FOR THE RECORD

Anu Ghosh, 1 Ph.D. and M. Seshadri, 1 Ph.D.

Human Y-Chromosomal Short Tandem Repeat DXYS156 in an Indian Population Sample

POPULATION: Allele frequencies for Y-specific short tandem repeat (STR) locus DXYS156 was determined for 120 male individuals from India. DXYS156 locus maps to the short arm of the Y-chromosome (Y_p) and consists of a pentanucleotide repeat (TAAAA)_n. The samples used for the present study belonged to four endogamous population groups: Konkanastha Brahmins, Marathas, Ezhavas and Nairs. The former two populations belonged to the western region while the latter two groups are from the southwestern region of India.

KEYWORDS: forensic science, short tandem repeat, DXYS156, Indian population, paternity testing

Peripheral blood samples were collected from healthy, unrelated adult male individuals. Informed consent was obtained from each donor at the time of blood collection. DNA extraction was performed using the salt-precipitation method (1). PCR primers were as described by Chen et al. (2) with the modification that the forward primer was fluorescently labeled at the 5' end. Annealing was carried out at 56°C and a hot-start was employed. The amplified products were analyzed on ALFTM Express DNA Sequencer (Amersham Biosciences Pvt., Uppasala, Sweden). Internal ladders were used in each lane to offset lane-to-lane mobility shifts. Allelic ladders were used for correct allelic classifications

Allele frequencies were computed using the gene-counting method. Gene diversity was calculated as $1 - \sum p_i^2$, where p_i is the allele frequency.

Table 1 shows the allele frequency distribution at DXYS156Y locus among the study populations. We observed a total of 6 alleles in a sample of 240 chromosomes. The X-chromosome and Y-chromosome alleles were classified according to Chen et al. (2) and Karafet et al. (3). Three smaller alleles (allele 7–9) were found to be X-chromosome specific while three larger alleles (allele 11, 12, and 14) were found to be Y-chromosome specific. Gene diversity was found to be moderate with values ranging between 0.61 and 0.65. The database on DYS156Y for the Indian population groups will be a prerequisite for use of this locus in forensics and paternity testing.

The complete data set is available upon request via electronic mail from the authors at anugh@magnum.barc.ernet.in or msesh@apsara.barc.ernet.in

TABLE 1—Allele frequency distribution at DXYS156 locus among Indian

	Konkanasthas $(n = 32)$		Marathas $(n = 108)$		Ezhavas $(n = 52)$		Nairs $(n = 48)$	
Allele	X	Y	X	Y	X	Y	X	Y
7	0.87		0.92		0.96		0.88	
8	0.06		0.02		0.04		0.12	
9	0.06		0.05					
10								
11		0.25		0.20		0.19		0.25
12		0.75		0.77		0.77		0.75
13								
14		0		0.02		0.04		
Gene Diversity	0.65		0.62		0.61		0.65	

n = Number of chromosomes.

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Additional information and reprint requests: M. Seshadri, Ph.D. Low Level Radiation Studies Section Bio-Science Group Bhabha Atomic Research Center Trombay, Mumbai—400 085 India

E-mail: msesh@apsara.barc.ernet.in

¹ Low level Radiation Studies Section, Bio-Science Group, Bhabha Atomic Research Center, Trombay, Mumbai—400 085, India.