

FOR THE RECORD

Kristina A. Tabbada,¹ B.Sc.; *Michelle M. F. Magno*,¹ B.Sc.; *Frederick C. Delfin*,¹ B.Sc.; *Gayvelline C. Calacal*,¹ B.Sc.; *Michael Tan*,¹ M.Sc.; *Josephine C-Ferreon*,¹ Ph.D.; *Saturnina C. Halos*,¹ Ph.D.; and *Maria Corazon A. De Ungria*,¹ Ph.D.

Allele Frequencies of Eight Short Tandem Repeat Loci in Three Visayas Regional Populations of the Philippines

POPULATION: Random population sample from Region 6 ($n = 114$), Region 7 ($n = 140$), and Region 8 ($n = 92$), constituting the major islands of the Visayas, Philippines.

KEYWORDS: forensic science, population genetics, short tandem repeat, Philippines, DNA typing

The Philippine Archipelago, composed of 7,100 islands and more than 70 ethno-linguistic groups, is divided into 15 regions on the basis of geographical, cultural, and political variations. Each region is classified under three major island groups: Luzon, Visayas, and Mindanao. The National Capital Region (NCR) is situated south of Luzon, and its population genetic database has been reported (1). However, because the NCR is geographically separated by sea from the rest of the island groups, and because each island group has its own distinct cultural identity, there is a need to study and compare the genetic composition of other regional populations to that of NCR. The present study reports population data at eight short tandem repeat (STR) loci, namely HUMvWA, HUMCSF1PO, HUMTH01, HUMTPOX, HUMF13A01, HUMFES/FPS, HUMFOLP23, and D8S306 for the Visayas. Visayas refers to the central group of islands in the Philippine Archipelago, where the major language spoken is the Visaya or Bisaya, instead of the more common Filipino (Tagalog) language. It is composed of three political regions, namely, Region VI, VII, and VIII. Blood samples were collected in Region VI (Aklan, Iloilo, $n = 114$), Region VII (Cebu, $n = 140$), and Region VIII (Leyte, $n = 92$) and blotted on FITZCO FTA™ cards. Genomic DNA was purified according to manufacturer's instructions (Flinder's Technology, Massachusetts). PCR amplification was performed as described previously (1). Amplified products were detected with the ALFExpress sequencer and using ALFwin and Allelelinks software (Pharmacia Biotech) using automated fluorescence technology. Hardy-Weinberg equilibrium (HWE) and linkage equilibrium (LE) were checked by the Exact Test using the DNA View software (2). Homogeneity tests were performed using Popgene ver 1.32 (3).

The allele frequencies of each regional population are given in Table 1. All three populations are in Hardy-Weinberg equilibrium except for Region VI at locus HUMFOLP23 ($p = 0.0265$). Upon Bonferroni equation, no linkage disequilibrium between all loci pairs was observed ($p < 0.002$). Combined power of discrimination (PD) and the average power of paternity exclusion (PPE) are given in Table 2, with the pooled Region VI and VII having the highest values ($PD = 0.99999981$, $PPE = 0.9935$).

G-statistics show that Region VI and Region VII are homogeneous in all loci and may therefore be combined into one database. In contrast, Region VIII database is not homogeneous with Regions VI and VII at HUMFOLP23 ($p = 0.0007$) and may not be pooled with these databases. This may be partly explained by the closer geographical proximity of the islands comprising Regions VI and VII, compared to those of Region VIII. The databases were also found to be non-homogeneous with the NCR database at HUMF13A01 and HUMFOLP23 (pooled Regions VI-VII) and HUMvWA, HUMFOLP23, and HUMTPOX (Region VIII). The results show that genetic variations exist across some regional populations of the Philippines that may be attributed to geographical location or demography of distinct groups of people within the archipelago. The STR profiles observed in the Visayas islands are quite distinct from that of the NCR, hence these databases should be considered separately. The complete data are available to any interested researcher upon request to the authors.

