FOR THE RECORD

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Data on Eight STR Loci in Shan, Akha, Lisu, Lahu, and Hmong Populations of Northern Thailand

POPULATIONS: Ethnic minorities of Northern Thailand i.e., Shan, Akha, Lisu, Lahu and Hmong.

KEYWORDS: forensic science, short tandem repeat, population data, Shan, Akha, Lisu, Lahu, Hmong, Northern Thailand

We present data from previous paternity tests of unrelated individuals: up to 49 Shan, 42 Akha, 42 Lisu, 72 Lahu, and 41 Hmong people. DNA was extracted from blood using the Chelex method (1). Each 10 µL PCR contained 1 µL Chelex extract, 1× Taq buffer, 1.5 mM MgCl$_2$, 100 µM each dNTP, 0.2 µM each primer (2,3), and 0.2 U Taq DNA polymerase. Amplifications were performed in a Hybaid thermocycler for 30 cycles: 94°C 1 min, 58°C 1 min, 72°C 1 min. Amplicons were separated by vertical native polyacrylamide gel electrophoresis and stained with silver (4). Alleles were typed using ladders of known alleles. The parameters dealing with forensic genetics were calculated using the computer program POWERSTATS (5), see Tables 1–8. The genotype distribution was analyzed for the Hardy-Weinberg equilibrium using the Chi-square test. All loci met Hardy-Weinberg equilibrium with the exception of TPOX in the Hmong. The combined power of discrimination was calculated for the Shan as 0.99999996,

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TABLE 1—*Population data and forensic value of D3S1358 in Shan, Akha, Lisu, Lahu and Hmong.*

Locus: D3S1358					
	Shan $n=36$	Akha $n=41$	Lisu $n=42$	Lahu $n=67$	Hmong $n=37$
Forensic identification					
Matching Probability	0.136	0.122	0.204	0.171	0.135
Expressed as 1 in . . .	7.4	8.2	4.9	5.8	7.4
Power of Discrimination	0.864	0.878	0.796	0.829	0.865
PIC	0.67	0.68	0.58	0.65	0.68
Paternity					
Power of Exclusion	0.463	0.367	0.314	0.478	0.432
Typical Paternity Index	1.80	1.46	1.31	1.86	1.68
Allele Frequencies					
Homozygotes	27.8%	34.1%	38.1%	26.9%	29.7%
Heterozygotes	72.2%	65.9%	61.9%	73.1%	70.3%
Total Alleles	72	82	84	134	74

Allele	Frequency				
12	. . .	. . .	2.4%	. . .	. . .
14	2.8%	3.7%	. . .	3.7%	4.1%
15	33.3%	28.0%	36.9%	35.1%	33.8%
16	34.7%	25.6%	44.0%	38.8%	17.6%
17	20.8%	35.4%	15.5%	11.9%	33.8%
18	8.3%	6.1%	1.2%	9.0%	10.8%
19	. . .	1.2%	. . .	1.5%	. . .

n: number of individuals, PIC: polymorphic information content.

TABLE 2—*Population data and forensic value of D5S818 in Shan, Akha, Lisu, Lahu and Hmong.*

Locus: D5S818					
	Shan $n=47$	Akha $n=41$	Lisu $n=42$	Lahu $n=71$	Hmong $n=41$
Forensic identification					
Matching Probability	0.103	0.111	0.094	0.102	0.123
Expressed as 1 in . . .	9.7	9.0	10.6	9.8	8.1
Power of Discrimination	0.897	0.889	0.906	0.898	0.877
PIC	0.72	0.74	0.76	0.73	0.72
Paternity					
Power of Exclusion	0.339	0.479	0.490	0.413	0.654
Typical Paternity Index	1.38	1.86	1.91	1.61	2.93
Allele Frequencies					
Homozygotes	36.2%	26.8%	26.2%	31.0%	17.1%
Heterozygotes	63.8%	73.2%	73.8%	69.0%	82.9%
Total Alleles	94	82	84	142	82

Allele	Frequency				
7	1.1%	1.2%	1.2%	. . .	2.4%
9	5.3%	11.0%	3.6%	6.3%	2.4%
10	22.3%	14.6%	20.2%	21.1%	23.2%
11	34.0%	34.1%	25.0%	28.9%	29.3%
12	22.3%	20.7%	28.6%	27.5%	28.0%
13	14.9%	18.3%	15.5%	15.5%	14.6%
14	. . .	. . .	3.6%	0.7%	. . .
15	. . .	. . .	2.4%	. . .	. . .

n: number of individuals, PIC: polymorphic information content.

