Admixture Studies in Latin America: From the 20th to the 21st Century

MÓNICA SANS[1]

Abstract   The present study is a review of admixture studies in Latin America, an interesting subject because of the unique history of the area, in which populations from 3 different origins had contact and inter-crossed. The most often used methods of analysis of admixture in Latin America and some problems related to them, such as the determination of the parental populations and selection of genetic markers, are briefly reviewed. Several sources of data for admixture studies (surnames, quantitative traits, proteins, and molecular information) are summarized. The results obtained using protein systems and blood groups, the most often used markers in Latin America, are considered. They are classified according to their application in 3 groups of populations: urban centers, native Americans, and African-descended subjects. The data show that almost every population is dihybrid or trihybrid, and when African influence is not detected, it is probably due more to the method than to an absence of that contribution. A special section is dedicated to the direction of gene flow, and results about directional mating based on mtDNA, Y-chromosome, and nuclear DNA or proteins are also given. From these studies it is possible to conclude that Amerindian admixture came mainly from female lineages, but it is difficult to establish what happened with the African contribution. A last subject considered is the relation between interethnic crosses and diseases; it is easy to analyze that relation when the pathological condition is related to a unique allele, but when complex diseases are considered, the results are not as clear because of the influence of nongenetic factors. Finally, the perspectives for admixture studies in the 21st century are considered, and some attempts to predict their future in Latin America are made.

Admixture studies have greatly contributed and are still contributing to the biological anthropology knowledge in Latin America (i.e., Central and South America). The interest for such a subject far exceeds its scientific limits: in different countries the newspapers have taken part in the diffusion of results

[1] Department of Biological Anthropology, University of the Republic, Magallanes 1577, 11200 Montevideo, Uruguay. E-mail: msans@adinet.com.uy.

KEY WORDS: ADMIXTURE STUDIES, HYBRID POPULATIONS, LATIN AMERICA

and in the support of analyses using different approaches [e.g., *Noticias* in Argentina (Markic 1991), *El Espectador* in Colombia (Rojas Posada 1992), and *El País* in Uruguay ("Encuesta: Desde el origin," 1998)]. The articles published in newspapers and magazines are usually debatable, but they reflect the population's interest in their origins.

There are several goals for admixture studies in Latin America. The understanding of the historical colonization process has been the most important, and it is related to the gene pool of the present populations. The knowledge of early native American populations is another objective; in this sense, intercrossing is not the focus, but the data are used to deduce the original characteristics of the starting populations, and discarding admixture is a basic condition for that. More recently, the relation between ethnic groups and certain diseases has become another topic of interest.

Latin America is probably the most analyzed region for admixture studies, but admixture investigations are not limited to this region. They have been performed in North America and the Caribbean area with similar aims. Admixture studies also have been performed in the Old World; in this case the level of differentiation of the populations considered parental is somewhat different, because these studies in part seek to revisit prehistoric migration waves. However, some Old World admixture studies have the same purpose as studies performed in Latin America, for example, the studies related to the African influence on Canary Islands (Spanish) populations (Morilla et al. 1988; Afonso et al. 1989; Pinto et al. 1996; Esteban et al. 1998).

Who Are the Participants in the Admixture Process?

The interest for admixture studies in Latin America is based on the region's unique and relatively homogeneous history. During the last 5 centuries 3 more or less diverse populations entered into contact with one another, interacted, and mixed. They are, in chronological order, Amerindians (a fairly homogeneous Asian-derived group), Europeans (mostly Spanish and Portuguese), and Africans (who were brought to Latin America as slaves). This process can also be seen as a natural experiment for genetic epidemiology and anthropology, in which polymorphic marker loci are used to infer a genetic basis for traits of interest (Chakraborty and Weiss 1988).

Diverse data show that Amerindians did not have contact with the other 2 groups for at least 12,500 years. Rosenblat (1954) estimated that at the time of the European conquest the native population in Latin America was 12,385,000, but Dobyns (1966) calculated 48,750,000 for South America only and between 80 and 104 million for Latin America and the Caribbean region. A review of these estimates is given by Ubelaker (1976). Crawford (1992) synthesized the information and concluded that Latin American inhabitants numbered 35 million at the end of the 15th century.

The introduction of people from Africa started early in the 16th century and ended around 1850, when the slave traffic stopped. Brazil was the last country to abolish slavery.

