

Genetic Admixture in Three Mexican Mestizo Populations Based on D1S80 and HLA-DQA1 Loci

RICARDO M. CERDA-FLORES,^{1,2,3} MARIA C. VILLALOBOS-TORRES,⁴
HUGO A. BARRERA-SALDAÑA,⁴ LIZETTE M. CORTÉS-PRIETO,⁵ LETICIA O. BARAJAS,⁵
FERNANDO RIVAS,⁵ ANGEL CARRACEDO,⁶ YIXI ZHONG,² SARA A. BARTON,^{2*} AND
RANAJIT CHAKRABORTY²

¹Departamento de Genética de Poblaciones, Centro de Investigación Biomédica del Noreste (CIBIN), Instituto Mexicano del Seguro Social, Monterrey, Nuevo León, México

²Human Genetics Center, The University of Texas School of Public Health, Houston, Texas

³Division de Postgrado, Facultad de Ciencias Biológicas, Universidad Autónoma de Nuevo León, Monterrey, Nuevo León, México

⁴Unidad de Laboratorios de Ingeniería y Expresión Genéticas, Departamento de Bioquímica, Facultad de Medicina, Universidad Autónoma de Nuevo León, Monterrey, México

⁵Immunology Division, Western Biomedical Research Center, Instituto Mexicano del Seguro Social, Guadalajara, Jalisco, México

⁶Unidad de Genética Forense, Departamento de Medicina Legal, Facultad de Medicina, Universidad de Santiago de Compostela, Galicia, Spain

ABSTRACT This study compares genetic polymorphisms at the D1S80 and HLA-DQA1 loci in three Mexican Mestizo populations from three large states (Nuevo León, Jalisco, and the Federal District). Allele frequency distributions are relatively homogenous in the three samples; only the Federal District population shows minor differences of the HLA-DQA1 allele frequencies compared with the other two. In terms of genetic composition, these Mestizo populations show evidence of admixture with predominantly Spanish-European (50–60%) and Amerindian (37–49%) contributions; the African contribution (1–3%) is minor. Together with the observation that in Nuevo León, the admixture estimates based on D1S80 and HLA-DQA1, are virtually the same as those reported earlier from blood group loci, suggests that DNA markers, such as D1S80 and HLA-DQA1 are useful for examining genetic homogeneity/heterogeneity across Mestizo populations of Mexico. The inverse relationship of the proportion of gene diversity due to population differences (G_{st}) to within population gene diversity (H_s) is also consistent with theoretical predictions, supporting the use of these markers for population genetics studies. *Am. J. Hum. Biol.* 14:257–263, 2002. © 2002 Wiley-Liss, Inc.

Cosmopolitan populations from large cities of Mexico consist of gene pools derived from three primary sources: Europeans (Spanish), Amerindians, and Africans (Lisker, 1981). Studies on blood groups and serum proteins describing gene frequencies and admixture estimates support this ethnohistory of Mexican Mestizo populations (Cerdeña-Flores et al., 1987, 1991, 1994; Cerdeña-Flores and Dávila-Rodríguez, 2000; Cerdeña-Flores and Garza-Chapa, 1988, 1989; Crawford et al., 1976a, 1976b; Garza-Chapa, 1983; Garza-Chapa et al., 2000; Lisker and Babinsky, 1986; Lisker et al., 1986, 1988, 1990; Tiburcio et al., 1978).

Because similar systematic studies with DNA markers have not yet been conducted, this report provides information for three Mexican states (Nuevo León, Jalisco, and the Federal District; Fig. 1) that have the largest populations in the Country, using two nuclear DNA polymorphisms (D1S80 and HLA-DQA1). The state of Nuevo León, one of the five states of Northeastern Mexico (that also includes Coahuila, San Luis

Potosí, Tamaulipas, and Zacatecas) has a population of over 3.8 million inhabitants. The state of Jalisco has a population of approximately 6.3 million, and the Federal District (which does not include all of the Mexico City metropolitan area) has nearly 8.6 million (Census, 2000).

