

FOR THE RECORD

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Y-Chromosomal Haplotypes for the PowerPlex[®] Y for Twelve STRs in a Peruvian Population Sample

POPULATION: Male population sample ($n = 79$) from Peru.

KEYWORDS: forensic science, Y chromosome, forensic DNA typing, multiplex PCR, Y-STR, DYS19, DYS385a/b, DYS389I/II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439, Peru, Andean, Hispanic, population genetics

TABLE 1—Distribution of sampled individuals from localities in the five areas (24 localities in Peru)*.

Area (N)	Locality	<i>n</i>	Area (N)	Locality	<i>n</i>
1 (13)	Cajamarca	3	4 (18)	Lima	15
	La Libertad	5		Ica	3
	Lambayeque	3	5 (28)	Apurimac	5
	Piura	1		Ayacucho	11
	Tumbes	1		Cusco	1
2 (3)	Amazonas	1	Puno	10	
	Iquitos	1	Tacna	1	
3 (17)	Ucayali	1			
	Ancash	4			
	Cerro de Pasco	2			
	Huancavelica	4			
	Huanuco	1			
	Junin	6			

n: number of samples of each locality and *N*: total number of samples for each area.

The biological samples used in this study consisted of blood stored on FTA[®] cards (Whatman Bioscience) from 79 unrelated males with paternal lineage (Andean -Quechuas and Aymaras- and Hispanic) from different localities of Peru, grouped by geographical criteria in five areas (Table 1). These samples were obtained of relatives of missing persons of the Case Mesa Redonda (4) and individuals from paternity and identification testing cases of Laboratorio Biomolecular y de Genética, Instituto de Medicina Legal, Ministerio Público Lima Peru.

TABLE 2—Private alleles for each of the five areas (localities grouped by Geographical criteria*) of paternal lineage.

Locus	Allele	Frequency	Area
DYS391	12	0,058824	3
DYS389I	15	0,071429	5
DYS389I	11	0,035714	5
DYS439	9	0,111111	4
DYS389II	33	0,055556	4
DYS438	13	0,058824	3
DYS437	13	0,055556	4
DYS19	16	0,111111	4
DYS392	12	0,055556	4
DYS393	15	0,076923	1
DYS390	26	0,076923	1
DYS385	16–17	0,035714	5
DYS385	11–15	0,071429	5
DYS385	13–15	0,058824	3
DYS385	13–13	0,058824	3
DYS385	12–13	0,058824	3
DYS385	12–12	0,058824	3
DYS385	16–16	0,055556	4
DYS385	15–20	0,333333	2
DYS385	17–18	0,076923	1
DYS385	16–18	0,076923	1
DYS385	11–13	0,076923	1
DYS385	null	0,076923	1
DYS385	13–19	0,076923	1
DYS385	12–18	0,076923	1

The DNA was amplified using the commercial typing kit, Promega PowerPlex[®] Y System-DYS19, DYS385a/b, DYS389I/II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438 and DYS439, using a quarter of the total volume of the manufacturer's instructions (Iannacone GC, et al. PowerPlex Y system in forensic cases at Laboratorio Biomolecular y Genética, IML Perú, personal

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* Information available at <http://www.mpfm.gob.pe/publicar> or by e-mail at adn@mpfm.gob.pe

TABLE 3—Allele frequencies and gene diversity of the 12 Y-STR loci.