Slaves who came to Spanish America (i.e., old Spanish colonies) were taken from different regions. Rout (1976) divided them into: Upper Guinea (Senegal, Guinea, Guinea-Bissau, Sierra Leone, western Mali, and Liberia), Lower Guinea (Ghana, Togo, Benin, Nigeria, and northern Cameroon), the Congo River delta and Angola (Gabon, Congo, Angola), and Mozambique. However, the slaves that arrived in Brazil were mostly from the Portuguese colonies in Africa. According to Ramos (1939), they belonged mainly to 3 cultures: Sudanese (Yoruba, Ewe, Fanti, and Ashanti), Sudanese-Islamized (Hausa, Tapa, Mandingo, and Fulah), and Bantu (Angola, Congo, Mozambique).

The number of slaves who entered Latin America is almost as unclear as the number of Amerindians present there when Europeans arrived. Curtin (1969) estimated the Amerindian population to be more than 3.6 million for Brazil and 1.5 million for Spanish America. Other calculations for Spanish America vary from 700,000 to 5–6 million (Rout 1976).

The estimation of the number of Europeans who entered Latin America has a different kind of complexity, because the influx continued in large numbers until recently. The origins and destinations of these populations depend on the time and reasons for the migration: the last wave occurred after World War II. Also, when populations are analyzed over different historical periods, data about "Europeans" may include "Criollos" (European descendants) and sometimes "Mestizos" (mixed European-Amerindian descendants), as in Rosenblat's (1954) analysis.

Contrary to the isolation of the Amerindian group, people living in Africa and the Iberian populations had had previous contacts. Spaniards and Portuguese have a long history of intermixture with other groups from either Africa or Asia. Reuter (1934) mentioned that the Portuguese have always mixed freely with the native populations of the countries they colonized.

To what extent this previous admixture is reflected in the admixture observed nowadays in Latin America is not clear, and it probably explains some hidden African contribution. Crawford et al. (1976) considered this problem in their analysis of the origin of the African contribution to the Tlaxcala, Mexico, population. They suggested that the African genes could have come from Spanish soldiers with Moorish ancestry or from coastal Amerindians who had interbred with slaves; they concluded that the answer lay between these 2 possibilities.

It is clear that the behavior of conquerors and colonizers in Latin America differed from their behavior in North America. There was much more interpopulation crossing in Latin America than in North America. The process was influenced by the previous history of contacts, religion, and sex of migrants (individual men vs. families).

The level of differentiation among the 3 populations that entered into contact should also be examined. Intrapopulation variation is always much greater than interpopulation variation. Moreover, the concept of human "races" has become anathema. However, as Salzano (1997, p. 225) asserted, "Wrong ideas about race and racist attitudes . . . should not lead us to inconsider the importance of interpopulation differences, just because this is not politically correct. Human heterogeneity should be studied at different levels of our biological hierarchy, and at distinct degrees of population differentiation . . . neglect[ing] to consider the interpopulation variation may lead to erroneous interpretations."

Therefore the existence of interpopulation variation justifies the performance of admixture studies. Because the populations' gene pools derive from different sources, they can be genetically treated as hybrids (Chakraborty 1986).

Most Used Markers and Methods

Even though admixture studies related to blood groups and proteins have been the most prevalent—and up to now these furnished a better knowledge of the populations' history in Latin America—it is necessary to mention the use of other markers, such as surnames, morphological traits, and DNA.

Use of surnames and morphological traits has the advantage of being cheaper than studies performed using proteins or DNA, and because of that, it is possible to analyze a larger number of populations or individuals. But there are difficulties related to the use of surnames or morphological traits.

Surnames have been applied in different countries to reflect African or Amerindian influences. There is a clear investigation advantage in Latin America compared with North America, because 4 surnames (2 from the father and 2 from the mother) are available in the records, giving information about both sides. But problems exist, such as losses or mutations. Moreover, African slaves frequently took their masters' surnames and Amerindians changed their names, usually after baptism, adopting the systems' names or others.

Studies in Brazil, such as the studies performed by E.S. Azevedo, indicate that Africans or their descendants many times adopted devotional names. Therefore the frequency of religious names could reflect African admixture. For example, 25% of the population identified as "white" in the state of Bahia had devotional names, but the percentage grows to 54% in the group considered "black" (Azevedo and Freire 1984).

