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FOR THE RECORD

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DNA Sequence Characterization of the FGA STR Locus in the Free State Population of South Africa

POPULATION: African ($n = 52$), Mixed Ancestry ($n = 5$), Caucasian ($n = 4$) SAN ($n = 1$).

KEYWORDS: forensic science, DNA typing, population genetics, free state province South Africa, FGA

TABLE 1—*Description of sequenced FGA alleles.*

Allele	*n*	Repeat Motif										bp
16.1	11	$(TTTC)_2$	TTTT	TTCT	$(CTTT)_5$	T	$(CTTT)_3$			CTCC	$(TTCC)_2$	224
18	1	$(TTTC)_2$	TTTT	TTCT	$(CTTT)_{10}$					CTCC	$(TTCC)_2$	231
18.2	1	$(TTTC)_2$	TTTT	TT	$(CTTT)_{11}$					CTCC	$(TTCC)_2$	233
19	4	$(TTTC)_2$	TTTT	TTCT	$(CTTT)_{11}$					CTCC	$(TTCC)_2$	235
19.2	1	$(TTTC)_2$	TTTT	TT	$(CTTT)_{12}$					CTCC	$(TTCC)_2$	237
20	2	$(TTTC)_2$	TTTT	TTCT	$(CTTT)_{12}$					CTCC	$(TTCC)_2$	239
21	2	$(TTTC)_2$	TTTT	TTCT	$(CTTT)_{13}$					CTCC	$(TTCC)_2$	243
21.2	1	$(TTTC)_2$	TTTT	TT	$(CTTT)_{14}$					CTCC	$(TTCC)_2$	245
22	4	$(TTTC)_2$	TTTT	TTCT	$(CTTT)_{14}$					CTCC	$(TTCC)_2$	247
22.2	2	$(TTTC)_2$	TTTT	TT	$(CTTT)_{15}$					CTCC	$(TTCC)_2$	249
23	2	$(TTTC)_2$	TTTT	TTCT	$(CTTT)_{15}$					CTCC	$(TTCC)_2$	251
23.2	1	$(TTTC)_2$	TTTT	TT	$(CTTT)_{16}$					CTCC	$(TTCC)_2$	253
24	1	$(TTTC)_2$	TTTT	TTCT	$(CTTT)_{16}$					CTCC	$(TTCC)_2$	255
24.2	1	$(TTTC)_2$	TTTT	TT	$(CTTT)_{17}$					CTCC	$(TTCC)_2$	257
25	2	$(TTTC)_2$	TTTT	TTCT	$(CTTT)_{17}$					CTCC	$(TTCC)_2$	259
26	3	$(TTTC)_2$	TTTT	TTCT	$(CTTT)_{18}$					CTCC	$(TTCC)_2$	263
26′	1	$(TTTC)_2$	TTTT	TTCT	$(CTTT)_{12}$	CCTT	$(CTTT)_5$			CTCC	$(TTCC)_2$	263
27	1	$(TTTC)_2$	TTTT	TTCT	$(CTTT)_{13}$	CCTT	$(CTTT)_5$			CTCC	$(TTCC)_2$	267
28	1	$(TTTC)_2$	TTTT	TTCT	$(CTTT)_{20}$					CTCC	$(TTCC)_2$	271
28′	1	$(TTTC)_2$	TTTT	TTCT	$(CTTT)_{14}$	CCTT	$(CTTT)_5$			CTCC	$(TTCC)_2$	271
29	1	$(TTTC)_2$	TTTT	TTCT	$(CTTT)_{15}$	CCTT	$(CTTT)_5$			CTCC	$(TTCC)_2$	275
29.2	3	$(TTTC)_4$	TTTT	TT	$(CTTT)_{13}$	$(CTTC)_3$	$(CTTT)_3$			CTCC	$(TTCC)_4$	277
30	1	$(TTTC)_3$	TTTT	TTCT	$(CTTT)_{16}$	CCTT	$(CTTT)_5$			CTCC	$(TTCC)_2$	279
30.2	1	$(TTTC)_4$	TTTT	TT	$(CTTT)_{14}$	$(CTCC)_3$	$(CTTT)_3$			CTCC	$(TTCC)_4$	281
31.2	2	$(TTTC)_4$	TTTT	TT	$(CTTT)_{15}$	$(CTCC)_3$	$(CTTT)_3$			CTCC	$(TTCC)_4$	285
40.2	6	$(TTTC)_4$	TTTT	TT	$(CTTT)_9$	$(CTGT)_3$	$(CTTT)_{12}$	$(CTTC)_3$	$(CTTT)_3$	CTCC	$(TTCC)_4$	321
41.2	1	$(TTTC)_4$	TTTT	TT	$(CTTT)_9$	$(CTGT)_3$	$(CTTT)_{13}$	$(CTTC)_3$	$(CTTT)_3$	CTCC	$(TTCC)_4$	325
43.2	16	$(TTTC)_4$	TTTT	TT	$(CTTT)_8$	$(CTGT)_5$	$(CTTT)_{13}$	$(CTTC)_4$	$(CTTT)_3$	CTCC	$(TTCC)_4$	333
43.2′	1	$(TTTC)_4$	TTTT	TT	$(CTTT)_{12}$	$(CTGT)_6$	$(CTTT)_9$	$(CTTC)_3$	$(CTTT)_3$	CTCC	$(TTCC)_4$	333
44.2	1	$(TTTC)_4$	TTTT	TT	$(CTTT)_9$	$(CTGT)_5$	$(CTTT)_{13}$	$(CTTC)_4$	$(CTTT)_3$	CTCC	$(TTCC)_4$	337

n = number of samples sequenced.

Whole blood was collected by venipuncture from individuals living in the Free State Province, South Africa. DNA was extracted using the Promega Wizard kit followed by PCR amplification using a 25 μL mixture containing 10 ng of genomic DNA, 200 μM of each dNTP (Promega Madison, WI), 25 pmol of each primer (MWG-Biotech AG Ebersberg, Germany), 1 U of Amplitaq (F. Hoffmann-La Roche, Basel, Switzerland) in Thermophilic DNA polymerase buffer and 1.5 mM $MgCl_2$. Samples were amplified in a GeneAmp PCR 2400 thermocycler (Applied Biosystems Norwalk, CT). The PCR product (5–10 μL) was electrophoresed on a 2.5% agarose gel containing 0.05 μg/mL ethidium bromide. The DNA fragments of interest were excised from the gel and purified using GenELute minus EtBr spin columns (Sigma-Aldrich, St.

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Louis, MO). Aliquots of 5 μL of the purified PCR product were amplified in second to fourth rounds of PCR (parameters as for first PCR) until a pure single fragment was obtained (1,2). Single band PCR products were purified using the High Pure PCR product purification kit (Roche) and were sequenced using the ABI Prism Big Dye Terminator Ready reaction version 3 kit (Applied Biosystems). Samples were run on a ABI Prism 310 Genetic Analyser using POP-6 polymer. Sequences were analysed using the ABI Prism Sequencing Analysis vs.3 Software.

Three new previously undescribed alleles were found in this study, i.e., alleles 29.2, 40.2, and 41.2 (Table 1). In addition, one of the 43.2 alleles and the only 44.2 allele observed in this study were new sequence variants.

The complete dataset is available at the following URL address: http://www.uovs.ac.za/admin/uploads/tmp_php4vd1eV_428b1fbfb274c_FGA.pdf

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