

FOR THE RECORD

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Genetic Variation at Five STR Loci (D10S2325, D13S325, D20S470, D18S51, and D19S253) in Korean Population

POPULATION: Korean

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Allele and genotype frequencies of the five STR loci (D10S2325, D13S325, D20S470, D18S51, and D19S253) were determined. Specimens were collected from unrelated volunteer blood donors from a population of Chungnam Province in South Korea ($n = 130$). DNA was obtained from the blood specimens using the Wizard genomic DNA purification kit (Promega, USA) and amplified using the multiplex PCR (triplex amplification of D10S2325, D13S325, and D20S470; duplex amplification of D18S51 and D19S253). The amplified DNAs were separated by denaturing polyacrylamide gel electrophoresis and then visualized by the silver staining (1). Exact χ^2 -test for Hardy-Weinberg equilibrium and pairwise disequilibrium were analyzed using the GDA program written by Lewis P.O. and Zaykin D (2). The chance of exclusion of combined system was 0.9986.

The data set can be accessed at <http://www.dnatyping.co.kr/genedata/str1.html>.

References

1. Bassam BJ, Caetano-Anolles G, Gresshoff PM. Fast and sensitive silver staining of DNA in polyacrylamide gels. *Anal Biochem* 1991;196:80-3.
2. Weir BS. Genetic data analysis II. Massachusetts: Sinauer, Sunderland, 1991.

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| Alleles | D10S2325 | D13S325 | D20S470 | D18S51 | D19S253 |
|----------------------|----------|---------|---------|--------|---------|
| 3 | | 0.004 | | | |
| 4 | | 0.004 | | | |
| 5 | | 0.062 | 0.004 | | |
| 6 | 0.023 | 0.300 | | | 0.235 |
| 7 | 0.288 | 0.238 | | | 0.038 |
| 8 | 0.023 | 0.204 | 0.015 | | 0.004 |
| 9 | 0.142 | 0.119 | 0.019 | | 0.012 |
| 10 | 0.081 | 0.031 | 0.135 | | 0.088 |
| 11 | 0.096 | 0.027 | 0.015 | 0.008 | 0.300 |
| 12 | 0.158 | 0.008 | 0.042 | 0.054 | 0.269 |
| 13 | 0.112 | | 0.104 | 0.238 | 0.038 |
| 14 | 0.065 | 0.004 | 0.162 | 0.204 | 0.015 |
| 15 | 0.004 | | 0.138 | 0.162 | |
| 16 | 0.008 | | 0.173 | 0.135 | |
| 17 | | | 0.131 | 0.042 | |
| 18 | | | 0.054 | 0.062 | |
| 19 | | | 0.004 | 0.038 | |
| 20 | | | 0.004 | 0.035 | |
| 21 | | | | 0.023 | |
| P (exact test)* | 0.060 | 0.965 | 0.646 | 0.199 | 0.964 |
| Heterozygosity (exp) | 0.841 | 0.795 | 0.877 | 0.849 | 0.784 |
| Heterozygosity (obs) | 0.885 | 0.854 | 0.931 | 0.838 | 0.785 |
| PD† | 0.947 | 0.920 | 0.963 | 0.951 | 0.902 |
| PIC‡ | 0.820 | 0.760 | 0.860 | 0.830 | 0.740 |
| CE§ | 0.764 | 0.702 | 0.859 | 0.672 | 0.557 |

*Based on 3200 shufflings.

†PD: Power of discrimination.

‡PIC: Polymorphism information content.

§CE: Chance of exclusion.