TABLE 3—*Population data and forensic value of D7S820 in Shan, Akha, Lisu, Lahu and Hmong.*

Locus: D7S820					
	Shan $n = 41$	Akha $n = 37$	Lisu $n = 32$	Lahu $n = 44$	Hmong $n = 30$
Forensic identification					
Matching Probability	0.105	0.080	0.123	0.094	0.164
Expressed as 1 in . . .	9.5	12.6	8.1	10.6	6.1
Power of Discrimination	0.895	0.920	0.877	0.906	0.836
PIC	0.74	0.77	0.69	0.76	0.63
Paternity					
Power of Exclusion	0.608	0.432	0.565	0.337	0.291
Typical Paternity Index	2.56	1.68	2.29	1.38	1.25
Allele Frequencies					
Homozygotes	19.5%	29.7%	21.9%	36.4%	40.0%
Heterozygotes	80.5%	70.3%	78.1%	63.6%	60.0%
Total Alleles	82	74	64	88	60

Allele	Frequency				
7	1.2%	. . .	. . .	. . .	. . .
8	14.6%	18.9%	12.5%	26.1%	10.0%
9	8.5%	5.4%	9.4%	10.2%	5.0%
10	17.1%	16.2%	14.1%	19.3%	10.0%
11	34.1%	24.3%	42.2%	23.9%	51.7%
12	23.2%	27.0%	21.9%	19.3%	20.0%
13	1.2%	8.1%	. . .	1.1%	3.3%

n: number of individuals, PIC: polymorphic information content.

TABLE 4—*Population data and forensic value of D8S1179 in Shan, Akha, Lisu, Lahu and Hmong.*

Locus: D8S1179					
	Shan $n = 41$	Akha $n = 33$	Lisu $n = 38$	Lahu $n = 45$	Hmong $n = 36$
Forensic identification					
Matching Probability	0.071	0.085	0.061	0.060	0.080
Expressed as 1 in . . .	14.1	11.7	16.4	16.7	12.5
Power of Discrimination	0.929	0.915	0.939	0.940	0.920
PIC	0.82	0.80	0.81	0.82	0.79
Paternity					
Power of Exclusion	0.800	0.814	0.629	0.599	0.420
Typical Paternity Index	5.13	5.50	2.71	2.50	1.64
Allele Frequencies					
Homozygotes	9.8%	9.1%	18.4%	20.0%	30.6%
Heterozygotes	90.2%	90.9%	81.6%	80.0%	69.4%
Total Alleles	82	66	76	90	72

Allele	Frequency				
8	. . .	. . .	. . .	. . .	1.4%
10	18.3%	12.1%	14.5%	10.0%	26.4%
11	8.5%	4.5%	10.5%	6.7%	15.3%
12	11.0%	15.2%	11.8%	13.3%	4.2%
13	12.2%	24.2%	25.0%	22.2%	15.3%
14	17.1%	10.6%	18.4%	12.2%	9.7%
15	24.4%	24.2%	14.5%	22.2%	23.6%
16	6.1%	9.1%	5.3%	13.3%	2.8%
17	2.4%	. . .	. . .	. . .	1.4%

n: number of individuals, PIC: polymorphic information content.

TABLE 5—*Population data and forensic value of D13S317 in Shan, Akha, Lisu, Lahu and Hmong.*

Locus: D13S317					
	Shan $n = 49$	Akha $n = 42$	Lisu $n = 42$	Lahu $n = 72$	Hmong $n = 41$
Forensic identification					
Matching Probability	0.093	0.117	0.080	0.089	0.202
Expressed as 1 in . . .	10.8	8.6	12.4	11.3	5.0
Power of Discrimination	0.907	0.883	0.920	0.911	0.798
PIC	0.78	0.73	0.78	0.75	0.56
Paternity					
Power of Exclusion	0.630	0.414	0.617	0.609	0.367
Typical Paternity Index	2.72	1.62	2.63	2.57	1.46
Allele Frequencies					
Homozygotes	18.4%	31.0%	19.0%	19.4%	34.1%
Heterozygotes	81.6%	69.0%	81.0%	80.6%	65.9%
Total Alleles	98	84	84	144	82

Allele	Frequency				
6	. . .	. . .	. . .	0.7%	. . .
8	28.6%	29.8%	26.2%	28.5%	59.8%
9	13.3%	15.5%	19.0%	27.1%	1.2%
10	15.3%	21.4%	15.5%	15.3%	15.9%
11	22.4%	26.2%	16.7%	13.9%	11.0%
12	13.3%	3.6%	19.0%	12.5%	9.8%
13	6.1%	2.4%	3.6%	2.1%	1.2%
14	1.0%	1.2%	. . .	. . .	1.2%

n: number of individuals, PIC: polymorphic information content.

