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SHORT COMMUNICATION

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Analysis of the short tandem repeat systems HumVWA and HumF13B in a population sample from northern Thailand

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Abstract Two STR systems (HumVWA, HumF13B) were analysed in a northern Thailand population sample using PCR and gel electrophoresis. No deviations from Hardy-Weinberg equilibrium were observed. A rare VWA allele was detected, sequenced and the molecular structure is presented. Interpopulation comparisons revealed that the Thai allele frequencies were most similar to data from other Asian populations.

Key words Short tandem repeat · HumVWA · HumF13B · Thailand

Introduction

STR systems are extremely useful for forensic case work and human identification (Gill et al. 1994). But our knowledge of allelic distribution in different populations is still limited. We therefore inform about the distribution of two such systems (HumVWA, HumF13B) in a population sample from northern Thailand.

Materials and methods

Population samples

Blood samples were taken from 127 healthy 18-year-old males from the rural areas of the districts of Chiangdao, Chomtong, Maewang and Prao of the Chiang Mai province in northern Thailand. All individuals had parents who were born in the respective districts and were speakers of the local dialect (Lemmens-Zygulska et al. 1996) and only one donor was chosen from each village. The populations used for comparisons were Ovambos (Bantu) from Namibia, Caucasoid Germans from North-western Germany (Münsterland), Chinese (Han race) from the Shen Yong area and Japanese from the Shiga area.

DNA extraction, amplification and electrophoresis

DNA was isolated (Miller et al. 1986), amplified by PCR (Kimpton et al. 1992; Möller et al. 1994; Nishimura and Murray 1992) and identified by gel electrophoresis (Allen et al. 1989; Budowle et al. 1991). Allelic ladders were used for sizing, allowing for an absolute accuracy of the length determination and recognition of structure variation.

Sequence analysis

Alleles with irregular migration were isolated (Möller and Brinkmann 1994), reamplified and sequenced on an ABI-373-DNA-Sequencer using the Taq Dye-Deoxy-Terminator Cycle Sequencing Kit (Perkin Elmer/Applied Biosystems, Foster City, CA).

Statistics

The evaluation of the Hardy-Weinberg equilibrium was carried out with the software HWE-Analysis 3.2 (C. Puers, Institute of Legal Medicine, Münster Germany). The frequency profile comparisons between different populations were carried out with a test for heterogeneity (2-way RxC contingency table, G. Carmody, Ottawa, Canada).

Results and discussion

The phenotypes observed in the two STR systems were used to calculate allele frequencies (Table 1) and tested for the presence of Hardy-Weinberg equilibrium with the χ^2-test. All systems studied were found to be in Hardy-Weinberg equilibrium (P-values above 5% Table 2). Additionally, we compared the observed and expected het-

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Table 1 Allele frequencies in the STR systems HumVWA and HumF13B in a northern Thai population sample

HumVWA		HumF13B	
Allele	Frequency (%)	Allele	Frequency (%)
14	26.2	6	1.2
14*	0.4	7	0.4
15	4.0	8	10.4
16	19.4	9	22.8
17	20.2	9c	0.4
18	19.4	10	64.4
19	8.7	11	0.4
20	1.2		
21	0.4		

Table 2 Observed and expected heterozygosity rates (H), discrimination power (DP) and *P*-values of the χ2-test of the observed phenotype configuration. Degrees of freedom are the maximum number of possible phenotypes minus the number of alleles

	HumVWA	HumF13B
H observed	0.81	0.568
H expected	0.809 ± 0.016	0.524 ± 0.056
DP	0.93210	0.69798
χ^2-value	21.9	18.4
d.f.	36	21
P-value	0.969	0.6236

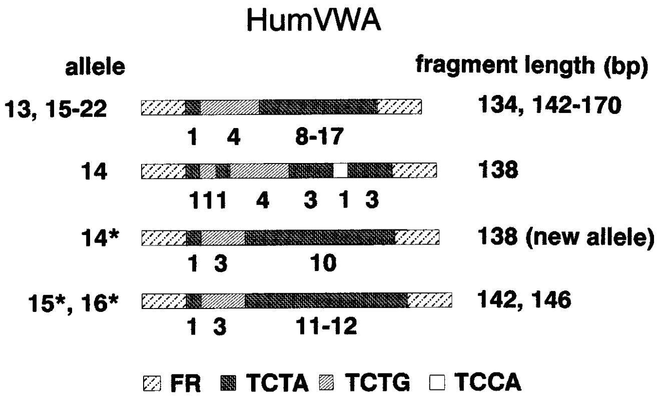

Fig. 1 Schematic representation of the structure of the STR system HumVWA

erozygosity rate (calculated according to Nei and Roychoudhury 1974) and found good agreement. The discrimination power according to Jones (1972) was higher in the system HumVWA (Table 2).

Interpopulation comparisons using a χ^2-test according to Carmody revealed significant differences when comparing Thais with the sub-Saharan African population of Ovambos and the Caucasoid population of Germans (Table 3), while the differences between the Thais and the two Asian population samples (Japanese and Chinese) were less pronounced. Significant ($P > 0.05$) relationships only were observed for HumVWA and HumF13B between Thais and Chinese and in the HumVWA system between Thais and Japanese. According to Cavalli-Sforza et al. (1994), Thais are closely related to Viet Muong living in Vietnam, Mon Khmer living in Kampuchea and many other groups also in Vietnam and to South Chinese. Information on STR allele frequencies of these populations is rare. Nevertheless, our data demonstrate that the northern Thai population sample resembles an asiatic allele distribution.

In the HumVWA system, one allele migrated slightly slower than allele 14 of the ladder and sequencing revealed a rare structure (Fig. 1). The new allele fits into the structural order of alleles 15′ and 16′ (Möller et al. 1994b) since the repeat structure is $(TCTA)_1(TCTG)_3(TCTA)_{10}$ and was thus denominated 14′. Alleles of this type are extremely rare in all populations investigated so far and have been described only once in the literature (Walsh et al. 1996).

In the system HumF13B, alleles 7, 11 and 9c were found only once in the population sample. “C” indicates that migration of this allele shifted slightly towards the cathode, relative to allele 9 of the ladder.

The data presented in this work will allow the calculation of matching probabilities in forensic case work if Thais are considered as a source of DNA evidence. Additionally, our data demonstrate the close relationship between Thais and other Asian populations such as Chinese and Japanese, based on to similar allele frequency distribution.

Table 3 χ^2-values for the degree of relationship between two populations determined in the test according to Carmody

North. Thais	Chinese		Japanese		Germans		Ovambos	
	χ^2	*P*	χ^2	*P*	χ^2	*P*	χ^2	*P*
HumF13B	5.6032	0.507 ± 0.0185	18.4426	0.001 ± 0.001	58.1354	0.00	744.8660	0.00
HumVWA	9.3486	0.278 ± 0.0142	12.2912	0.123 ± 0.0104	31.4181	0.00	148.2102	0.00

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