# FOR THE RECORD

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# Allele Frequencies of 15 Loci using AmpFℓSTR Identifiler Kit in Japanese Population

**POPULATION:** Japanese

**KEYWORDS:** forensic science, short tandem repeats, DNA typing, AmpFℓSTR® Identifiler™ PCR Amplification Kit, Japan, population genetics, D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, FGA

Blood samples were collected from 1350 unrelated individuals in Japan. DNA was isolated from the blood samples using MagNA Pure LC instrument (Roche Diagnostic). We reported allele frequency data for nine STR loci from 1200 Japanese previously (1). In this study, 1103 out of 1350 samples are the same DNA sample that were used in previous population study.

The co-amplification of D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818 and FGA loci were performed using AmpFℓSTR® Identifiler™ PCR Amplification Kit (Applied Biosystems), according to manufacture's recommendation (2). Multiplex PCR amplification was carried out using a GeneAmp® PCR System 9700 Thermal Cycler (Applied Biosystems).

The amplified products were electrophoresed on an ABI PRISM® 310 Genetic Analyzer or an ABI PRISM® 3100 Genetic Analyzer (Applied Biosystems). The analysis of the amplified products and allele designation were performed automatically using GeneMapper™ ID software (version 3.1, Applied Biosystems).

Allele frequencies were calculated by direct counting method (Table 1). Statistical test for fit to Hardy-Weinberg equilibrium expectations was performed using the computer program GENEPOP software (web version of 3.4, http://wbiomed.curtin. edu.au/genepop/) (3). Power of discrimination was calculated following Fisher's method (4). The results demonstrate that all loci were in Hardy-Weinberg equilibrium. The combined match probability of all loci is $1.8 \times 10^{-17}$.

The complete data are available to any interested researcher upon request from the corresponding author Dr. Kanako Yoshida at kana@nrips.go.jp

## References

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TABLE 1—*The distribution of allele frequencies at fifteen STR loci in a Japanese population (n = 1350).*

