Identifiler® PCR Amplification Kit in a 96-well GeneAmp® PCR System 9700, according to the manufacturer's recommendations, in a 12.5-μl reaction volume.

Table 1
Observed allele frequencies in an El Salvadoran population sample (228 individuals)

| | D8S1179 | D21S11 | D7S820 | CSF1PO | D3S1358 | TH01 | D13S317 | D16S539 | D2S1338 | D19S433 | VWA | TPOX | D18S51 | D5S818 | FGA | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 6 | | | | | | 0,364 | 0,0023 | | | | | 0,0088 | | | | 6 |
| 7 | | | 0,0044 | 0,0132 | | 0,3114 | 0,0023 | | | | | 0,0022 | | 0,0373 | | 7 |
| 8 | 0,0044 | | 0,0855 | 0,0066 | | 0,068 | 0,0658 | 0,0066 | | | | 0,4846 | | 0,0132 | | 8 |
| 9 | 0,0066 | | 0,0504 | 0,0307 | | 0,1031 | 0,2083 | 0,0987 | | | | 0,0373 | | 0,0526 | | 9 |
| 9,3 | | | | | | 0,1447 | | | | | | | | | | 9,3 |
| 10 | 0,0899 | | 0,2478 | 0,2149 | | 0,0088 | 0,114 | 0,2039 | | | | 0,057 | 0,0021 | 0,0592 | | 10 |
| 10,2 | | | | | | | | | | | | | 0,0021 | | | 10,2 |
| 11 | 0,0526 | | 0,3136 | 0,2763 | | | 0,1776 | 0,3136 | | 0,0023 | | 0,2478 | 0,0088 | 0,4627 | | 11 |
| 12 | 0,1513 | | 0,2566 | 0,3662 | | | 0,239 | 0,261 | | 0,0767 | | 0,1579 | 0,0987 | 0,2631 | | 12 |
| 12,2 | | | | | | | | | | 0,0109 | | | 0,0022 | | | 12,2 |
| 13 | 0,2961 | | 0,0395 | 0,0877 | | | 0,1096 | 0,1009 | | 0,1886 | 0,0066 | 0,0044 | 0,0987 | 0,0987 | | 13 |
| 13,2 | | | | | | | | | | 0,1557 | | | | | | 13,2 |
| 14 | 0,2588 | | 0,0022 | | 0,0614 | | 0,0789 | 0,0153 | | 0,2961 | 0,0724 | | 0,1557 | 0,0088 | | 14 |
| 14,2 | | | | | | | | | | 0,0439 | | | | | | 14,2 |
| 15 | 0,1096 | | | 0,0044 | 0,4825 | | 0,0022 | | | 0,1535 | 0,0833 | | 0,1601 | 0,0044 | | 15 |
| 15,2 | | | | | | | | | | 0,0373 | | | | | | 15,2 |
| 16 | 0,0263 | | | | 0,2303 | | | | 0,0373 | 0,0197 | 0,3662 | | 0,1382 | | | 16 |
| 16,2 | | | | | | | | | | 0,0153 | | | | | | 16,2 |
| 17 | 0,0044 | | | | 0,1403 | | | | 0,1009 | | 0,307 | | 0,1689 | | | 17 |
| 18 | | | | | 0,0811 | | | | 0,0679 | | 0,1228 | | 0,068 | | 0,0044 | 18 |
| 19 | | | | | 0,0044 | | | | 0,1952 | | 0,0373 | | 0,0373 | | 0,0987 | 19 |
| 20 | | | | | | | | | 0,1557 | | 0,0022 | | 0,0285 | | 0,0504 | 20 |
| 21 | | | | | | | | | 0,0439 | | 0,0022 | | 0,0066 | | 0,1031 | 21 |
| 22 | | | | | | | | | 0,0811 | | | | 0,0153 | | 0,1118 | 22 |
| 23 | | | | | | | | | 0,1908 | | | | 0,0066 | | 0,1623 | 23 |
| 24 | | | | | | | | | 0,0811 | | | | 0,0022 | | 0,1689 | 24 |
| 25 | | | | | | | | | 0,0351 | | | | | | 0,1491 | 25 |
| 26 | | 0,0022 | | | | | | | 0,0088 | | | | | | 0,1096 | 26 |
| 27 | | 0,0219 | | | | | | | 0,0022 | | | | | | 0,0329 | 27 |
| 28 | | 0,0833 | | | | | | | | | | | | | 0,0088 | 28 |
| 29 | | 0,2237 | | | | | | | | | | | | | | 29 |
| 30 | | 0,2741 | | | | | | | | | | | | | | 30 |
| 30,2 | | 0,0109 | | | | | | | | | | | | | | 30,2 |
| 31 | | 0,0329 | | | | | | | | | | | | | | 31 |
| 31,2 | | 0,1294 | | | | | | | | | | | | | | 31,2 |
| 32 | | 0,0132 | | | | | | | | | | | | | | 32 |
| 32,2 | | 0,1491 | | | | | | | | | | | | | | 32,2 |
| 33 | | 0,0044 | | | | | | | | | | | | | | 33 |
| 33,2 | | 0,0373 | | | | | | | | | | | | | | 33,2 |
| 34,2 | | 0,0132 | | | | | | | | | | | | | | 34,2 |
| 35 | | 0,0022 | | | | | | | | | | | | | | 35 |
| 35,2 | | 0,0022 | | | | | | | | | | | | | | 35,2 |
| Min Freq | 0,0126 | 0,0131 | 0,0121 | 0,0125 | 0,0116 | 0,0121 | 0,0129 | 0,0122 | 0,0136 | 0,0132 | 0,0122 | 0,0118 | 0,0136 | 0,012 | 0,0136 | Min Freq |