Another example of the use of surnames is the analysis done in Bolivia by Chakraborty et al. (1989). The sample was separated by taking into account the number of Aymara surnames, and after that the groups were analyzed genetically using 17 polymorphic loci. The results showed a strong correlation

between the amount of Amerindian admixture and the number of Amerindian surnames. For example, the group that had 3 or 4 Aymara surnames showed an Amerindian contribution of 89%, and the group with no Aymara surnames had an Amerindian contribution of 2%.

In North America Spanish surnames have been taken as a marker of Mexican ancestry (Bean and Bradshaw 1970; Murguia and Frisbie 1977; Gottlieb 1983).

Morphological traits have also provided information about population admixture. Some of these studies were based on 1 character only, such as skin color, Mongolian or sacral spot, or shovel-shaped incisors. Chakraborty (1983, 1990) pointed out that the analysis of quantitative traits is important to understand the different sources of evolution acting on genetic variability; they reflect more complex processes than traits determined by only 1 gene and can provide information equivalent to that given by many monogenic traits. However, the percentages of the different contributions cannot be quantitatively determined because of the scarce knowledge of the quantity of genes involved and the ways in which the genes interact. Pollitzer and Elston (1973) discussed the applicability of such markers, considering the correlation among traits, the range of individual variation, and other aspects.

In some cases morphological traits have been used to classify individuals for medical purposes or to select more homogeneous samples. For example, a study done in Brazil that focused on the frequency of hemoglobin S carriers divided the population into classes according to skin color, showing that the darker the skin, the higher the frequency of hemoglobin S (Salzano and Tondo 1982).

Other studies have used skin color to classify individuals and, subsequently, to analyze the degree of admixture in each class. Krieger et al. (1965) correlated morphological and monogenic markers; they took into consideration pigmentation of the abdomen, color and type of hair, and the conformation of nose and lips as a basis to analyze admixture in "Nordestinos" (people from the northeast) living in São Paulo, Brazil. Krieger et al. used 17 polymorphic loci and concluded that "white" people had 17% African admixture, "medium mulattoes" had 32% African admixture, and "Negroes" had 49% African admixture.

In other cases morphological markers were used simply to show that a population is admixed, despite some popular beliefs. This was the aim of some studies in Uruguay, where the national identity refers to the population as composed entirely of European descendants. When the frequency of the Mongolian spot was investigated, the results gave intermediate values between Europeans on one hand and Africans and Amerindians on the other (Sans et al. 1986, 1991; Sans, Mañé-Garzón et al. 1993). These studies were the basis for justifying blood group, protein, and DNA analyses that were performed to determine the percentages of the different contributions (Sans,

Sosa et al. 1993; Bravi et al. 1997; Sans et al. 1997; Bonilla 1998; Sans, Bonilla et al. 1999; Sans, Weimer et al. 1999).

The use of blood groups and proteins can be divided into studies using unique alleles (i.e., alleles that are present in only 1 of the parental populations) and studies based on loci with alleles that vary only in frequency among them.

In Latin America the use of unique alleles or rare variants is relatively common. In an early study Saldanha (1962) applied the formula developed by Ottensooser (1944) [basically an extension of the equation designed by Bernstein (1931)], using the alleles $DI*A$ and RH cDe, to quantify the Amerindian and African contributions, respectively. The use of these markers continues up to the present, despite the fact that trihybrid populations must be, in this type of analysis, sequentially treated as dihybrid.

After the appearance of the general formula of Bernstein (1931), several other methods were derived that consider 2 as well as 3 parental populations and multiple alleles and systems (Ottensooser 1944, 1962; Krieger et al. 1965; Elston 1971; Chakraborty 1975, 1985; Szathmary and Reed 1978; Long 1991; Long et al. 1991). Most of these methods are based on the least-squares method to compute an overall estimate of admixture, using maximum likelihood to provide it. Less frequent is the use of genetic identity, as in the method developed by Chakraborty (1975, 1985). Chakraborty's (1985) study included a least-squares approach to give more stability to the estimations. Some methods also contemplate genetic drift, mutations, and size of the groups, but population size is usually the most criticized part. Chakraborty (1986) provided a detailed review of the characteristics of the different methods.

A study performed among the Tlaxcaltecans of Mexico included a review of the different methods and applied several of them to the data from this population (Crawford et al. 1976). Crawford et al. considered the population both dihybrid and trihybrid. When the trihybrid approach was considered, they obtained a variation for the Amerindian contribution of 67–76% and a variation for the African contribution of 7–9%. They concluded that the estimates were stable and that maximum likelihood mildly overestimated the Amerindian contribution.

