

FOR THE RECORD

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Population Data of 10 Y-chromosomal STR Loci in Cebu Province, Central Visayas (Philippines)

POPULATION: 103 unrelated male individuals from Cebu province, Central Visayas region of the Philippines.

KEYWORDS: forensic science, Y-STR, Y-plexTM 5, Y-plexTM 6, DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385, DYS438, DYS439, haplotype, Philippines

The Philippine archipelago is subdivided into 15 geopolitical groups, namely Regions I–XIII, the Cordillera Autonomous Region, and the Autonomous Region of Muslim Mindanao. Cebu province is located in the Central Visayas region (Region VII), the region that has become the economic and political center of Visayas. People of the Visayas generally speak “Visaya” or “Bisaya,” a dialect that differs with Tagalog, Tagalog being the basis of the Filipino language. The Y-short tandem repeat (STR) minimal haplotype database of a representative National Capital Region (NCR) population has been reported previously (<http://www.ystr.org/asia>; 1). This present study reports the population data of 10 Y-STR loci (eight of which define the Y-minimal haplotype) of 103 males living in the Central Visayas region.

Blood from 103 unrelated male volunteers living in Cebu province, the urban center of Central Visayas region, were collected and stored on FTA[®] cards (Whatman [registered mark] BioScience, Newton, MA). Genomic DNA from 1.2 mm FTA[®] discs was extracted according to the manufacturer’s procedure (Whatman[®] BioScience). Amplification of DNA was carried out using the Y-plexTM 5 and Y-plexTM 6 multiplex systems following the manufacturer’s instructions (Reliagene Technologies Inc., New Orleans, LA; 2,3). PCR products were analyzed on an ABI310 automatic sequencer using GeneScan[®] and Genotyper[®] 3.7 analysis software (Applied Biosystems Inc., Forster City, CA). Alleles were designated using the Y-plexTM 5 and Y-plexTM 6 genotyping macros (Reliagene Technologies Inc.; 2,3).

Analysis of Data

Allele and haplotype frequencies were determined by the gene count method. Gene and haplotype diversities were calculated based on the equations proposed by Nei (4). For comparative population study, Analysis of Molecular Variance (AMOVA) was performed using the Arlequin software version 2.000 (CMPG, Institute of Zoology, University of Berne, Berne, Switzerland; 5).

Tables 1 and 2 show the frequencies of alleles and most common haplotypes observed in the Central Visayas regional

population, respectively. Gene diversity (g) values for all 10 Y-STR loci decrease in the following order: DYS385, DYS390, DYS439, DYS389II, DYS392, DYS393, DYS19, DYS389I, DYS391, and DYS438. A total of 90 different haplotypes were observed, 81 of which are unique in the population. A comparison of the number of haplotypes produced and respective haplotype diversity (h) between the 10 Y-STR haplotype and the Y-STR minimal haplotype (Table 2) shows that the extended Y-STR haplotype has a higher diversity index value ($h = 99.66\%$) and is therefore more informative than the Y-STR minimal haplotype core set ($h = 99.22\%$). Thus, DYS438 ($g = 23.28\%$) and DYS439 ($g = 68.63\%$) provide additional information useful for forensic and population genetic studies.

A comparison of the Y-STR minimal haplotypes of Central Visayas with those found in the database of the NCR included in the Y-STR Haplotype Reference Database (YHRD) showed that only 17 out of 81 haplotypes are shared by NCR and Visayan populations with 64 unique haplotypes in Central Visayas (<http://www.ystr.org/asia>; 1). An earlier study on autosomal STR DNA typing of individuals within NCR and Region 7 reported significant regional variation (6). However, a comparison of the two populations using AMOVA showed no significant variation amongst males belonging to these two populations (R_{st} value = -0.00242 ; $p = 0.63343$). Based on current Y-STR data, these two populations may be pooled to increase the number of haplotypes to 247 (207 of which are unique) and haplotype diversity (99.57%). Further work to study the genetic diversity of these two regional populations is warranted.