The aims of this study were: 1) to estimate the contribution of the ancestral populations (i.e., Spanish, Amerindian, and African) to the Mestizo populations of these three states using two nuclear DNA polymorphisms, D1S80 and HLA-DQA1; 2) to compare admixture proportions of these three Mestizo populations; and 3) to compare admixture estimates of the Nuevo

Contract grant sponsor: CONACYT, Mexico; contract grant number: 113518 (to R.M. Cerdeña-Flores); Contract grant sponsor: U.S. Public Health Service Research, U.S. National Institutes of Health; Contract grant numbers: GM 41399 and GM45861.

*Correspondence to: Sara A. Barton, Human Genetics Center, School of Public Health, P.O. Box 20186, Houston, TX 77225. E-mail: sabarton@sph.uth.tmc.edu

Received 5 June 2001; Revision received 22 August 2001; Accepted 24 August 2001



Fig. 1. Location of the states of Nuevo León, Jalisco, and Federal District in Mexico.

León population with estimates based on five blood group markers from the same region (Cerde-Flores et al., 1994).

The rationale of this study was to examine whether or not the genetic compositions of the large urban Mestizo populations of Mexico are similar in terms of DNA polymorphisms. Answers to such questions will be helpful in designing case-control studies of disease-gene association involving DNA markers.

MATERIALS AND METHODS

Sample description

Genetic data from these populations were collected as part of a larger investigation of the genetic structure of the Mexican Mestizo populations. Venous blood samples from unrelated healthy individuals were collected in tubes containing EDTA.

The Nuevo León sample consists of 103 individuals, interviewed at the Universidad Autónoma de Nuevo León (74 students) and in the Instituto Mexicano del Seguro Social (29 white-collar workers) from 1997 to 1998. In the Jalisco sample, 129 individuals who

were scored for D1S80 and 63 for HLA-DQA1, were unrelated individuals living in the Guadalajara metropolitan area. All of them had Mexican Mestizo parents and grandparents, mainly from the state of Jalisco. The sampled individuals were either family members of Instituto Mexicano del Seguro Social employees or university student volunteers. The sample from the Federal District, chosen for comparative purposes, consists of allele frequency data for D1S80 and HLA-DQA1, obtained from the compilation of Peterson et al. (2000).

Sample preparation

For the Nuevo León sample, DNA was obtained by the lysis method with Triton X-100 and sodium dodecyl sulfate, purified by extraction with phenol-chloroform, and precipitated with ethanol (Martínez-Soriano et al., 1993). For the Jalisco sample, DNA was extracted from peripheral blood leukocytes by the method of Miller et al. (1988).

D1S80 typing

Extracted DNA was amplified by polymerase chain reaction (PCR) using the

D1S80 primers described by Kasai et al. (1990). In Nuevo León, DNA fragments were scanned with a Gel Doc 1000 system (Bio Rad Laboratories, Hercules, CA) on ethidium bromide stained gels, and the bands were analyzed with Bio Rad software. For the Jalisco samples, allele sizes were assigned on silver stained acrylamide gels by visual comparison. A commercial D1S80 allelic ladder (PE Applied Biosystems, Branchburg, NJ) was used as a reference in all cases.

HLA-DQA1 typing

For the HLA-DQA1 typing in Nuevo León, a PCR amplification and a reverse dot-blot procedure with biotinylated DQA primers and immobilized oligonucleotide probes was done using the AmpliType HLA-DQA1 PCR Amplification and Typing Kit (Perkin Elmer Applied Biosystems, Branchburg, NJ), whereas the Jalisco sample was typed by the PCR-SSP (sequence specific primers) method (Olerup et al., 1993). Some alleles were pooled to reduce categories to six alleles and make results comparable with the commercial kit used in Nuevo León (*0101 + *0104 = 1.1, *0401 + *0501 + *0601 = 4).