TABLE 6—*Population data and forensic value of THO1 in Shan, Akha, Lisu, Lahu and Hmong.*

Locus: TH01					
	Shan $n = 45$	Akha $n = 42$	Lisu $n = 41$	Lahu $n = 48$	Hmong $n = 41$
Forensic identification					
Matching Probability	0.142	0.172	0.141	0.202	0.264
Expressed as 1 in . . .	7.1	5.8	7.1	4.9	3.8
Power of Discrimination	0.858	0.828	0.859	0.798	0.736
PIC	0.65	0.60	0.63	0.58	0.51
Paternity					
Power of Exclusion	0.379	0.414	0.274	0.441	0.402
Typical Paternity Index	1.50	1.62	1.21	1.71	1.58
Allele Frequencies					
Homozygotes	33.3%	31.0%	41.5%	29.2%	31.7%
Heterozygotes	66.7%	69.0%	58.5%	70.8%	68.3%
Total Alleles	90	84	82	96	82

Allele	Frequency				
5	. . .	. . .	1.2%	. . .	. . .
6	7.8%	6.0%	7.3%	8.3%	20.7%
7	23.3%	45.2%	26.8%	34.4%	15.9%
8	11.1%	4.8%	6.1%	5.2%	. . .
9	47.8%	34.5%	48.8%	47.9%	61.0%
10	10.0%	9.5%	8.5%	4.2%	2.4%
11	. . .	. . .	1.2%	. . .	. . .

n: number of individuals, PIC: polymorphic information content.

TABLE 7—*Population data and forensic value of TPOX in Shan, Akha, Lisu, Lahu and Hmong.*

Locus: TPOX					
	Shan $n = 34$	Akha $n = 42$	Lisu $n = 40$	Lahu $n = 46$	Hmong $n = 38$
Forensic identification					
Matching Probability	0.296	0.219	0.238	0.216	0.240
Expressed as 1 in . . .	3.4	4.6	4.2	4.6	4.2
Power of Discrimination	0.704	0.781	0.763	0.784	0.760
PIC	0.47	0.53	0.54	0.54	0.56
Paternity					
Power of Exclusion	0.121	0.149	0.291	0.207	0.331
Typical Paternity Index	0.85	0.91	1.25	1.05	1.36
Allele Frequencies					
Homozygotes	58.8%	54.8%	40.0%	47.8%	36.8%
Heterozygotes	41.2%	45.2%	60.0%	52.2%	63.2%
Total Alleles	68	84	80	92	76

Allele	Frequency				
8	64.7%	54.8%	56.3%	53.3%	36.8%
9	13.2%	26.2%	12.5%	8.7%	14.5%
10	· · ·	1.2%	2.5%	6.5%	· · ·
11	20.6%	17.9%	26.3%	31.5%	46.1%
12	· · ·	· · ·	2.5%	· · ·	2.6%
13	1.5%	· · ·	· · ·	· · ·	· · ·

n: number of individuals, PIC: polymorphic information content.

TABLE 8—*Population data and forensic value of VWA in Shan, Akha, Lisu, Lahu and Hmong.*

Locus: VWA					
	Shan $n = 49$	Akha $n = 42$	Lisu $n = 42$	Lahu $n = 49$	Hmong $n = 41$
Forensic identification					
Matching Probability	0.093	0.084	0.078	0.092	0.101
Expressed as 1 in . . .	10.8	11.9	12.8	10.9	9.9
Power of Discrimination	0.907	0.916	0.922	0.908	0.899
PIC	0.75	0.77	0.78	0.76	0.71
Paternity					
Power of Exclusion	0.451	0.617	0.530	0.630	0.520
Typical Paternity Index	1.75	2.63	2.10	2.72	2.05
Allele Frequencies					
Homozygotes	28.6%	19.0%	23.8%	18.4%	24.4%
Heterozygotes	71.4%	81.0%	76.2%	81.6%	75.6%
Total Alleles	98	84	84	98	82

Allele	Frequency				
14	34.7%	25.0%	28.6%	22.4%	29.3%
15	1.0%	· · ·	2.4%	4.1%	1.2%
16	9.2%	20.2%	19.0%	7.1%	13.4%
17	16.3%	21.4%	17.9%	27.6%	7.3%
18	22.4%	16.7%	17.9%	25.5%	34.1%
19	11.2%	14.3%	10.7%	10.2%	14.6%
20	5.1%	2.4%	2.4%	3.1%	· · ·
21	· · ·	· · ·	1.2%	· · ·	· · ·

n: number of individuals, PIC: polymorphic information content.

the Akha as 0.99999996, the Lisu as 0.99999997, the Lahu as 0.99999996 and the Hmong as 0.9999997. Since the population size of these ethnic minorities is far less than one-hundred thousand in Thailand, it means that practically any tribal individual there can be unambiguously be identified using this collection of STR loci. These markers are therefore very useful for paternity testing and forensic casework. The complete dataset can be accessed at http://www.med.cmu.ac.th/dept/forensic/DNA/Data.htm.

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