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Population genetic data for eight STR loci in the south of Africa

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1. Introduction

Population data for short tandem repeat (STR) loci, today's method of choice for human identification and paternity testing in forensic genetics, are available for numerous populations from the major ethnic groups. Nevertheless, the allele frequency data for Sub-Saharan Africans in particular are extremely generalized and little information is available for particular populations.

In this study, we present the allele frequency and the forensic efficiency values for eight STR polymorphisms (i.e. TH01, vWA, ACTBP2, FGA, D21S11, D3S1358, D8S1179, D18S51 in addition to the Amelogenin locus for gender identification) in two small population samples from Southern Africa (42 unrelated Himbas from Northwest Namibia, and 72 unrelated black South Africans from the Cape Town area).

The purpose of this work was to establish a database for forensic purposes including paternity testing and to increase our knowledge of STRs in African populations.

2. Materials and methods

Genomic DNAs from oral cotton swab samples were extracted by the Proteinase K/Chelex method [1]. The eight STR systems (ACTBP2, FGA, TH01, vWA, D3S1358, D8S1179, D18S51, D21S11 [2] plus Amelogenin) were simultaneously amplified in a

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multiplex PCR reaction (*gen*Res MPX-2, Serac, Bad Homburg, Germany). The amplification success was checked by native polyacrylamide gel electrophoresis with subsequent silver staining and the fragments sizing was done by denaturing capillary gel electrophoresis using an ABI PRISM 310 Genetic Analyzer (Applied Biosystems, Foster City, CA, USA) according to the manufacturer's instructions. Alleles were automatically called by the software Genotyper 2.5 and the template provided by Serac. Evaluation of Hardy–Weinberg equilibrium and other forensic statistical parameters was performed using the software package PowerStats (PROMEGA, Madison, WI) and software package HWE (Chr. Puers, Münster [3]).

3. Results and discussion

A typical electropherogram is shown in Fig. 1. Allele frequency and forensic parameters are given in Fig. 2 and Table 1, respectively. Analysis of the Amelogenin system revealed the expected gender in all cases (data not shown). Based on exact test, the Himba population sample fulfilled Hardy–Weinberg expectations, while the South African population samples displayed deviations from the Hardy–Weinberg equilibrium at D21S11, vWA and FGA. This may be due to a sampling effect or may indicate inbreeding. In interpopulation comparisons between Himbas and the South Africans using the program R×C (Mark P. Miller), that performs Fisher's exact test on contingency table through the use of the Metropolis algorithm, significant differences could be observed (Table 1).

In this study, our knowledge of autosomal STRs in two populations from Southern Africa has been increased. The eight MPX-2 loci are efficient for individualization purposes showing a combined PD of 0.99999998 (Himba) and 0.9999999998 (South

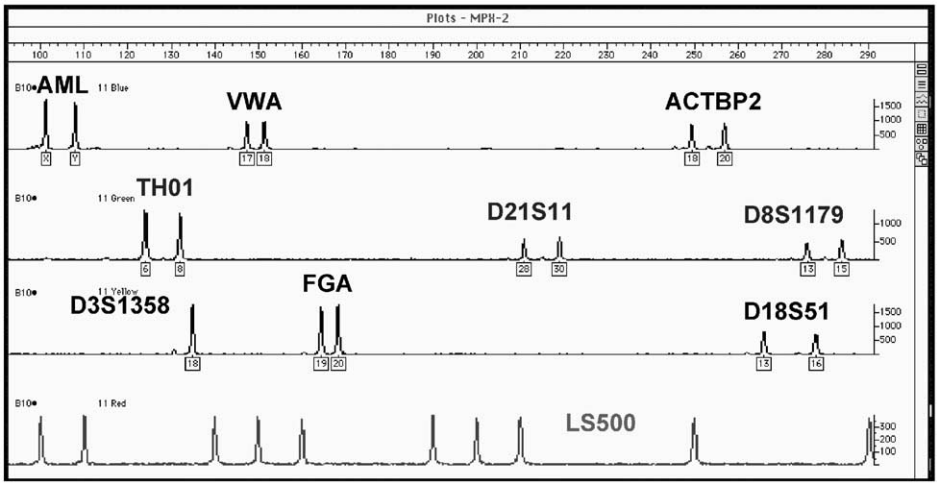

Fig. 1. Representative electropherogram of a Himba sample amplified with the MPX-2 kit.