Locus	Allele	Frequency	Gene Diversity	<i>n</i>	Locus	Allele	Frequency	Gene Diversity	<i>n</i>				
DYS391	9	0.051	0.443	79	DYS390	21	0.076	0.680	79				
	10	0.709				22	0.038						
	11	0.228				23	0.456						
	12	0.013				24	0.304						
DYS389I	11	0.013	0.589	79	DYS385I/II	25	0.114	0.942	78				
	12	0.076				26	0.013						
	13	0.519				11,13	0.013						
	14	0.367				11,14	0.064						
DYS439	15	0.025	0.733	79	11,15	0.026							
	9	0.025			12,12	0.013							
	10	0.051			12,13	0.013							
	11	0.228			12,18	0.013							
	12	0.380			13,13	0.013							
	13	0.253			13,14	0.038							
DYS389II	14	0.063	0.768	79	13,15	0.013							
	27	0.025			13,16	0.051							
	28	0.101			13,19	0.013							
	29	0.165			14,14	0.026							
	30	0.241			14,15	0.026							
	31	0.354			14,16	0.038							
	32	0.101			14,17	0.064							
	33	0.013			14,18	0.064							
	DYS438	9			0.051	0.562			79	14,19	0.051		
		10			0.165					15,15	0.026		
11		0.620	15,16	0.051									
12		0.152	15,17	0.064									
13		0.013	15,18	0.128									
DYS437	13	0.013	0.377	79	15,19	0.090							
	14	0.772			15,20	0.013							
	15	0.152			16,16	0.013							
	16	0.063			16,17	0.013							
DYS19	13	0.620	0.550	79	16,18	0.013							
	14	0.241			16,19	0.038							
	15	0.076			17,18	0.013							
	16	0.025											
	17	0.038											
DYS392	11	0.190	0.777	79									
	12	0.013											
	13	0.203											
	14	0.354											
	15	0.063											
	16	0.101											
DYS393	17	0.076	0.553	79									
	12	0.076											
	13	0.570											
	14	0.342											
	15	0.013											

communication) and it was carried out following the amplification conditions recommended by the manufacturer, in a Mastercycler gradient (Eppendorf) thermocycler. Fragments were analyzed on an ABI310 automated system (Applied Biosystems Divisions/Perkin Elmer). Data were analyzed using the softwares GenAlEx V5 and GDA V1.0 (1,3). The frequencies of private alleles in each area and STR alleles in this population sample are given in Tables 2 and 3. The analysis of Molecular Variance of the 5 areas ranged 0.03 among areas and 0.97 within areas. The haplotype data (76 distinct haplotypes, 75 of which were unique; one of these has a null allele in *DYS385-I/II*) are given in Table 4. Gene diversity values ranged between 0.377 for *DYS437* and 0.942 for *DYS385-I/II*. For Y chromosome specific markers, the allele distribution for each marker is less important than the haplotype diversity for the whole array of loci. The haplotype diversity value of the Y-chromosome corresponds to the value of the power of discrimina-

tion (PD) and the chance of exclusion (CE) for unrelated males. Since we used a random population sample to estimate the haplotype diversity for the total, the equation, $h = n(1 - \sum \chi^2)/(n-1)$ for an unbiased estimate of the haplotype diversity was employed according to Nei's (2) recommendation. The haplotype diversity for the PowerPlex[®] Y loci in the Peruvian Population was calculated to be 99.81%. This means that the PD and CE for unrelated males are also 99.81%. From a forensic point of view, the values obtained revealed that the twelve combined systems is a powerful tool for identification in combination with autosomal STR markers. Further characterization of these loci should include sequencing data for ethnic and geographical groups, mutation rates and evaluation of the performance of these STR's for different types of forensic evidences.

The complete dataset is available to any interested party at <http://www.mpfm.gob.pe/publicar>.

TABLE 4—The 76 haplotypes observed in 79 unrelated males from Peru.