| * | D8S1179 | D21S11 | D7S820 | CSF1PO | D3S1358 | TH01 | D13S317 | D16S539 | D2S1338 | D19S433 | vWA | TPOX | D18S51 | D5S818 | FGA |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 5 | | | | | | 0.0015 | | | | | | | | | |
| 6 | | | | | | 0.2233 | | | | | | | | | |
| 7 | 0.0004 | | 0.0030 | 0.0100 | | 0.2667 | 0.0011 | 0.0004 | | | | 0.0004 | | 0.0026 | |
| 8 | | | 0.1267 | 0.0011 | | 0.0663 | 0.2670 | 0.0019 | | | | 0.4544 | | 0.0067 | |
| 9 | 0.0007 | | 0.0456 | 0.0467 | | 0.3985 | 0.1289 | 0.3537 | | | | 0.1141 | | 0.0859 | |
| 9.1 | | | 0.0004 | | | | | | | | | | | | |
| 9.2 | | | | | | | | | | 0.0004 | | | | | |
| 9.3 | | | | | | 0.0348 | | | | | | | | | |
| 10 | 0.1326 | | 0.2189 | 0.2233 | | 0.0089 | 0.1148 | 0.1967 | | | | 0.0307 | 0.0022 | 0.2007 | |
| 10.1 | | | 0.0004 | | | | | | | | | | | | |
| 10.2 | | | | | | | | | | 0.0011 | | | | | |
| 10.3 | | | 0.0007 | | | | | | | | | | | | |
| 11 | 0.1089 | | 0.3285 | 0.2078 | | | 0.2211 | 0.1870 | | 0.0037 | | 0.3630 | 0.0044 | 0.2922 | |
| 11.2 | | | | | | | | | | 0.0007 | | | | | |
| 12 | 0.1226 | | 0.2348 | 0.4185 | 0.0019 | | 0.2022 | 0.1785 | | 0.0404 | | 0.0356 | 0.0478 | 0.2352 | |
| 12.2 | | | | | | | | | | 0.0052 | | | | | |
| 13 | 0.2248 | | 0.0348 | 0.0689 | 0.0007 | | 0.0511 | 0.0726 | | 0.2874 | 0.0004 | 0.0011 | 0.1993 | 0.1667 | |
| 13.2 | | | | | | | | | | 0.0300 | | | | | |
| 14 | 0.2048 | | 0.0059 | 0.0178 | 0.0289 | | 0.0130 | 0.0081 | | 0.3496 | 0.1941 | 0.0007 | 0.2222 | 0.0089 | |
| 14.2 | | | | | | | | | | 0.0881 | | | | | |
| 15 | 0.1344 | | 0.0004 | 0.0052 | 0.3959 | | 0.0007 | 0.0011 | | 0.0507 | 0.0267 | | 0.1681 | 0.0011 | |
| 15.2 | | | | | | | | | | 0.1148 | | | | | |
| 16 | 0.0641 | | | 0.0007 | 0.3063 | | | | 0.0085 | 0.0052 | 0.1841 | | 0.1256 | | |
| 16.2 | | | | | | | | | | 0.0193 | | | | | |
| 17 | 0.0063 | | | | 0.1996 | | | | 0.0974 | | 0.2826 | | 0.0815 | | 0.0033 |
| 17.1 | | | | | | | | | | | | | 0.0004 | | |
| 17.2 | | | | | | | | | | 0.0030 | | | | | |
| 18 | 0.0004 | | | | 0.0633 | | | | 0.1589 | 0.0004 | 0.2256 | | 0.0481 | | 0.0215 |
| 19 | | | | | 0.0030 | | | | 0.2089 | | 0.0737 | | 0.0363 | | 0.0670 |
| 20 | | | | | | | | | 0.1056 | | 0.0100 | | 0.0219 | | 0.0889 |
| 21 | | | | | 0.0004 | | | | 0.0148 | | 0.0026 | | 0.0156 | | 0.1307 |
| 22 | | | | | | | | | 0.0504 | | 0.0004 | | 0.0130 | | 0.2015 |
| 22.2 | | | | | | | | | | | | | | | 0.0019 |
| 23 | | | | | | | | | 0.1467 | | | | 0.0074 | | 0.2052 |
| 23.2 | | | | | | | | | | | | | | | 0.0048 |
| 24 | | | | | | | | | 0.1078 | | | | 0.0037 | | 0.1570 |
| 24.2 | | | | | | | | | | | | | | | 0.0011 |
| 25 | | | | | | | | | 0.0615 | | | | 0.0015 | | 0.0733 |
| 25.2 | | | | | | | | | | | | | | | 0.0019 |
| 26 | | | | | | | | | 0.0289 | | | | 0.0007 | | 0.0319 |
| 27 | | 0.0011 | | | | | | | 0.0085 | | | | 0.0004 | | 0.0078 |
| 28 | | 0.0422 | | | | | | | 0.0022 | | | | | | 0.0022 |
| 28.2 | | 0.0048 | | | | | | | | | | | | | |
| 29 | | 0.2467 | | | | | | | | | | | | | |
| 30 | | 0.3370 | | | | | | | | | | | | | |
| 30.2 | | 0.0044 | | | | | | | | | | | | | |
| 30.3 | | 0.0011 | | | | | | | | | | | | | |
| 31 | | 0.1033 | | | | | | | | | | | | | |
| 31.2 | | 0.0711 | | | | | | | | | | | | | |
| 32 | | 0.0193 | | | | | | | | | | | | | |
| 32.2 | | 0.1189 | | | | | | | | | | | | | |
| 33 | | 0.0026 | | | | | | | | | | | | | |
| 33.1 | | 0.0022 | | | | | | | | | | | | | |
| 33.2 | | 0.0404 | | | | | | | | | | | | | |
| 34 | | 0.0007 | | | | | | | | | | | | | |
| 34.2 | | 0.0041 | | | | | | | | | | | | | |
| Ob.H | 0.822 | 0.792 | 0.779 | 0.734 | 0.727 | 0.702 | 0.807 | 0.771 | 0.864 | 0.754 | 0.784 | 0.627 | 0.844 | 0.770 | 0.856 |
| Ex.H. | 0.841 | 0.793 | 0.770 | 0.725 | 0.705 | 0.715 | 0.807 | 0.764 | 0.870 | 0.769 | 0.792 | 0.647 | 0.853 | 0.784 | 0.857 |
| PD | 0.955 | 0.929 | 0.910 | 0.885 | 0.855 | 0.870 | 0.935 | 0.907 | 0.969 | 0.913 | 0.924 | 0.812 | 0.961 | 0.920 | 0.961 |
| P | 0.377 | 0.235 | 0.990 | 0.150 | 0.262 | 0.340 | 0.938 | 0.447 | 0.322 | 0.146 | 0.745 | 0.170 | 0.151 | 0.082 | 0.130 |

Ob.H: observed heterozygosity, Ex.H: expected heterozygosity, PD: power of discrimination, P: Probability value of exact test.