A problem in these analyses is the determination of the parental populations because of the scarcity of historical data, differences in the time since the original parental populations came to the Americas and the moment when the hybrid populations are analyzed, and the lack of information about some ethnic groups, because some may have been extinguished or mixed.

Although descendants of the 3 basic original populations seem to be present in any urban center, Latin American populations are not homogeneous, and parental populations vary from 1 region to another. Most of the admixture studies use only Spanish or Portuguese as the European parental population. Our own studies on the Uruguayan population have shown that,

at least for Uruguay, better results are obtained by using a mix of different European populations (Sans et al. 1997). However, because some areas in Latin America had a stronger Iberian migration, the first option can be justified.

Another problem is related to the number of systems and loci that are considered, the number of parental populations, and the confidence obtained depending on the method. The credibility of some results is affected when only a few markers and or when in mixed Amerindian and European countries biparental models are used, avoiding consideration of the African contribution. Some researchers also omit data about the chi-square values or other error estimators.

The newest approach is based on analysis at the molecular level. Most of these studies use restriction fragment length polymorphisms (RFLPs). Admixture estimates can be done with the same methods used for proteins, taking into consideration that there is no recombination when mtDNA or Y-chromosome markers are used. Shriver et al. (1997) estimated the ethnic contribution for major US resident populations based on population-specific DNA markers; a similar analysis was done by Bravi et al. (1997) for an African-derived group in Uruguay. However, because the frequency of some of these markers in different populations is not well known or because it is not easy to find markers that are restricted to 1 population, the use of molecular markers is still difficult. Point mutation frequencies have also been used. Despite the absence of recombination, the results seem to be fairly adequate because more data can be used independently of the unique presence of a marker in a specific population (Sans, Weimer et al. 1999).

DNA-based admixture analyses, especially analyses that use mtDNA and/or Y-chromosome markers, are especially interesting because the maternal and paternal contributions can be determined.

Last, there is the question of the estimation of individual admixture. Even if the results have not been satisfactory up to now, it is necessary to mention that some new methods and applications have been developed (MacLean and Workman 1973a,b; Chakraborty 1986; Hanis et al. 1986; Shriver et al. 1997).

Populations Analyzed

Latin American populations can be divided into 3 categories: (1) urban populations, usually di- or trihybrid, without considering possible substructures; (2) African-derived populations in fairly isolated communities; and (3) Amerindian groups. In the last 2 groups the emphasis is generally the degree of European admixture.

A complete review of admixture studies would be a complex and hard task, especially because most of the studies were published in journals or

annals that are available in only a few places; however, it is possible to analyze some of the data.

Urban Populations.   The different ethnic contributions to Latin American populations can be analyzed considering the biocultural regions defined by Harris (1964) and lately by others (Morner 1967; Wagley 1968, 1971; Ribeiro 1969; Stepan 1991). Nevertheless, it should be pointed out that these studies did not consider any quantitative estimation based on genetic contributions to the different groups to support their ethnic classifications.

In general, the genetic data agree with the delimitation of the regions. For instance, there is usually a clear difference among "Amerindian" (Mexico, Chile), "European" (Argentina, Uruguay), and "African" (Brazil) countries, but this is not always true.

The population of Mexico is 1 of the best analyzed, but although the population can be considered mixed Amerindian and European, there are some regional differences related to the African contribution. Mexico City probably reflects most of the population; for it Lisker et al. (1986) calculated 41% European, 56% Amerindian, and 3% African contributions. However, on the Caribbean coast the African contribution increases: In Veracruz it reaches 26%, and in Tamahihua, in the same state of Veracruz, the calculated value is 40% (Lisker and Babinsky 1986). These last values are similar to those found in "African" countries.

Cerda-Flores and Garza-Chapa (1989) performed a different type of analysis on the Mexican population. They analyzed the degree of admixture that 3 different generations of people living in Monterrey would have and concluded that the oldest generation (people born between 1896 and 1925) had more Spanish contribution than the other generations.

Another example of a mixed Amerindian-European country is Chile. For Santiago Rothhammer (1987) calculated 57% European and 43% Amerindian contributions; a more recent study established that the degree of admixture was related to socioeconomic class (Rothhammer 1993).

