Announcement of Population Data

Genetic population data of 12 Y-chromosome STRs loci in Mendoza population (Argentina)

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ABSTRACT

The 12 Y-chromosome STRs included in the "minimal haplotype" plus "SWGDAM core set" (DYS438 and DYS439) and DYS437, were typed in 224 unrelated males from Mendoza province, Argentina. The amplifications were performed using PowerPlex®Y Systems (Promega Corp.) and AmpFISTR YFiler Amplification Kit (AB Applied Biosystems). A total of 203 different haplotypes were identified, of which 186 were unique and 17 were found in two or more individuals. Allele frequency and haplotype diversity (HD) were calculated.

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Population: Two hundred twenty four unrelated males living in Mendoza province (Fig. 1) were sampled using FTA® Classic Card (Whatman). Sample donors signed an informed consent or were order by judges.

DNA extraction: Blood samples were collected and the DNA was extracted according to FTA® protocols.

PCR: One hundred and forty six samples were genotyped by PowerPlex®Y System (Promega Corp.) and the others 78 samples were typed by AmpFISTR YFiler Amplification Kit (AB Applied Biosystems) following manufacturer's recommendations.

STRs typing: Amplified samples were analyzed with the help of an ABI Prism® 3130 Genetic Analyzer (AB Applied Biosystems).

Results: See Tables 1–3.

Quality control: Proficiency testing of the GEP-ISFG WG 2008 (Spanish–Portuguese Speaking Working Group of International Society for Forensic Genetics, http://www.gep-isfg.org), the proficiency testing of the Argentine Society for Forensic Genetics 2008 (http://www.sagf.org.ar), and the Y-STR Haplotyping Quality Assurance Exercise 2008 (http://www.yhrd.org).

Data analysis: Haplotype and allele frequencies were determined by direct counting, haplotype diversity (HD) was performed by using Arlequin software v3.11 [1].

Other remarks: Duplicated loci were observed in two samples, DYS19 in Mza39 and DYS437 in Mza166. We found no-consensus allele in Mza178 at DYS385 locus.

A list of the haplotypes found in Mendoza population is shown in Table 1, and was deposited in the YHRD (accession number: YA003472) [2].

In the 224 individuals sampled, we found 203 different haplotypes, 91.63% (N = 186) were unique, 14 with two, two with three and one with four records. The overall haplotype diversity (HD) was 0.9990, similar to that depicted by the already publish data from Mendoza province and European populations [3–6].

We searched the most frequent haplotype in Mendoza province (Mza88) in the YHRD, which includes a total of 13,751 haplotypes in 97 populations typed for the "*minimal haplotype*" + DYS438, DYS439 and DYS437. For this haplotype we found 69 records in 27 populations from Europe, Latin America and North America, with high number of matches in Ravenna (11/384) and Modena (6/130), north of Italy, Central Portugal (6/303) and Peru (5/311).

If we consider only the "*minimal haplotype*" the number of different haplotypes is 178, with a total number of uniquely found haplotypes of 148 (83.15%). Moreover, we found 25 haplotypes in two individuals, two haplotypes in three individuals, one in five, one in seven and one in eight individuals. The two most frequent "*minimal haplotype*" in our sample (14-13-29-24-10-13-13-11,14 and 14-13-29-24-11-13-13-11,14) are the most frequent in Argentina population [3] and represents the modal for the European Haplogroup R1b [7]. This corroborate previously

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Fig. 1. Map of Argentina indicating Mendoza province.

published conclusion of the impact of the European male genetic contribution to the extant population of Argentina [3,8].

Our results were compared with previously published Argentinean population data obtained by typing the *"minimal haplotype"*. The comparison included population samples of ten provinces: Buenos Aires ($n = 237$), Santa Fe ($n = 73$), Rio Negro ($n = 224$), Chubut ($n = 108$), Misiones ($n = 70$), Formosa ($n = 54$), Salta ($n = 35$), Chaco ($n = 33$), Corrientes ($n = 28$) [3] and Córdoba ($n = 100$) [9]. R_{st} based genetic distances between Mendoza population sample and the samples from other six provinces were not statistically significant. Nevertheless, the sample of Mendoza displayed significant distances with Salta, Cordoba, Misiones and Buenos Aires samples. The difference was highest with Cordoba ($R_{st} = 0.04847$; $P = 0.00010 \pm 0.0001$ and with Salta ($R_{st} = 0.02234$; $P = 0.04336 \pm 0.0021$). These differences can be explained by the different proportion of European immigrants received by the three provinces and the high contribution of the Native American to the extant gene pool of the Andean region of the country.