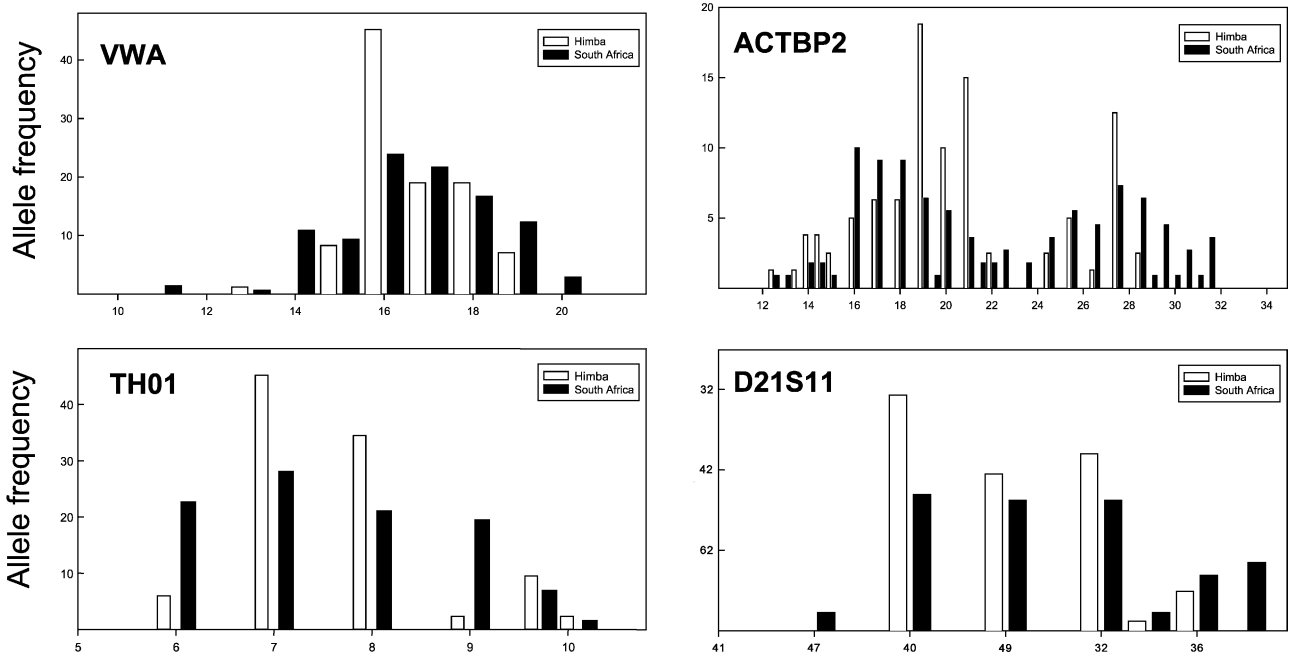

Fig. 2. Allele frequencies of the eight STR loci in the two populations from Southern Africa.