All PCR product separations were performed by capillary electrophoresis using an ABI PRISM® 310 Genetic Analyzer. GeneScan® v 3.7 and Genotyper® Software v 3.7 was used for automated STR analysis and allele designation.

Statistical analyses were performed using GDA Version 1.0 (d16c) (Lewis, P.O., and Zaykin, D. 2001) and PowerStats v1.2 (Allan Tereba, Promega) programs.

## 3. Results and discussion

The observed allele frequencies in the El Salvadoran population sample for the 15 STR loci are shown in Table 1. Minimum allele frequencies were also estimated using sample size and the observed heterozygosity at each locus.

The observed (Ho) and expected (He) heterozygosities, $p$ values of chi square test ($p$-Chi) and Fisher test ($p$-Fish) for departures from Hardy–Weinberg expectations (HWE), power of discrimination (PD), probability of exclusion (PE) and Polymorphism Information Content (PIC) are displayed in Table 2.

All loci are highly polymorphic with the locus D3S1358 having the lowest observed heterozygosity (Ho) (64.9%) and loci D18S51 and FGA both displaying the highest heterozygosity (86.4%).

The genotype distribution for the 15 loci showed no deviations ($p>0.01$) from Hardy–Weinberg Equilibrium expectation and an inter-class correlation test analysis showed no evidence for association of alleles between the 15 loci. The combined power of discrimination (PD) for the 15 loci was >0.9999999999999999 and the combined probability of exclusion (PE) was 0.99999544.

In conclusion, these results demonstrate that the AmpFlSTR® Identifiler® PCR Amplification Kit is a highly discriminating test suitable for paternity and identity testing in El Salvadoran population.

Table 2
Statistical parameters of forensic value for AmpFlSTR® Identifiler® Kit

| Loci STR | Alleles | He | Ho | $p$-Chi | $p$-Fisher | PD | PE | PIC |
|---|---|---|---|---|---|---|---|---|
| D8S1179 | 10 | 0.801 | 0.772 | 0.325 | 0.241 | 0.930 | 0.548 | 0.77 |
| D21S11 | 15 | 0.827 | 0.816 | 0.789 | 0.473 | 0.945 | 0.629 | 0.80 |
| D7S820 | 8 | 0.765 | 0.719 | 0.313 | 0.299 | 0.910 | 0.459 | 0.72 |
| CSF1PO | 8 | 0.736 | 0.759 | 0.574 | 0.668 | 0.878 | 0.525 | 0.69 |
| D3S1358 | 6 | 0.686 | 0.649 | 0.850 | 0.797 | 0.861 | 0.354 | 0.64 |
| TH01 | 6 | 0.736 | 0.719 | 0.079 | 0.091 | 0.881 | 0.459 | 0.69 |
| D13S317 | 10 | 0.834 | 0.798 | 0.627 | 0.590 | 0.950 | 0.596 | 0.81 |
| D16S539 | 7 | 0.773 | 0.724 | 0.500 | 0.404 | 0.916 | 0.466 | 0.74 |
| D2S1338 | 12 | 0.871 | 0.860 | 0.436 | 0.242 | 0.966 | 0.714 | 0.86 |
| D19S433 | 11 | 0.821 | 0.833 | 0.039 | 0.219 | 0.940 | 0.662 | 0.80 |
| VWA | 9 | 0.744 | 0.724 | 0.906 | 0.786 | 0.901 | 0.466 | 0.70 |
| TPOX | 8 | 0.675 | 0.671 | 0.233 | 0.605 | 0.852 | 0.385 | 0.63 |
| D18S51 | 17 | 0.878 | 0.864 | 0.929 | 0.824 | 0.970 | 0.723 | 0.86 |
| D5S818 | 9 | 0.700 | 0.697 | 0.378 | 0.522 | 0.870 | 0.424 | 0.66 |
| FGA | 11 | 0.876 | 0.864 | 0.294 | 0.176 | 0.967 | 0.723 | 0.86 |