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## FOR THE RECORD

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# Population Data of ABO Gene Applicable to Human Identification in Koreans*

**POPULATION:** A total of 100 unrelated healthy individuals living in Seoul, Korea

**KEYWORDS:** forensic science, ABO gene, human identification, Koreans

Genomic DNA was isolated from buccal swabs by the QIAamp DNA Mini Kit (QIAGEN). The primers used for amplification and sequencing of exon 6 and 7 of ABO gene were suggested by Lee and Chang (1), and Ogasawara et al. (2), respectively. About 1–2 ng of genomic DNA was used for PCR in 25 μL reaction volume. PCR mixture contained 10 mM Tris-HCl pH 8.5, 50 mM KCl, 1.5 mM $MgCl_2$, 200 μM of each dNTP, 0.25 μM of each primer, and 1 U of AmpliTaq Gold DNA Polymerase (Applied Biosystems). Thermal cycling was performed initially at 95°C for 10 min, then 35 cycles consisting of 95°C for 1 min, 60°C for 1 min for exon 6 and 63°C for 1 min for exon 7, 72°C for 1 min, followed by 10 min extension at 72°C in a GeneAmp PCR System 9600 (Perkin Elmer).

PCR products were purified by QIAquick PCR Purification kit (QIAGEN). The BigDye Terminator Cycle Sequencing kit (Applied Biosystems) and an ABI PRISM 310 Genetic Analyzer (Applied Biosystems) were used for direct DNA sequencing. Sequences were analyzed with Sequence Navigator software (Applied Biosystems). ABO genotype was determined by comparing those with the reported nucleotide sequences of ABO alleles (3,4).

Statistical analysis was performed using the Genetic Data Analysis software, (http://lewis.eeb.uconn.edu/lewishome/software.html) and the PowerStat (http://www.promega.com/geneticidtools/powerstats/) program of Promega Corporation. In case of mean exclusion chance (MEC), it was calculated according to Krüger et al. (5). We did not find significant deviation from Hardy-Weinberg equilibrium at ABO gene.

The complete data are available to any interested researcher upon request from the corresponding author.

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TABLE 1—*Allele frequencies and forensic efficiency of ABO gene in Koreans.*

| Allele | A101 | A102 | B101 | B102 | O01 | O02 | O04 | Number | Frequency |
|---|---|---|---|---|---|---|---|---|---|
| A101 | 3 | 1 | 1 | … | 2 | 2 | … | 12 | 0.060 |
| A102 | | 7 | 10 | … | 10 | 9 | … | 44 | 0.220 |
| B101 | | | 8 | 1 | 11 | 5 | … | 44 | 0.220 |
| B102 | | | | … | … | … | … | 1 | 0.005 |
| O01 | | | | | 9 | 13 | 1 | 55 | 0.275 |
| O02 | | | | | | 6 | 1 | 42 | 0.210 |
| O04 | | | | | | | … | 2 | 0.010 |

| | |
|---|---|
| Observed heterozygosity | 0.670 |
| Expected heterozygosity | 0.784 |
| Polymorphism information content (PIC) | 0.744 |
| Power of discrimination (PD) | 0.915 |
| Mean exclusion chance (MEC) | 0.564 |