For the Record

Allele Frequency Distributions for Three STR Loci in the Han and Thai Populations

Dai Xin Huang, Ph.D.[1], Lin Zhang, Ph.D.[1], and Mei Yun Wu, M.D.[1]

Populations: Han population living in Changdu, China and Thai population living in Bangkok, Thailand

Keywords: DNA typing, population genetics, D752846, D2S441, D752201, Han Chinese, Thai, China, Thailand

[1] School of Forensic Medicine, West China University of Medical Sciences, No. 17, Section 3, South Renmin Road, Chengdu (610041), The People's Republic of China.

Specimens were collected from unrelated volunteer blood donors. DNA was obtained from blood specimens using the nonorganic method (1). DNA typing by PCR, using 2 ng target DNA. Primer sequences: D2S441: 5′-att gga gct aag tgg ctg tg-3′, 5′-aaa agg ctg taa caa ggg ct-3′; D7S2846: 5′-tct aaa ctc ctt tgc aca gtc-3′, 5′-aca tgt gtc cat caa atg atg-3′; D7S2201: 5′-agt tca acc tgg gca aca ta-3′, 5′-tca agc caa ggc att ttc ta-3′. PCR conditions: one cycle of 2 min at 95°C, 30 cycles of 45s at 94°C, 45s at 58°C, 50s at 72°C followed by a 10 min extension period at 72°C. The amplified products were electrophoresed with PAG and then visualized using silver staining. Data were analyzed by The Promega Software, POWERSTATS. For testing Hardy-Weinberg equilibrium within each sample and for comparing gene counts between samples Chi-square tests were used throughout. The complete data set is available to any interested researcher upon request.

References

1. Grimberg J, Nawcschik S, Belluscio L, McKee R, Turck A, Eisenberg A. A simple and efficient nonorganic procedure for the isolation of genomic DNA from blood. Nucl Acids Res 1989;17:83–90.

Allele	D2S441		D7S2846		D7S2201	
	Han (*n* = 260)	Thai (*n* = 145)	Han (*n* = 376)	Thai (*n* = 131)	Han (*n* = 262)	Thai (*n* = 119)
9	0.002	0.007	…	…	…	…
9.1	0.017	0.007	…	…	…	…
10	0.229	0.200	…	…	…	…
11	0.352	0.293	…	…	0.004	0
11.3	0.064	0.200	…	…	…	…
12	0.173	0.097	…	…	0.029	0.050
13	0.023	0.007	…	…	0.382	0.387
14	0.131	0.103	0.005	0.008	0.536	0.513
15	0.010	0.086	0.083	0.069	0.034	0.042
16	…	…	0.472	0.397	0.013	0.008
17	…	…	0.206	0.309	0.002	0
18	…	…	0.196	0.187	…	…
19	…	…	0.032	0.027	…	…
20	…	…	0.005	0.004	…	…
21	…	…	0.001	0	…	…
DP	0.908	0.923	0.857	0.860	0.704	0.735
H	0.789	0.855	0.692	0.687	0.599	0.588
PE	0.578	0.705	0.415	0.408	0.290	0.277
PIC	0.739	0.780	0.645	0.655	0.479	0.501
HWE test*	0.392	0.053	0.194	0.896	0.872	0.634
p†	$P < 0.01$		$0.01 < P < 0.05$		$P > 0.05$	

* Probability values.
† Probability values for comparing gene counts between samples.
… means that allele not applicable to that locus.
DP: discriminating power.
H: heterozygosity.
PE: power of exclution.
PIC: polymorphism information content.