Statistical methods

The statistical analyses were conducted in five parts. First, allele frequencies were estimated by the gene counting method (Li, 1976), because for codominant systems such as D1S80 and HLA-DQA1 this method requires no assumption regarding the genetic structure of the sampled populations. Second, possible deviation from Hardy-Weinberg expectations (HWE) was tested by three methods: the homozygosity test in which the unbiased estimate of the expected homozygote/heterozygote frequencies (Nei, 1978) were compared with those observed, the log likelihood ratio test criterion (Weir, 1992), and the exact test (Guo and Thompson, 1992). Third, an $R \times C$ contingency table exact test was used to test for homogeneity of the three Mestizo populations for D1S80 and HLA-DQA1 loci separately (Roff and Bentzen, 1989). Fourth, the percent contribution of ancestral populations to the Mestizo population was calculated by the method of Elston (1971), each Mestizo population being considered the product of the admixture of three parental populations: Spanish (Central Spain), Amerindian (Pueblo), and African (Zimbabwe).

Gene frequency data on the three ancestral populations were obtained from the compilation of Peterson et al. (2000) for African, Scholl et al. (1995) for Amerindian, and http://www.ertzaintza.net/adn_nuclear for Spanish. Fifth and finally, the Mestizo populations were compared using heterogeneity of admixture proportions by the χ^2 heterogeneity test (Rao, 1973).

RESULTS

Allele frequency distributions and their comparisons in three populations

The distribution of D1S80 allele frequencies for three Mexican Mestizo populations and three ancestral populations is shown in Table 1. The most common alleles in the Nuevo León, Jalisco, and Federal District populations were alleles 18 and 24. For Nuevo León, Jalisco, and the Federal District, the gene diversity (unbiased estimate of heterozygosity) values were 0.878, 0.806, and 0.827, respectively. There was no significant difference between the three Mestizo populations (G-statistic = 65.40, $P > 0.05$).

The distribution of HLA-DQA1 allele frequencies for the three Mexican Mestizo populations and three ancestral populations is shown in Table 2. There were a total of six alleles. The most common allele was 4 in the Nuevo León, Jalisco, and Federal District populations. For Nuevo León, Jalisco, and Federal District the allelic diversity values were 0.759, 0.737, and 0.691, respectively. No difference between Nuevo León and Jalisco populations was detected ($G = 9.14$, $P = 0.11$) but when they were merged, the pooled distribution was significantly different from the Federal District sample ($G = 29.16$, $P < 0.05$). Allele 2 seems to be less frequent in the Federal District population with a corresponding increase of alleles 3 and 4, compared with the other two samples.

Conformity of genotype frequencies with HWEs

The genotype frequency distributions for the D1S80 loci do not deviate from HWE based on any of the three tests (homozygosity test, likelihood ratio test, and the exact test) in the Nuevo León and Jalisco populations. In contrast, whereas the likelihood ratio and exact tests do not detect deviation of HLA-DQA1 genotype frequencies from HWE in the Nuevo León and

TABLE 1. *D1S80* allele frequencies (%) in three Mexican Mestizo populations and three ancestral populations

Allele	Nuevo León	Jalisco	Federal District ^a	Spain ^b	Native American ^c	African ^a
N	103	129	230	297	93	101
15	0.97	0.00	0.00	0.00	0.00	0.00
16	3.88	1.16	2.20	0.00	10.80	0.50
17	0.48	0.39	0.40	0.34	0.50	1.49
18	23.30	30.21	32.20	22.90	25.30	2.48
19	3.40	0.39	0.40	0.50	2.70	0.00
20	0.98	1.55	0.90	2.19	0.50	0.50
21	2.43	2.33	1.30	3.20	1.10	14.36
22	1.46	1.55	1.50	5.39	1.10	12.87
23	1.94	0.39	0.20	1.18	0.00	2.97
24	20.39	29.07	20.90	35.86	30.10	12.87
25	7.77	6.98	9.60	5.05	9.10	5.94
26	2.43	1.16	1.70	1.51	0.00	0.00
27	0.00	0.78	1.50	0.67	2.20	2.97
28	7.28	5.04	5.90	6.73	2.70	11.88
29	5.34	2.33	5.00	6.23	0.00	1.98
30	7.28	5.81	8.00	0.67	5.90	1.49
31	7.77	9.30	6.30	4.38	7.50	6.93
32	0.97	0.39	0.70	0.17	0.00	1.49
33	0.00	0.00	0.00	0.00	0.00	0.00
34	0.97	0.00	0.70	0.50	0.00	16.34
35	0.00	0.39	0.20	0.34	0.00	0.00
36	0.48	0.39	0.20	0.50	0.00	0.00
37	0.00	0.39	0.00	0.67	0.00	0.00
38	0.00	0.00	0.20	0.17	0.00	0.00
39	0.00	0.00	0.00	0.19	0.00	0.00
≥40	0.48	0.00	0.00	0.67	0.50	2.97
H	0.878	0.806	0.827	0.802	0.818	0.897