Hap	DYS391	DYS389I	DYS439	DYS389II	DYS438	DYS437	DYS19	DYS392	DYS393	DYS390	DYS385I/II	n
1	9	13	11	30	11	14	13	13	14	25	15-15	1
2	9	14	10	30	10	14	13	11	13	24	13-14	1
3	9	14	10	31	10	14	13	11	13	24	13-14	1
4	9	14	12	32	11	14	13	14	13	24	16-17	1
5	10	11	11	27	11	14	13	14	13	22	14-17	1
6	10	12	10	28	10	16	14	11	13	22	13-16	1
7	10	12	11	28	10	16	14	11	14	22	13-14	1
8	10	12	12	27	11	15	14	14	12	23	15-20	1
9	10	12	12	29	10	16	15	11	15	21	14-15	1
10	10	12	13	28	9	14	15	11	12	24	16-19	1
11	10	12	13	28	9	15	17	11	12	24	15-18	1
12	10	13	9	31	11	14	13	13	13	24	13-16	1
13	10	13	9	31	11	14	13	15	14	24	13-16	1
14	10	13	10	30	11	14	13	14	13	24	15-18	1
15	10	13	11	28	10	15	17	11	13	23	12-12	1
16	10	13	11	28	11	14	13	14	13	25	14-17	1
17	10	13	11	29	9	14	15	13	13	23	14-16	1
18	10	13	11	29	11	14	13	14	13	23	14-15	1
19	10	13	11	30	11	14	13	14	13	23	15-16	1
20	10	13	11	30	11	14	13	14	13	24	15-18	1
21	10	13	11	31	11	14	13	14	13	25	14-18	1
22	10	13	11	31	11	14	13	14	13	25	15-16	1
23	10	13	12	28	12	14	15	13	13	24	12-13	1
24	10	13	12	29	9	16	14	11	12	23	13-16	1
25	10	13	12	29	10	14	14	11	12	23	13-15	1
26	10	13	12	29	11	14	14	14	13	23	14-19	1
27	10	13	12	30	10	14	13	11	13	23	16-16	1
28	10	13	12	30	10	14	13	11	13	24	17-18	1
29	10	13	12	30	11	14	13	14	13	24	14-19	1
30	10	13	12	30	11	14	13	14	13	24	15-17	1
31	10	13	12	30	12	14	13	13	13	24	13-13	1
32	10	13	12	30	12	14	13	14	13	23	14-17	1
33	10	13	12	31	11	14	13	14	13	25	14-18	1
34	10	13	13	31	11	14	13	14	14	23	14-16	1
35	10	13	12	31	11	14	15	11	14	21	15-17	1
36	10	13	13	29	11	14	13	14	13	21	14-17	1
37	10	13	13	30	11	14	13	15	14	23	15-17	1
38	10	13	13	30	11	14	17	11	14	21	16-18	1
39	10	13	13	31	11	14	13	13	13	24	14-18	1
40	10	13	14	30	11	14	13	16	14	23	15-19	1
41	10	14	11	31	10	14	14	11	12	23	12-18	1
42	10	14	11	33	11	14	16	14	14	23	15-17	1
43	10	14	12	31	10	14	13	15	13	24	14-18	1
44	10	14	12	31	11	14	14	14	13	25	14-16	1
45	10	14	12	31	11	13	14	14	13	25	15-16	1
46	10	14	12	31	11	14	13	16	14	23	15-18	1
47	10	14	12	32	11	14	13	14	13	25	16-19	1
48	10	14	13	31	11	14	13	14	13	24	14-14	1
49	10	14	13	31	11	14	14	16	14	23	15-19	1
50	10	14	13	31	11	14	13	16	14	23	15-18	1
51	10	14	13	31	11	14	13	17	14	23	15-18	4
52	10	14	13	31	11	14	13	17	14	23	15-19	1
53	10	14	13	32	11	14	13	14	13	21	14-18	1
54	10	14	13	32	11	14	13	14	13	24	14-14	1
55	10	14	14	30	11	14	13	16	14	23	16-19	1
56	10	14	14	31	11	14	13	17	14	23	15-18	1
57	10	15	14	32	11	14	13	16	14	23	15-19	1
58	11	13	11	29	12	15	14	13	14	26	11-14	1
59	11	13	11	29	12	15	14	13	13	24	11-15	1
60	11	13	11	32	11	14	13	14	14	23	14-19	1
61	11	13	12	29	12	15	14	13	13	23	11-13	1
62	11	13	12	29	12	15	14	13	13	23	11-14	1
63	11	13	12	29	12	15	14	13	13	24	null	1
64	11	13	12	28	10	15	16	12	14	23	15-15	1
65	11	13	12	31	11	14	13	14	13	21	15-17	1
66	11	13	13	30	11	14	13	15	13	24	14-19	1
67	11	13	14	30	12	16	14	13	13	23	11-15	1
68	11	14	11	32	11	14	13	14	13	24	14-17	1
69	11	14	12	30	10	14	15	13	14	25	13-19	1
70	11	14	12	30	13	15	14	13	13	23	11-14	1
71	11	14	12	31	11	14	13	16	14	23	15-19	1
72	11	14	12	31	12	15	14	13	13	23	11-14	1
73	11	14	12	32	11	14	13	14	13	24	15-16	1
74	11	14	13	31	12	14	13	16	14	23	15-19	1
75	11	15	13	31	11	14	13	15	14	23	15-19	1
76	12	13	11	29	12	15	14	13	13	24	11-14	1

Hap: haplotype number; n: individuals observed for each haplotype.

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