Access to Data

The complete dataset can be obtained from the corresponding author, Dr. Maria Corazon A. De Ungria, at mcaadu@uplink.com.ph.

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TABLE 1—Allele/genotype frequencies and gene diversity (g) values of 10 Y-STR loci in the Central Visayas regional population database (n = 103).

Allele	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS438	DYS439	Genotype	DYS385
8								0.0097		11,11	0.0097
9					0.0680			0.0194		11,14	0.0291
10					0.6602	0.0194		0.8738	0.0097	11,15	0.0097
11					0.2718	0.0388		0.0680	0.3592	11,16	0.0194
12	0.0388	0.6602				0.1262	0.2136	0.0291	0.3689	12,12	0.0194
13	0.0485	0.2427				0.4854	0.6019		0.2330	12,13	0.0291
14	0.1068	0.0777				0.3107	0.1650		0.0291	12,14	0.0583
15	0.6117	0.0194				0.0194	0.0194			12,15	0.0388
16	0.1748									12,16	0.1359
17	0.0194									12,17	0.0388
21				0.0583						12,18	0.0097
22				0.0680						12,19	0.0194
23				0.3689						12,20	0.0097
24				0.3398						12,22	0.0097
25				0.1650						13,13	0.0971
27			0.0388							13,14	0.0680
28			0.4757							13,15	0.0097
29			0.2816							13,20	0.0485
30			0.1553							13,21	0.0097
31			0.0388							13,22	0.0097
32			0.0097							14,14	0.0194
										14,15	0.0291
										14,17	0.0097
										14,19	0.0097
										14,25	0.0097
										15,15	0.0388
										15,16	0.0097
										15,17	0.0194
										15,19	0.0097
										16,17	0.0097
										16,18	0.0097
g	0.5854	0.5037	0.6737	0.7202	0.4904	0.6560	0.5700	0.2328	0.6863		0.9547
SE	0.0082	0.0072	0.0032	0.0017	0.0061	0.0033	0.0059	0.0105	0.0009		0.0056

SE, standard error.

TABLE 2—Haplotype frequencies of the most frequent haplotypes for the extended Y-STR haplotype and Y-STR minimal haplotype in Central Visayas regional population (n = 103).

Haplotype	Most frequent haplotypes	frequency
Extended Y-STR haplotype: DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385, DYS438, and DYS439 (h ± SE = 0.9966 ± 0.001)	15-12-28-24-10-13-13-12,16-10-12	0.0388
	15-12-28-23-10-14-13-13,13-10-12	0.0291
	15-13-29-23-11-12-14-15,15-10-11	0.0291
	12-14-30-23-11-14-13-14,15-10-11	0.0194
	13-13-29-25-10-13-13-13,20-10-12	0.0194
	15-12-28-23-10-14-13-12,14-10-13	0.0194
	15-12-28-24-11-13-12-12,16-10-13	0.0194
	15-12-28-23-10-14-13-13,14-10-11	0.0194
	14-13-30-24-11-10-14-13,17-11-13	0.0194
	15-12-28-23-10-14-13-13,13	0.0583
	15-12-28-24-10-13-13-12,16	0.0485
	15-13-29-23-11-12-14-15,15	0.0291
	15-12-28-24-11-13-12-12,16	0.0291
Y-STR minimal haplotype: DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, and DYS385 (h ± SE = 0.9922 ± 0.002)	13-13-29-25-10-13-13-13,20	0.0291
	12-14-30-23-11-14-13-14,15	0.0194
	15-12-28-23-10-14-13-12,14	0.0194
	17-12-28-23-10-14-13-13,14	0.0194
	15-12-28-23-10-14-13-13,14	0.0194
	14-13-30-24-11-10-14-13,17	0.0194
	15-12-28-24-11-13-12-12,12	0.0194
	15-12-28-24-10-13-14-15,17	0.0194

h ± SE, haplotype diversity ± standard error.

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