Nuevo León vs. Jalisco vs. Federal District: G-statistic = 65.40, *P* > 0.05.

H, Gene diversity (unbiased estimate of heterozygosity).

^aPeterson et al. (2000).

^bhttp://www.ertzaintza.net/adn_nuclear.

^cScholl et al. (1995).

TABLE 2. *HLA-DQA1* allele frequencies (%) in three Mexican Mestizo and three ancestral populations

Allele	Nuevo León	Jalisco	Federal District ^a	Spain ^b	American Indian ^c	African ^a
N	103	63	230	360	103	106
1.1	8.74	15.87	8.50	13.06	5.80	13.21
1.2	10.19	3.97	8.50	16.25	1.00	34.43
1.3	4.85	3.18	2.00	7.64	1.50	12.26
2	13.59	10.32	5.40	16.11	3.40	5.66
3	24.27	26.98	31.70	15.56	12.10	4.72
4	38.35	39.68	43.90	31.39	76.20	29.72
H	0.759	0.737	0.691	0.803	0.402	0.759

Nuevo León vs. Jalisco vs. Federal District: G-statistic = 29.16, *P* < 0.05.

Nuevo León vs. Jalisco: G-statistic = 9.14, *P* > 0.05.

H, Gene diversity (unbiased estimate of heterozygosity).

^aPeterson et al. (2000).

^bhttp://www.ertzaintza.net/adn_nuclear.

^cScholl et al. (1995).

Jalisco samples, the homozygosity test reveals a significant deficiency of observed homozygotes in the Jalisco sample (*P* = 0.019, based on 1,000 permutations of alleles; Edwards et al., 1992).

Genetic admixture analysis

Table 3 presents the estimated values of admixture proportions along with their standard errors based on the two loci together. The trihybrid model of admixture

(consisting of contributions of Spanish, Amerindian, and African genes) is the best fitting admixture model for all three samples. The respective admixture proportions (60%, 37%, and 3% in Nuevo León; 56%, 43%, and 1% in Jalisco; and 50%, 49%, and 1% in Federal District from the ancestral gene pools) are not significantly different as tested by the heterogeneity χ^2 statistic (shown in the last row of Table 3). However, the proportion of Amerindian genes appear

TABLE 3. Percentage contribution from Spanish, Amerindian, and African gene pools to the three Mexican Mestizo populations

Population	Spanish	Amerindian	African
Nuevo León ^a	59.03 ± 2.01	31.03 ± 1.82	9.94 ± 0.89
Nuevo León ^b	59.99 ± 5.94	36.99 ± 5.05	3.02 ± 2.76
Jalisco ^b	56.03 ± 7.87	43.03 ± 6.43	0.94 ± 4.41
Federal District ^b	50.03 ± 4.11	49.03 ± 3.76	0.94 ± 1.27
χ^2	2.02	3.71	0.46

^aPrevious results. The computation are done with five polymorphic loci (ABO, Rh, MNSs, Duffy, Kidd); see Cerda-Flores et al. (1994).

^bThe computation is done with D1S80 and HLA-DQA1.

to be somewhat larger in the Central and Western states (Federal District and Jalisco) compared with Nuevo León, with a corresponding decrease of the African contribution in their gene pool. The Nuevo León population showed similar ancestral contributions with the Northeastern populations using nuclear DNA markers and blood groups markers (Cerda-Flores et al., 1994) by the heterogeneity χ^2 statistic ($\chi^2 = 0.002$, $P > 0.05$).