Brazil is a good example of a mixed African-European country. Two early studies, done in the 1960s (Saldanha 1962; Krieger et al. 1965), considered northeastern migrants tested in the southern city of São Paulo. Besides the correlation between morphological and blood polymorphisms, Krieger et al.'s article was of interest because it developed a method that estimated admixture from 3 parental populations.

One problem related to admixture studies in Brazil is that some of the studies analyze the admixture inside separate groups of individuals (as "blacks," "whites," or others). Sometimes these groups are based on data coming from censuses where "race" is evaluated, but that division can lead to confusion when analyzing the whole population.

It is interesting to note that the African contribution in Brazil is distributed from 4% in Parintins (Amazonas) to 34% in Aracaju (northeastern re-

gion) (Schüler et al. 1982; Conceição et al. 1987); the Amerindian contribution also varies, being almost 0% in the south and increasing to 27% in Manaus, in the north (Franco et al. 1982; Santos et al. 1983).

Unexpected results were found in "European" countries. In Uruguay the capital city, Montevideo, has about 10% non-European contribution; however, this contribution increases to at least 49% in the northern city of Tacuarembó (Sans et al. 1997).

For another "European" country, Argentina, an article in a popular magazine (Markic 1991) stated that the present population had only 1% Amerindian ancestry, without reference to the African contribution. The European fraction was mostly Italian (40%) and Spanish (35%); no mention was made about admixed Amerindians or admixed blacks. But a recent study done in La Plata, close to Buenos Aires, showed a composition that was unusual considering common beliefs: 30% Amerindian and 7% African contributions (López Camelo et al. 1996).

A summary of data for some urban centers, presented in chronological order, can be seen in Table 1.

Native Populations.   Studies on Amerindian populations are mostly focused on the degree of European admixture in more or less isolated groups and rarely on the African admixture. This kind of analysis is in some cases related to the interest in inferring the characteristics of those populations before the European conquest.

One of the conclusions reached by Lisker et al. (1996), who were studying native populations of Mexico, is that every Amerindian group shows a variable degree of admixture, mostly with Europeans, but African admixture is also frequent on the coast. This conclusion can be extended to the other countries: Amerindian groups without European or African admixture are almost nonexistent, including the groups that are more isolated.

Salzano and Callegari-Jacques (1988) summarized the admixture data for several Amerindian groups of South America. Table 2 shows some of them and also other results. The apparent absence of African admixture is probably due to the fact that most researchers do not consider it or to the choice of some methods that do not allow the separation of the European and African contributions.

African-Derived Populations.   As it happens with Amerindian groups, the degree of isolation of African-derived communities varies considerably, but no population with only African-derived genes was observed. In some cases the whole population can be considered "African," as in Venezuela, northern Brazil, and the Caribbean region; in others cases the individuals constitute an auto-defined group inside a more hybridized population, as in Uruguay and southern Brazil.

Table 1. Admixture in Urban Dihybrid or Trihybrid Latin American Populations

Population	Number of Systems Used	Amount of Admixture (%)			Reference[a]
		European	Amerindian	African	
"Nordestinos," São Paulo, Brazil	17	59	11	30	1
Tlaxcala, Mexico	9	16	76	8	2
Santiago, Chile	1	57	43	n/c	3
Puerto Montt, Chile	1	47	53	n/c	3
Concepción, Chile	1	65	35	n/c	3
Belem, Brazil	1	54	20	27	4
Saltillo (Chamizal), Mexico	1	45	52	3	5
Natal, Brazil	8	58	17	8	6
Porto Alegre, Brazil (whites)	12	92	0	8	6
Parintins, Brazil	9	67	29	4	7
Manaus, Brazil	7	61	27	12	8
Veracruz, Mexico	9	35	39	26	9
Tamahihua, Veracruz, Mexico	9	29	31	40	9
Mexico City, Mexico	6	41	56	3	10
Aracajú, Brazil	14	62	4	34	11
Isla Margarita, Venezuela	3	>50	<40	10	12
Oriximiná, Brazil	7	57	28	15	13
Puebla, Mexico	11	33	56	11	14
Oaxaca, Mexico	9	30	68	2	15
Mérida, Mexico	9	43	51	6	15
La Plata, Argentina	9	63	30	7	16
Montevideo, Uruguay	11	90	1	9	17
Tacuarembó, Uruguay	20	65	20	15	17
Laitec, Chile	5	20	80	n/c	18
Poposo, Chile	5	40	60	n/c	18

n/c, not considered

a. (1) Krieger et al. (1965); (2) Crawford et al. (1976); (3) Rothhammer and Cruz Coke (1977); (4) Schneider and Salzano (1979); (5) Crawford and Devor (1980); (6) Franco et al. (1982); (7) Schüler et al. (1982); (8) Santos et al. (1983); (9) Lisker and Babinsky (1986); (10) Lisker et al. (1986); (11) Conceição et al. (1987); (12) de Díaz Ungria (1987); (13) Santos et al. (1987); (14) Lisker et al. (1988); (15) Lisker (1990); (16) López Camelo et al. (1996); (17) Sans et al. (1997); (18) Harb et al. (1998).

