For the Record

Allele Frequency Distributions for Four VNTR Loci in the Chinese Han Population

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Population: Han population living in Chengdu, China

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Specimens were collected from unrelated volunteer blood donors. DNA was obtained from blood specimens using the organic extraction (1). DNA typing by PCR, using 20 ng target DNA. Primer sequences: D4S43: 5′-gac cac aga gag ctt agt gga gct t-3′,

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5′-gac cac ttc act gac atc cac atc t-3′; D4S111: 5′-tag gtg tct cct cag aga gg-3′, 5′-agg acc tgg tgg aca cct ca-3′; HVR-Ig: 5′-ggg ccc tgt ctc agc tgg gga-3′, 5′-tgg cct ggc tgc cct gag cag-3′; Ha-ras: 5′-gag cta gca ggg cat gcc gc-3′, 5′-agc acg gtg tgg aag gag cc-3′. PCR conditions: D4S43: 30 cycles of 1 min at 94°C, 1 min at 55°C, 1 min, 30 s at 72°C followed by a 10 min extension at 72°C; D4S111: start at 95°C of 7 min, 30 cycles of 1 min at 93°C, 1 min at 65°C, 1 min, 30 s at 71°C followed by a 10 min extension at 71°C; HVR-Ig: 30 cycles of 1 min at 94°C, 1 min at 65°C, 2 min at 72°C followed by a 10 min extension at 72°C; Ha-ras: 30 cycles of 1 min at 94°C, 2 min at 65°C, 4 min at 71°C followed by a 10 min extension at 71°C. The amplified products of D4S43 and D4S111 were electrophoresed in 2% ethidium bromide stained agarose gel, while those of HVR-Ig and Ha-ras were electrophoresed in 1.5% ethidium bromide stained agarose gel by using PBR322/HaeIII for D4S43, 100bp ladder for both D4S111 and HVR-Ig and 123 bp ladder for Ha-ras as size marker. Data were analyzed by The Promega Software, POWERSTATS. Chi-square test was carried out for testing Hardy-Weinberg equilibrium for each locus.

The complete data set is available to any interested researcher upon request.

Reference

1. Sambrook J, Fritsch EF, Maniatis T. Molecular cloning. A laboratory manual. 2nd ed. Cold Spring Harbor NY: Cold Spring Harbor Laboratory Press, 1989.

Allele	D4S43 (n = 107)	D4S111 (n = 110)	HVR-Ig (n = 114)	Ha-ras (n = 119)
A1	0.897	0.214	. . .	. . .
A2	0.065	0.241	. . .	. . .
A3	0.023	0.545	. . .	. . .
A4	0.005	. . .	. . .	. . .
A5	0.009	. . .	. . .	. . .
5	. . .	. . .	0.759	. . .
6	. . .	. . .	0.009	. . .
7	. . .	. . .	0.022	. . .
8	. . .	. . .	0.044	. . .
9	. . .	. . .	0.096	. . .
10	. . .	. . .	0.004	. . .
13	. . .	. . .	0.066	. . .
859 bp	. . .	. . .	. . .	0.004
915 bp	. . .	. . .	. . .	0.004
971 bp	. . .	. . .	. . .	0.025
999 bp	. . .	. . .	. . .	0.050
1027 bp	. . .	. . .	. . .	0.307
1111 bp	. . .	. . .	. . .	0.450
1167 bp	. . .	. . .	. . .	0.004
1335 bp	. . .	. . .	. . .	0.025
1475 bp	. . .	. . .	. . .	0.004
1559 bp	. . .	. . .	. . .	0.008
1839 bp	. . .	. . .	. . .	0.101
2595 bp	. . .	. . .	. . .	0.017
DP	0.284	0.765	0.599	0.781
H	0.121	0.618	0.298	0.681
PE	0.011	0.313	0.063	0.399
PIC	0.180	0.530	0.390	0.640

Based on Chi-square test, the four loci meet Hardy-Weinberg equilibrium expectations ($p > 0.05$).
DP: discriminating power.
H: heterozygosity.
PE: power of exclution.
PIC: polymorphism information content.