DISCUSSION

The contribution of the Spanish, Amerindian, and African ancestries in the three Mexican Mestizo populations are similar using two DNA markers D1S80 and HLA-DQA1. In the United States, almost identical admixture components have been reported in Mexican Americans in the states of Texas and Arizona but not using nuclear DNA polymorphisms (Hanis et al., 1991; Cerda-Flores et al., 1992; Long et al., 1991; Tseng et al., 1998; Williams et al., 1992).

Of the two analyzed systems, the D1S80 locus is more polymorphic than HLA-DQA1, both in terms of number of segregating alleles as well as gene diversity (heterozygosity). In this sense, the allele frequency homogeneity of the D1S80 locus across the three samples, and a minor indication of heterogeneity for the HLA-DQA1 locus is worth noting. Chakraborty and Jin (1992) showed that heterogeneity of allele frequencies across populations is expected to be inversely related within population heterozygosity (H_s). The present data follows this prediction; the proportion of gene diversity ascribed to allele frequency differences of three Mestizo populations (G_{ST}) is 3.14% for D1S80 and 6.70% for HLA-DQA1

with their within-population heterozygosities being 83.7% and 72.9%, respectively.

It is worth noting that D1S80 allele frequencies were reported for another Mestizo sample from Jalisco in a recent survey of Rangel-Villalobos et al. (1999). Although the residential history of the 173 individuals in that study were not mentioned, the summary measures of D1S80 polymorphism are very similar to those of the Jalisco sample of the present study (i.e., 19 segregating alleles, 83.6% gene diversity and the heterogeneity statistic for allele frequency differences of 17.89, $P = 0.63$). The authors also concluded that the allele frequencies at the D1S80 locus of their sample are statistically similar to the ones obtained in U.S. Hispanics (Budowle et al., 1997).

The Nuevo León population show similar ancestral contributions with Northeastern populations using either nuclear DNA markers or blood groups markers (Cerda-Flores et al., 1994). This observation suggests that D1S80 and HLA-DQA1 markers are also well suited for measuring genetic admixtures.

In conclusion, Mestizos of the States of Nuevo León, Jalisco, and Federal District have similar ancestral contributions, at least with respect to the two nuclear DNA loci typed. If this result holds true for other DNA markers as well (e.g., short tandem repeats and other microsatellites), it will have a deeper implication for disease-gene association studies in Mexican Mestizo populations. Genetic homogeneity of the urban Mestizo populations will facilitate easy sampling of both affected and control individuals without detailed information of their residential history or inter-state migration history, leading to the possibility for easier collection of large case-control series. Of course, the increased trend of African contribution in the gene pool of the Northeastern region of the country (even though not statistically significant in this study) should be examined with a larger set of DNA markers, including loci that exhibit marked differences of allele frequencies in the African and non-African populations.

ACKNOWLEDGMENTS

The authors gratefully acknowledge the assistance from the Universidad Autonoma in Nuevo León and Guadalajara, Jalisco, as well as the Instituto Mexicano del Seguro

Social personnel in Monterrey, Nuevo León and Guadalajara, Jalisco for the use of their facilities to sample and interview the study participants. IRB (Institutional Review Board) approval from these two organizations were obtained for all sample collections.