In Table 2 are allele frequencies for 10 Y-STRs and in Table 3 are the genotypic frequencies for the DYS385 locus. In bold number are indicated the most frequent allele/genotype.

This paper follows the guidelines for publication of population data request by the journal [10].

Table 1
Observed Y-chromosome haplotypes in Mendoza population.

Hpt	n	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS385a/b	DYS438	DYS439	DYS437
Mza1	1	12	14	32	25	10	16	13	17–17	11	12	14
Mza2	1	13	12	29	23	10	11	13	16–18	10	12	13
Mza3	1	13	12	30	23	10	10	13	17–17	10	12	14
Mza4	1	13	12	30	24	10	11	13	14–18	10	11	15
Mza5	1	13	13	29	24	11	14	13	14–14	12	11	14
Mza6	1	13	13	29	24	11	14	13	14–19	12	11	14
Mza7	1	13	13	29	24	9	11	13	13–13	10	10	14
Mza8	1	13	13	29	25	9	11	13	14–14	10	10	14
Mza9	1	13	13	30	23	10	13	13	13–14	11	12	14
Mza10	1	13	13	30	24	10	11	13	15–18	10	12	14
Mza11	2	13	13	30	24	10	11	13	16–18	10	12	14
Mza12	1	13	13	30	24	10	11	13	16–19	10	12	14
Mza13	1	13	13	30	24	10	13	15	13–19	11	13	14
Mza14	1	13	13	30	24	11	11	13	16–18	10	13	14
Mza15	1	13	13	30	24	9	11	13	15–15	10	11	14
Mza16	2	13	13	30	25	10	11	13	15–18	10	12	14
Mza17	1	13	13	31	23	10	11	13	16–16	10	12	14
Mza18	1	13	13	31	23	10	14	15	14–17	11	13	14
Mza19	1	13	13	31	24	10	11	14	15–17	10	11	14
Mza20	1	13	13	31	25	9	12	13	18–19	10	12	14
Mza21	1	13	13	31	25	9	12	13	18–19	10	13	14
Mza22	2	13	14	29	22	10	13	13	12–15	9	11	15
Mza23	1	13	14	30	23	10	11	13	17–21	10	11	14
Mza24	1	13	14	30	23	9	11	13	13–14	10	10	14
Mza25	1	13	14	30	23	9	11	13	13–16	10	10	14
Mza26	1	13	14	30	24	10	14	14	14–15	12	11	14
Mza27	2	13	14	30	24	9	11	13	13–14	10	10	14
Mza28	1	13	14	30	25	11	13	13	12–13	12	12	15
Mza29	1	13	14	30	25	11	15	13	15–18	11	11	14
Mza30	2	13	14	30	25	9	14	13	14–18	10	12	14
Mza31	1	13	14	30	25	9	14	13	14–18	14	12	10
Mza32	1	13	14	31	23	10	15	14	15–18	11	12	14
Mza33	1	13	14	31	23	10	16	14	15–18	11	12	14
Mza34	1	13	14	31	23	10	16	14	15–18	11	14	14
Mza35	1	13	14	31	23	10	16	14	15–19	11	13	14
Mza36	1	13	14	31	24	10	16	14	15–17	11	12	14
Mza37	1	13	14	31	24	9	11	13	13–14	10	10	14
Mza38	1	13	14	31	25	10	16	14	15–19	11	14	14
Mza39	1	14–15	14	31	21	10	11	13	14–15	10	11	16
Mza40	1	14	12	27	24	10	14	12	11–14	12	13	14
Mza41	1	14	12	28	22	10	11	13	13–14	10	11	16
Mza42	1	14	12	28	23	10	11	13	13–14	10	11	16
Mza43	1	14	12	28	23	10	11	13	14–14	10	11	15