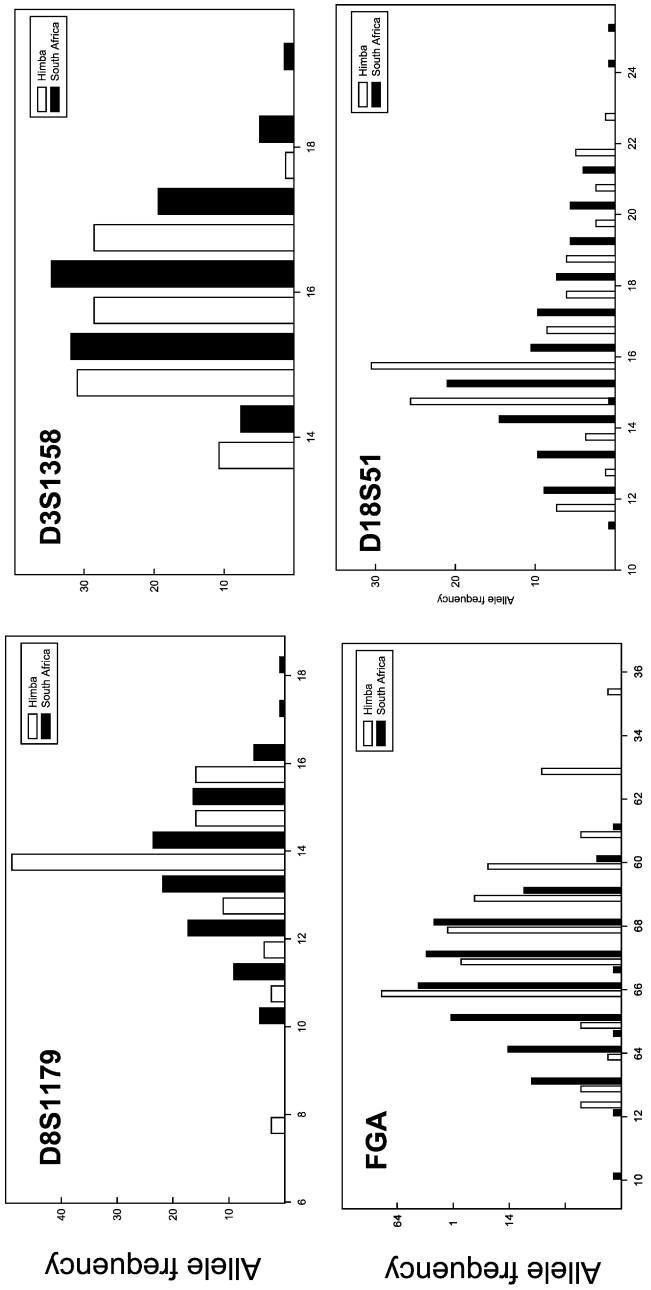

Fig. 2 (*continued*).

Table 1
Forensic statistical parameters of the eight STR loci in the two populations from Southern Africa

	vWA	ACTBP2	TH01	D21S11	D8S1179	D3S1358	FGA	D18S51
Himba								
n	84	80	84	80	82	84	84	82
H_{obs}	0.714	0.900	0.548	0.769	0.732	0.571	0.905	0.854
PD	0.872	0.959	0.833	0.882	0.869	0.785	0.951	0.909
PE	0.451	0.795	0.233	0.543	0.479	0.258	0.805	0.702
P value	0.003	0.119	0.058	0.007	0.051	0.084	0.033	0.404
South Africa								
n	138	110	128	130	110	144	138	124
H_{obs}	0.725	0.927	0.734	0.769	0.855	0.806	0.913	0.855
PD	0.937	0.976	0.915	0.951	0.925	0.857	0.939	0.963
PE	0.467	0.851	0.483	0.543	0.704	0.609	0.822	0.704
P value	0.865	0.192	0.069	0.885	0.9	0.115	0.715	0.051
P (R × C)	0.002	0.018	0.000	0.000	0.000	0.000	0.000	0.001

P value = HWE exact test probability, PE = exclusion power, H_{obs} = observed heterozygosity, PD = discrimination power, *n* = number of chromosomes analyzed, *P* values of R × C were calculated by the R × C program (http://www.public.asu.edu/~mmille8).

Africa). The combined power of exclusion (PE) of all 11 loci was 0.9991 and 0.9998, respectively.

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