Table 2. Admixture in Amerindian Latin American Populations

Population	Number of Systems Used[a]	Amount of Admixture (%)		Reference[c]
		European/African[b]	Amerindian	
Aymara, Chile	1	4	96	1
Mapuche, Chile	1	27	73	1
Pehuenche, Chile	1	5	95	1
Alacaluf, Chile	4, 6	11	89	2
Caingang, Brazil	6, 10	9	91	2
Chané, Bolivia	4, 6	3	97	2
Chiriguano, Bolivia	4, 6	19	81	2
Cófan, Ecuador	7	0	100	2
Mataco, Argentina	9	10	90	2
Quechua, Peru	10	22	78	2
Parakanã, Brazil	6, 9	1	99	2
Warao, Venezuela	8	1	99	2
Yupa, Colombia	5, 7	1	99	2
Yanomama, Venezuela	10, 12	0	100	2
Boruca, Costa Rica	6	14, 4	82	3
Cabécar, Costa Rica	6	4, <1	95	3
Huétar, Costa Rica	6	33, 4	63	3
Guaymí, Panamá	6	7, 2	91	3
Kuna, Panamá	6	4, >1	95	3
Mapuche, Argentina	5	6	94	4
Huasteca, Mexico	9	37	63	5
Huichol, Mexico	9	9	91	5
Gavião, Brazil	13	4	96	6
Zoró, Brazil	13	0	100	6

a. When 2 values are given, the first value corresponds to the number of systems considered for the estimation of the possible European admixture, and the second value corresponds to the number of systems considered for possible African admixture. The value given for European and African admixture is the average of these 2 estimates.

b. When 2 values are given, the first value corresponds to the estimated value of the European admixture and the second value corresponds to the African admixture; when only 1 value is given, the admixture could be due to either Europeans or Africans.

c. (1) Rothhammer (1987); (2) Salzano and Callegari-Jacques (1988); (3) Barrantes (1993); (4) Carnese et al. (1993); (5) Lisker et al. (1996); (6) Salzano et al. (1998).

The outside contributions to African-derived groups can be European or Amerindian, depending on the geographic regions and historical facts. Castro de Guerra et al. (1993) did an interesting study in 2 Venezuelan populations. One population, Patanemo, showed strong European admixture, whereas the other population, Ganga, had mostly Amerindian admixture. Castro de Guerra et al. concluded that their results were due to differentiated origins; the Patanemo population was founded by fugitive blacks who escaped slavery, and the Ganga population was founded by free blacks (*libertos*).

Data about African-derived groups or populations are shown in Table 3.

Direction of Gene Flow

In an analysis of the direction of gene flow, Cavalli-Sforza et al. (1993, p. 55) stated that "in certain circumstances the gene flow, as it is called, may occur only, or mostly, in one direction. This is the case for Black Americans,

Table 3. Admixture in Latin American African-Derived Populations or Subpopulations

Population	Number of Systems Used	Amount of Admixture (%)			Reference[a]
		European	Amerindian	African	
Livingston, Guatemala	1		29	70	1
Punta Gorda, Belize	1	5	24	71	2
Trombetas, Brazil	11	19	11	70	3
Bluefields, Nicaragua	7	1	33	66	4
Ganga, Venezuela	6	0	24	76	5
Patanemo, Venezuela	6	34	13	53	5
Cametá, Brazil	14	18	34	48	6
Paredão, Brazil	14	18	3	79	6
Curiepe, Venezuela	14	28	14	58	6
Panaquire, Venezuela	12	15	26	59	7
Porto Alegre, Brazil (blacks)	12	59	0	41	8
Melo, Uruguay (blacks)	11	35	13	52	9
Mimbó, Brazil	10	17	22	61	10
Sítio Velho, Brazil	10	12	16	72	10

a. (1) Crawford et al. (1981); (2) Schanfield et al. (1984); (3) Schneider et al. (1987); (4) Biondi et al. (1988); (5) Castro de Guerra et al. (1993); (6) Bortolini et al. (1995); (7) Castro de Guerra et al. (1996); (8) Bortolini et al. (1997); (9) Sans, Weimer et al. (1999); (10) Arpini-Sampaio et al. (1999).

who, in the 300 or more years since they were forcibly taken from Africa to America have received genes from Caucasoid people in a small proportion at every generation."