LITERATURE CITED

- Budowle B, Smerick JB, Keys KM, Moretti TR. 1997. United States population data on the multiplex short tandem repeat loci—HUMTHO1, TPOX, and CSF1PO and the variable number of tandem repeat locus D1S80. *J Forensic Sci* 42:846–849.
- Census. 2000. Instituto Nacional de Estadística Geografía e Informática. 2000: XII Censo general de población y vivienda. Mexico, DF: Instituto Nacional de Estadística Geografía e Informática (<http://www.I-NEGI.gob.mx>).
- Cerda-Flores RM, Barton SA, Hanis CL, Chakraborty R. 1994. Genetic variation by birth cohorts in Mexican Americans of Starr County, Texas. *Am J Hum Biol* 6:669–674.
- Cerda-Flores RM, Dávila-Rodríguez MI. 2000. Natural fertility in northeastern Mexico: Genetic structure by birthyear and birthplace. *Arch Med Res (Mexico)* 31:520–525.
- Cerda-Flores RM, Garza-Chapa R. 1988. Cambios en las frecuencias de incompatibilidad para ABO y Rh(D) en tres generaciones de la población del área metropolitana de Monterrey, Nuevo León, Mexico. *Arch Med Res (Mexico)* 19:79–89.
- Cerda-Flores RM, Garza-Chapa R. 1989. Variation in the gene frequencies of three generations of humans from Monterrey, Nuevo León, Mexico. *Hum Biol* 61:249–261.
- Cerda-Flores RM, Kshatriya GK, Barton SA, Leal-Garza CH, Garza-Chapa R, Schull WJ, Chakraborty R. 1991. Genetic structure of the populations migrating from San Luis Potosi and Zacatecas to Nuevo León in Mexico. *Hum Biol* 63:309–327.
- Cerda-Flores RM, Kshatriya GK, Bertin TK, Hewett-Emmett, Hanis CL, Chakraborty R. 1992. Gene diversity estimation of genetic admixture among Mexican-Americans of Starr County, Texas. *Ann Hum Biol* 19:347–360.
- Cerda-Flores RM, Ramírez-Fernández E, Garza-Chapa R. 1987. Genetic admixture and distances between populations from Monterrey, Nuevo León, Mexico and their putative ancestral populations. *Hum Biol* 59:31–49.
- Chakraborty R, Jin L. 1992. Heterozygote deficiency, population substructure and their implications in DNA fingerprinting. *Hum Genet* 88:267–272.
- Crawford MH, Lisker R, Perez-Briceño R. 1976a. Genetic microdifferentiation of two transplanted Tlaxcaltecan populations. In: Crawford MH, editor. *The Tlaxcaltecan, prehistory, demography, morphology and genetics: Publications in Anthropology 7*. Lawrence, KS: University of Kansas. p 169–175.
- Crawford MH, Workman PL, McLean C, Lees FC. 1976b. Admixture estimates and selection in Tlaxcala. In: Crawford MH, editor. *The Tlaxcaltecan, prehistory, demography, morphology and genetics: Publications in Anthropology 7*. Lawrence, KS: University of Kansas. p 161–168.
- Edwards A, Hammond H, Jin L, Caskey CT, Chakraborty R. 1992. Genetic variation at five trimeric and tetrameric repeat loci in four human population groups. *Genomics* 12:241–253.
- Elston RC. 1971. The estimation of admixture in racial hybrids. *Ann Hum Genet* 35:9–17.
- Garza-Chapa R. 1983. Genetic distances for ABO and Rh (D) blood groups in the state of Nuevo León, Mexico. *Soc Biol* 30:24–31.
- Garza-Chapa R, Rojas-Alvarado MA, Cerda-Flores RM. 2000. Prevalence of NIDDM in Mexicans with paraphyletic and polyphyletic surnames. *Am J Hum Biol* 12:721–728.
- Guo SW, Thompson EA. 1992. Performing the exact test of Hardy-Weinberg proportion for multiple alleles. *Biometrics* 48:361–372.
- Hanis CL, Hewett-Emmett D, Bertin TK, Schull WJ. 1991. Origins of U.S. Hispanics: Implications for diabetes. *Diabetes Care* 14:618–627.
- Kasai K, Nakamura Y, White R. 1990. Amplification of a variable number of tandem repeats (VNTR) locus (pMCT118) by the polymerase chain reaction (PCR) and its application to forensic science. *J Forensic Sci* 35:1196–1200.
- Li CC. 1976. *First course in population genetics*. Pacific Grove, CA: The Boxwood Press.
- Lisker R. 1981. Estructura genética de la población Mexicana: Aspectos médicos y antropológicos. Mexico: Salvat Mexicana de Ediciones.
- Lisker R, Babinsky V. 1986. Admixture estimates in nine Mexican Indian groups and five east coast localities. *Rev Invest Clin* 38:145–149.
- Lisker R, Perez-Briceño R, Granados J, Babinsky V, De Rubens J, Armendares S, Buentello L. 1986. Gene frequencies and admixture estimates in a Mexico City population. *Am J Phys Anthropol* 71:203–207.
- Lisker R, Perez-Briceño R, Granados J, Babinsky V. 1988. Gene frequencies and admixture estimates in the state of Puebla, Mexico. *Am J Phys Anthropol* 76:331–335.
- Lisker R, Ramirez E, Perez-Briceño R, Granados J, Babinsky V. 1990. Gene frequencies and admixture estimates in four Mexican urban centers. *Hum Biol* 62:791–801.
- Long JC, Williams RC, McAuley JE, Medis R, Partel R, Tregellas WM, South SF, Rea AE, McCormick SB, Iwaniec U. 1991. Genetic variation in Arizona Mexican Americans: Estimation and interpretation of admixture proportions. *Am J Phys Anthropol* 84:141–157.
- Martínez-Soriano JP, Cab-Barrera EL, Tamez-González R, Leal-Klevezas DS. 1993. Detección de brucella abortus por medio de la reacción en cadena de la polimerasa. *Bioquímica* 72:10–16.
- Miller SA, Dykes DD, Polesky HF. 1988. A simple salting out procedure for extracting DNA from human nucleated cells. *Nucleic Acids Res* 16:1215.
- Nei, M. 1978. Estimation of average heterozygosity and genetic distance from a small number of individuals. *Genetics* 89:583–590.
- Olerup O, Aldener A, Fogdell A. 1993. HLA-DQB1 and -DQA1 typing by PCR amplification with sequence-specific primers (PCR-SSP) in 2 hours. *Tissue Antigens* 41:119–134.
- Peterson BL, Su B, Chakraborty R, Budowle B, Gaenslen RE. 2000. World population data for the HLA-DQA1, PM® and D1S80 loci least and most common profile frequencies for combinations of loci estimated following NRCII guidelines. *J Forensic Sci* 45:118–146.
- Rangel-Villalobos H, Rivas F, Torres-Rodríguez M, Jaloma-Cruz AR, Gallegos-Arreola MPO, López-Satow J, Cantú JM, Figueroa LE. 1999. Allele frequency distributions of six-Amp-FLPS (D1S80, APO-B, VWA, THO1, CSF1PO and HPRTB) in a Mexican population. *Forensic Sci Intl* 105:125–129.