Acknowledgment

This work was supported by the Natural Sciences Research Institute of the University of the Philippines, the Philippine Anti-Crime Commission, and the Philippine Council for Advanced Science and Technology Research and Development. The authors would also like to acknowledge Ms. Lyre Espada, Dr. Leo Uy, and

¹ DNA Analysis Laboratory, Natural Sciences Research Institute, University of the Philippines, Diliman, Quezon City, Philippines.

TABLE 1A—Observed pooled allele frequencies of Region VI and Region VII at the 8 STR loci.

	HUMF13A01	HUMFES/FPS	HUMvWA	HUMD8S306	HUMFOLP23	HUMCSF1PO	HUMTPOX	HUMTH01
3				0.0023				
3.2	0.1889							
4	0.0415			0.0161				
5	0.0714			0.0277				0.0069
6	0.6705			0.1429	0.0599			0.1083
7	0.0069			0.1797	0.4309			0.3088
8				0.2258	0.1452	0.0023	0.4677	0.0991
9		0.0092		0.2028	0.1936	0.0184	0.1705	0.3894
9.3								0.0207
10		0.0438		0.1221	0.1705	0.2880	0.0138	0.0668
11		0.4009		0.0484		0.2696	0.3226	
12	0.0023	0.3618		0.0184		0.3502	0.0230	
13		0.1590	0.0023	0.0115		0.0622		
14	0.0069	0.0254	0.1682	0.0023		0.0092		
15	0.0092		0.0991					
16	0.0023		0.1152					
17			0.2719					
18			0.2696					
19			0.0576					
20			0.0161					

TABLE 1B—Observed allele frequencies of Region VIII at the 8 STR loci.

	HUMF13A01	HUMFES/FPS	HUMvWA	HUMD8S306	HUMFOLP23	HUMCSF1PO	HUMTPOX	HUMTH01
3				0.0122				
3.2	0.1964							
4	0.0714			0.0122				
5	0.0952			0.0061				
6	0.6131			0.0915	0.1389			0.1467
7				0.2134	0.3111			0.2772
8				0.2256	0.1778	0.0054	0.5380	0.0435
9				0.1951	0.2167	0.0489	0.1772	0.4457
9.3								0.0163
10		0.0330		0.1220	0.1556	0.3750		0.0707
11		0.4011		0.0854		0.2446	0.2722	
12		0.3626		0.0244		0.2935	0.0127	
13		0.1813		0.0122		0.0272		
14	0.0119	0.0165	0.1685			0.0054		
15	0.0119	0.0055	0.0815					
16			0.1033					
17			0.3859					
18			0.2120					
19			0.0489					
20								

TABLE 2—Table of power of discrimination and combined power of paternity exclusion.

Locus	Pooled Region VI–VII	Region VIII
HUMF13A01	0.7187	0.8081
HUMFES/FPS	0.8394	0.8353
HUMvWA	0.9306	0.9030
HUMD8S306	0.9526	0.9560
HUMFOLP23	0.8839	0.9271
HUMCSF1PO	0.9462	0.8701
HUMTPOX	0.8108	0.7994
HUMTH01	0.8920	0.8689
Combined power of discrimination	0.999999981	0.999999966
Combined power of paternity exclusion	0.9935	0.9944

the Philippine National Red Cross for the samples used in the study.

References

- Halos SC, Chu JY, Ferreon ACM, Magno MMF. Philippine population database at nine microsatellite loci for forensic and paternity applications. *Forensic Sci Int* 1999;101:27–32.
- Brenner C. DNAVIEW (version 2.1): DNA forensic analysis programs. User's Manual. 1998.
- Yeh FC, Boyle TJB. Population genetic analysis of co-dominant and dominant markers and quantitative traits. *Belgian J Botany*:129:157.

Additional information and reprint requests:

Maria Corazon A. De Ungria, Ph.D.
DNA Analysis Laboratory
Natural Sciences Research Institute
University of the Philippines
Diliman, Quezon City 1101
Fax: (632)9252965
E-mail: mcadu@uplink.com.ph