If this is true for North America (and it is so because of cultural, not biological, reasons), it is not possible to assert the same for Latin America. In Latin America the gene flow between populations usually gave rise to a new, hybrid group, such as the "Mestizos" or the "Mulattos" (Pardos). These 2 groups sometimes appear differentiated in censuses and could have had different legal rights in the past. Some regions, especially those that received European populations early in the colonization process, elaborated a complex system of castes that never functioned efficiently.

Depending on the country, the population was involved in a more or less fast "whitening" process. This process sometimes had a legal connotation: African descendants had the opportunity to purchase a license (cédula de gracias al sacar) that would favor them. It was the king's prerogative to place the Africans and their descendants in the privileged social class, their economic status being the condition for that (Morner 1967).

It is true that most of the African descendants had difficulties integrating into other populations, and they maintained their identity as an ethnic group.

but it is possible to assert that some of them mixed more or less freely, creating new social groups, the castes (castas).

On the contrary, Amerindians, especially in the areas where they had a stratified social structure before European conquest, were easily assimilated in the "Spanish" group or in a new group inside the society, the "Mestizo." Sometimes, the union between a conqueror and an Amerindian had political or religious reasons: the domination of a territory or the conversion to Catholicism.

Population admixture became an ideology, such as J. Vasconcelo's concept of the cosmic race or G. Freyre's idea of a racial democracy. However, this idealistic view of admixture was not true in most cases, and discrimination against some groups, depending on the country, became common fact. Bieber (1997) provided a critical analysis of these ideologies.

One approach to analyzing the way in which admixture has occurred is to separate the male and female contributions. In the last years the possibility of Y-chromosome or mtDNA molecular analysis has furnished that opportunity.

When Amerindian admixture is analyzed, all the results are coherent in suggesting that the female contribution is much higher than the male contribution. Dipierri et al. (1998) performed an interesting analysis of the European contribution to Amerindian populations. Dipierri et al. considered 2 populations from the province of Jujuy, Argentina: San Salvador and Humahuaca. Both populations have 100% Amerindian mtDNA, but Humahuaca, at a higher altitude (2,500–3,500 m above sea level compared with 1,200 m for San Salvador) showed a much smaller European contribution (28% vs. 64%) of Y chromosomes.

On the contrary, the direction of the African contribution is not as clear. This may be due to difficulties of analysis when RFLPs are considered, because RFLPs do not always allow separation of the African and European contributions. An example is a study of African descendants in Melo, Uruguay (Bravi et al. 1997).

In trihybrid populations data about the African contribution are absolutely insufficient from the molecular point of view. In African-descended populations the situation is a little better but also somewhat unclear: When African admixture is analyzed, the higher contribution can come from the maternal or from the paternal lineages, such as what happens in different groups in Brazil. In contrast, in Amerindian or tryhibrid populations the Amerindian contribution is always higher when maternal lineages are analyzed (Bortolini et al. 1999).

Another complex issue is that the admixture values from autosomal markers can be lower or higher compared with mtDNA or Y-chromosome estimates, such as in Ribeirão Preto, Paredão, and Trombetas (Bortolini et al. 1999); data in process from Tacuarembó, Uruguay, seem to indicate the same

situation (Bertoni 1999). The explanation for that is not simple, and it will probably require deeper analysis in future studies.

Some results about directional mating studies in Latin American populations are shown in Table 4. In some cases only Amerindian or European contributions are given, without considering the African contribution, as in some studies using protein markers.

Diseases and Population Admixture

The existence of alleles that are restricted to certain populations is well known. Some of them, such as hemoglobin S or $GD*A-$, are directly related to the existence of pathological conditions in Africa or southern Europe (Acquaye and Oldham 1973; Livingstone 1984, 1989; Beutler 1991). These conditions are also present in the hybrid populations formed by those who carried the allele, although the frequencies are usually lower than expected, probably because the selective value they had in the past was lost.

