

## FOR THE RECORD

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# Evaluation of Five Short Tandem Repeat Loci Among North Indian Muslim Populations

**POPULATIONS:** Muslim Sunni ( $n = 200$ ), Muslim Shia ( $n = 200$ )

**KEYWORDS:** forensic science, DNA typing, short tandem repeats, polymerase chain reaction, population genetics, Uttar Pradesh-India, TPO, vWA, TH01, vWF-1, FES

Whole blood obtained by venipuncture was collected in EDTA vacutainer tubes from individuals residing in different parts of Uttar Pradesh, India. The DNA was extracted by phenol chloroform method (1) and purified by ethanol precipitation. PCR amplification was performed using flanking primers described by Perez-Lezaun et al. (2). The amplified product was separated and detected on 9% PAGE using silver staining. The data were analyzed using software POPGENE (3) and CERVUS (4). The allele frequency data is tabulated in Table 1.

The complete data are available to any interested researcher upon request.

## References

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ment length polymorphism analysis. *J Forensic Sci* 1994;39:1254–69.

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TABLE 1—STR allele frequency data for North Indian Sunni ( $n=200$ ) and Shia Muslims ( $n=200$ ).

Bp	Hum vWA		Hum TH01		Hum vWF-1		TPO		FES	
	Sunni	Shia	Sunni	Shia	Sunni	Shia	Sunni	Shia	Sunni	Sunni
96					0.15	0.13				
100					0.15	0.11				
104					0.30	0.25				
108					0.01	0.05				
110							0.01	0.02		
114							0.39	0.40		
116					0.25	0.30				
118							0.12	0.10		
120					0.02	0.01				
122							0.09	0.08		
124					0.12	0.15				
126							0.35	0.35		
130							0.03	0.05		
134							0.01	-		
138	0.14	0.18							0.04	0.05
142	0.04	0.05							0.11	0.06
146	0.34	0.34							0.08	0.05
150	0.14	0.16							0.29	0.36
154	0.29	0.25	-	0.01					0.20	0.18
158	0.02	0.02	0.27	0.28					0.22	0.26
162	0.03	0.02	0.16	0.12					0.04	0.04
166			0.09	0.08					0.01	-
170			0.15	0.17						
173			0.27	0.26						
174			0.06	0.08						
H	0.680	0.650	0.680	0.670	0.655	0.630	0.600	0.640	0.668	0.835
PIC	0.739	0.742	0.779	0.783	0.771	0.781	0.676	0.673	0.777	0.724
PE	0.334	0.352	0.320	0.323	0.403	0.412	0.292	0.282	0.441	0.369

H: Observed heterozygosity.

PIC: Polymorphism information content.

PE: Power of exclusion.