- Rao CR. 1973. *Linear statistical inference and its applications*, 2nd Ed. New York: John Wiley.
- Roff DA, Bentzen P. 1989. The statistical analysis of mitochondria DNA polymorphisms: χ^2 and the problem of small samples. *Mol Biol Evol* 6:539-545.
- Scholl W, Budowle B, Radecki K, Salvo M. 1995. Navajo, Pueblo, and Sioux population data on the loci HLA-DQA1, LDLR, GYPA, HBGG, D7S8, Gc, and D1S80. *J Forensic Sci* 41:47-51.
- Tiburcio V, Romero A, De Garay AL. 1978. Gene frequencies and racial intermixture in a Mestizo population from Mexico City. *Ann Hum Biol* 5:131-138.
- Tseng M, Williams RC, Maurer KR, Schanfield MS, Knowler WC, Everhart JE. 1998. Genetic admixture and gallbladder disease in Mexican Americans. *Am J Phys Anthropol* 106:361-371.
- Weir BS. 1992. Independence of VNTR alleles defined by fixed bins. *Genetics* 130:873-887.
- Williams RC, Knowler WC, Pettitt DJ, Long JC, Rokala DA, Polesky HF, Hackenberg RA, Steinberg AG, Bennett PH. 1992. The magnitude and origin of European-American admixture in the Gila River Indian Community of Arizona: A union of genetics and demography. *Am J Hum Genet* 51:101-110.