Int J Legal Med (2001) 114 : 349–351

CASE REPORT

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Tibetan population data on the PCR-typed loci D16S539, D7S820, D13S317, HUMF13A01, FESFPS, vWA, HUMTH01, TPOX and CSF1PO

Received: 8 February 2000 / Accepted: 7 November 2000

Abstract Frequency data for nine tetrameric short tandem repeat loci (D16S539, D7S820, D13S317, HUMF13A01, FESFPS, vWA, HUMTH01, TPOX and CSF1PO) were investigated in a population sample of 107 unrelated Tibetan individuals by using a multiplex polymerase chain reaction (PCR), followed by 4% polyacrylamide gel electrophoresis (PAGE) and silver staining. All loci met the Hardy-Weinberg expectations. The forensically relevant parameters were calculated. This is the first time that Chinese Tibetan population data on DNA loci have been reported that are of forensic importance.

Keywords Forensic science · DNA typing · Population genetics · Tibetan

Introduction

Recent advances of polymorphic short tandem repeats (STRs) as genetic markers have led to their wide application in forensic science such as human identification and paternity [1, 2, 3, 4, 5, 6, 7, 8]. The commercially available kits enable multiplex PCR of the STR loci D16S539, D7S820, D13S317, HUMF13A01, FESFPS, vWA, HUMTH01, TPOX and CSF1PO. Currently, there are few data on allele frequencies and genotype distributions in the Tibetan population for STR loci. This paper presents the first report of the allele frequency data for these nine STR loci in a Chinese Tibetan population sample.

Materials and methods

Blood samples were taken from 107 unrelated Tibetan volunteer donors living in the Gannan area of Tibetan, which is located in the east of the Tibetan plateau in Gansu Province, China. For all individuals tested the last three generations were endogamous. Genomic DNA was extracted using chelex-100 resin [9]. The co-amplification of D16S539, D7S820, D13S317, HUMF13A01, FESFPS, vWA, HUMTH01, TPOX and CSF1PO and typing were performed using the GenePrint STR system according to the manufacturer's recommendations (Promega corporation, Madison, Wis.).

Allele designations were determined by comparison with those of the allelic ladders (Promega corporation, Madison, Wis.). Unbiased estimates of expected heterozygosity were computed as described by Edwards et al [2]. Possible divergence from Hardy-Weinberg expectations (HWE) was tested by calculating the unbiased estimate of the expected homozygote/heterozygote frequencies [10, 11, 12, 13], the likelihood ratio test [2, 11, 14] and the exact test [15], based on 2,000 random shuffling experiments. The value of forensic and paternity statistics was computed using the PowerStats software (Promega Corporation, Madison, Wis.).

Result and discussion

The distribution of observed allelic frequencies for the nine STR loci are shown in Table 1. There was no detectable deviation from HWE for the nine loci based on the homozygosity test, likelihood ratio test, and the exact test. Forensically relevant parameters of the loci are summarised in Table 2. These calculated statistical scores (i.e. heterozygosity, PD, PIC, Pe, $PI_{typical}$) were found to be highly informative among this Tibetan population from northwest China. In conclusion, a Tibetan population database has been established for nine PCR-typed polymorphic STR loci. The data obtained in this paper are potentially useful for forensic analyses and paternity testing in this area.

Acknowledgments This work was supported by a major project grant (GK979–2-111A) from the Science and Technology Committee of the Gansu Province. Any points of view or opinions given in this document are those of the authors and do not necessarily represent the official position.

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Table 1 Allele frequencies of nine STRs in a Chinese Tibetan population sample (n = 107)

Allele	STR loci								
	D16S539	D7S820	D13S317	F13A01	FESFPS	vWA	TH01	TPOX	CSF1PO
3.2	–	–	–	0.346	–	–	–	–	–
4	–	–	–	0.159	–	–	–	–	–
5	–	–	–	0.131	–	–	–	–	–
6	0.009	–	–	0.360	–	–	0.075	–	–
7	0.173	–	0.005	0.005	–	–	0.201	–	–
8	0.122	0.159	0.248	–	–	–	0.131	0.477	–
9	0.266	0.103	0.173	–	0.005	–	0.495	0.140	0.061
9.3	–	–	–	–	–	–	0.056	–	–
10	0.164	0.196	0.121	–	0.093	–	0.042	0.047	0.248
11	0.168	0.257	0.187	–	0.435	–	–	0.308	0.276
12	0.098	0.252	0.215	–	0.308	–	–	0.028	0.318
13	–	0.033	0.042	–	0.154	–	–	–	0.093
14	–	–	0.009	–	0.005	0.201	–	–	0.005
15	–	–	–	–	–	0.009	–	–	–
16	–	–	–	–	–	0.266	–	–	–
17	–	–	–	–	–	0.276	–	–	–
18	–	–	–	–	–	0.164	–	–	–
19	–	–	–	–	–	0.065	–	–	–
20	–	–	–	–	–	0.019	–	–	–
Observed homozygosity	0.215	0.234	0.196	0.337	0.245	0.253	0.330	0.390	0.270
Expected homozygosity (unbiased)	0.241	0.250	0.227	0.364	0.273	0.211	0.312	0.310	0.241
HWE homozygosity test (*P*)	0.278	0.520	0.336	0.388	0.356	0.286	0.313	0.236	0.111
Likelihood ratio test	0.385	0.990	0.154	0.949	0.938	0.895	0.434	0.687	0.119
Exact test	0.353	0.911	0.124	0.914	0.893	0.918	0.470	0.711	0.209

Table 2 Forensic and paternity statistics for nine STR loci in the Tibetan population sample (*PIC* polymorphism information content)

STR loci	Matching probability	Power of discrimination	PIC	Power of exclusion	Typical paternity index
D16S519	0.045	0.955	0.83	0.549	2.20
D7S820	0.050	0.950	0.81	0.510	2.00
D13S317	0.043	0.957	0.82	0.491	1.92
F13A01	0.091	0.909	0.73	0.337	1.38
FES/FPS	0.091	0.909	0.74	0.472	1.83
vWA	0.053	0.947	0.81	0.580	2.38
TH01	0.056	0.944	0.82	0.463	1.80
TPOX	0.056	0.944	0.81	0.379	1.50
CSF1PO	0.067	0.933	0.77	0.379	1.50

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