

## FOR THE RECORD

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# Mitochondrial DNA Hypervariable Region I and II Sequence Polymorphism in the Dravidian Linguistic Group of India

**POPULATION:** Blood samples were collected from 131 unrelated individuals of four predominant and endogamous populations of Karnataka: Iyengar Brahmin, Lingayats, Gowda, and Bhovi. The population size for all of the four communities varied in between eight to eighty hundred thousand approximately (3).

**KEYWORDS:** forensic science, mitochondrial DNA, hypervariable region I and II, Gowda, Iyengar Brahmin, Lingayat, Bhovi, India.

Mitochondrial DNA is an important tool for studying maternal lineage that has been widely used in the study of human identification and population structure as well. In this study, HV I and HV II sequence polymorphism is studied in four important populations belonging to the Dravidian linguistic family of Karnataka, India. The information on some polymorphic autosomal STR loci is already available for these populations (1).

Genomic DNA was extracted from the whole blood samples following phenol-chloroform extraction method (4). A total of 10–15 ng of the isolated DNA was used as template for amplification of the Hypervariable (HV I and II) segments of the control region using two sets of primers as listed in Table 1. PCR was carried out in a 25  $\mu$ L reaction volume consisting of 0.5  $\mu$ M primer, 250  $\mu$ M each dNTP, 2  $\mu$ g/ $\mu$ L BSA, 0.5mM MgCl<sub>2</sub> and 5U Taq Polymerase (GIBCO BRL). Amplification was carried out in a PE 2400 thermocycler, with initial denaturation at 95°C for 1 min, followed by a cycling condition of 95°C for 10 sec, 60°C for 30 sec, and 72°C for 30 sec for 30 cycles.

ExoSap-IT™ (USB Corp.) was used to clean the amplified product following the manufacturer's instructions. Sequencing was performed at 96°C for 15 sec, 50°C for 1 sec, 60°C for 1min, followed by a final hold for 10 min at 15°C for 25 cycles using the BigDye™ Terminator Cycle Sequencing ready reaction (Applied Biosystems, Foster City, CA). The amplified product was ethanol precipitated before being run on the ABI 377 automated sequencer (Applied Biosystems, Foster City, CA).

The sequences were edited between positions 16050 to 16400 for HV I region and 90 to 415 for HV II region, which were then aligned and compared with the Anderson reference sequence (5) using BioEdit software (6). Gene and nucleotide diversity (7,8) were calculated using the Arlequin package (9).

Results obtained from the sequencing of the HV I and HV II segments of mt. DNA for each of the four populations are presented as haplotype data in Table 2. The values for gene and nucleotide diversity are given in Table 3. The Gene diversity for all studied populations was 1.00 while the nucleotide diversity varied from 0.037 for Lingayat to 0.066 for Gowda population. A total of 127 haplotypes were observed out of 131 samples. The Bhoivis share two haplotypes 7 and 10 with the Gowda, and also haplotype 3 and 17, with Brahmin and Lingayat, respectively. The data generated in this study will add on to the mitochondrial control region sequence polymorphism marker databases available for other world populations.

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TABLE 2G—Continued.

SAMPLE	HAPLOTYPE Number	16069	16086	16093	16095	16102	16111	16126	16129	16145	16152	16153	16154	16157	16158	16168	16169	16170	16172	16176	16179	16184	16185	16186	16188	16189	16192	16193	16198	16199	16201	16206	16207	16209	16213	16214	16217	16218	16221	16222	16223	16227	16230	16231	16234	16239	16240	16242				
	<b>Anderson</b>	C	T	T	C	T	C	T	G	T	G	T	G	T	A	C	C	A	T	C	C	C	C	C	C	T	C	C	T	T	C	A	A	T	G	C	T	C	C	C	A	A	T	C	A	C						
G1	89									A																																										
G2	90																																																			
G3	91																																																			
G4	92	T	C					C		A									C																																	
G5	93																																																			
G6	94																																																			
G7	95																																																			
G8	96																																																			
G9	10																																																			
G10	97							C													T																															
G11	98																																																			
G12	99																																																			
G13	100																																																			
G14	101																																																			
G15	102																																																			
G16	7																																																			
G17	103																																																			
G18	104																																																			
G19	105																																																			
G20	106																																																			
G21	107							T																																												
G22	108																																																			
G23	109																																																			
G24	110																																																			
G25	111																																																			
G26	112																																																			
G27	113																																																			
G28	114																																																			
G29	115									A																																										
G30	116																																																			
G31	117																																																			
G32	118																																																			
G33	119																																																			
G34	120																																																			
G35	121																																																			
G36	122																																																			
G37	123																																																			
G38	124																																																			
G39	125																																																			
G40	126																																																			
G41	127																																																			

B- Bhovi, Bh- Brahmin, L- Lingayat, G- Gowda. 'D' - deletion, an insertion is designated by the appropriate position followed by a dot.





TABLE 2I—Continued.

SAMPLE	HAPLOTYPE Number	16356	16359	16360	16362	16366	16368	16380	16381	111	140	146	150	151	152	153	174	182	194	195	196	199	200	204	214	224	227	234	239	242	246	250	263	264	271	279	283	285	309.1	309.2	315.1	355	343	372	373				
<b>Anderson</b>		T	T	C	T	C	T	C	T	A	C	T	C	C	T	A	A	C	C	T	C	T	A	T	A	T	A	A	T	C	T	T	A	C	C	T	T	C			A	C	T	A					
G1	89																																																
G2	90	C			C																																												
G3	91																																																
G4	92																																																
G5	93	C													C																																		
G6	94															G																																	
G7	95																							C																									
G8	96														C																																		
G9	10																																																
G10	97																																																
G11	98																																																
G12	99																																																
G13	100																																																
G14	101	C			C																																												
G15	102	C																																															
G16	7																																																
G17	103																						C																										
G18	104	C										T											C																										
G19	105																																																
G20	106																																																
G21	107				C																																												
G22	108															C																																	
G23	109										C																																						
G24	110	C																																															
G25	111				C																																												
G26	112																																																
G27	113																																																
G28	114																																																
G29	115																																																
G30	116											T																																					
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TABLE 3—Gene and nucleotide diversity of mitochondrial DNA hypervariable regions I and II in the four studied populations of Karnataka.

Population	Bhovi	Brahmin	Lingayat	Gowda
Gene diversity	HV I + HV II 1.000 ± 0.008	HV I + HV II 1.000 ± 0.006	HV I + HV II 1.000 ± 0.012	HV I + HV II 1.000 ± 0.005
Nucleotide diversity	0.054 ± 0.027	0.056 ± 0.029	0.037 ± 0.021	0.066 ± 0.034

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