A general review of hemoglobinopathies and enzyme deficiencies in Latin American populations was made by Arends (1971). Arends showed that almost every country in Central America and South America has hemoglobin S and that some of them also have other hemoglobin variants, β-thalassemia, and G6PD deficiency.

The presence of sickle cell disease, a result of hemoglobin S, is well known in Brazil. Salzano (1985) estimated that approximately 45,000 Brazilian inhabitants present sickle cell disease, whereas the frequency of carriers varied from 5–6% for individuals considered black to 1% for those considered white. The variability of hemoglobin types in Brazil has been reviewed by Salzano and Tondo (1982) and Zago and Costa (1985).

Interestingly, the presence of hemoglobin S was also observed in high proportion in Mexico; on the Gulf coast the frequency of the allele reaches 6%, and the frequency of β-thalassemia heterozygotes reaches 15% (Ruiz-Reyes 1998). These results agree with the African admixture present in that area.

Some studies have investigated associations between genetic markers and malaria. Arends (1971) tested the levels of hemoglobin A2 and hemoglobin F in malaria patients from Venezuela. Santos et al. (1983) found in the ABO blood group system a higher frequency of individuals with B and AB types in malaria patients. Restrepo et al. (1988) considered 2 Amerindian, 1 African-derived, and 1 mixed group in Colombia and determined that when some European HLA alleles are present, there is a smaller resistance to malaria. This fact was explained by a shorter exposure to Plasmodium vivax or P. falciparum; the European descendants have been in contact with malaria only in the past 65 years, because the disease was not endemic before that in the region where the mixed group lives.

Table 4. Evidence for Directional Mating in Latin American Populations.

Population	DNA and Proteins			Amount of Admixture (%) mtDNA			Y Chromosome			Reference
	European	Amerindian	African	European	Amerindian	African	European	Amerindian	African	
European-derived or Mexican populations										
Hispanics, Colorado	67		n/c		85	n/c		56	n/c	1
Humahuaca, Argentina		33		10	90	0		72	0	2
Andean region, Peru				0	100	0		36	0	3
San Salvador, Argentina				64	100	0				4
Tucumán, Uruguay	65	20	15	40	57	0	44	6	19	5
Melo, Uruguay (all)	73	14	13	61	39	n/c	28	n/c	20	5
African-derived populations								64		6
Melo, Uruguay (blacks)	38	15	46	19	29	52	64	6	19	5
Porto Alegre, Brazil (blacks)	46	0	34	11	14	75	80	n/c	20	6
Camaçã, Brazil	24	22	53	17	24	59	54	18	28	7
Ribeirão Preto, Brazil (blacks)	22	5	73	8	10	82	4	0	96	6
Irombeta, Brazil	32	10	58	7	13	80	13	3	84	6
Paeáño, Brazil	38	13	49	15	27	58	35	0	65	6
Coriepe, Venezuela	23	6	70	0	25	58	80	20	0	7
Panaquire, Venezuela	19	26	55	0	25	75	69	31	0	7

n/c, not considered.

a. (1) Merriwether et al (1997); (2) Rodriguez-Delfin et al (1998); (3) Dipierri et al (1998); (4) Sans et al (1997) and Bonilla (1998); (5) Sans, Bonilla et al (1999) and Sans et al (unpublished data, 1999); (6) Sans, Weimer et al (1990); (7) Bortolini et al (1999).

Recently, the association between complex diseases and admixture has also been analyzed. The list of pathological conditions with different frequencies in distinct ethnic groups continues to grow, but the derived inferences are not always straightforward because of the number of factors involved (customs, diet, physical environment, etc.).

One of the most studied diseases is non-insulin-dependent diabetes mellitus (NIDDM). Some studies have shown that Mexican Americans have a higher frequency of NIDDM. For instance, Weiss et al. (1989) found a frequency of NIDDM of 6.9–9.5% in Mexican Americans compared with 1.9–4.2% in white Americans. Moreover, Gardner et al. (1984) analyzed 3 different neighborhoods according to socioeconomic class; they obtained rates of NIDDM of 14.5%, 10%, and 5% for low-, middle-, and high-income areas, respectively; the estimation of native American admixture, according to skin color, gave 46%, 27%, and 18%.

On the other hand, in a study done in Durango, Mexico, Guerrero Romero et al. (1997) found a low prevalence of NIDDM. They concluded that this result was related to the low level of obesity found in the study population.

Another widely analyzed pathological condition is gallbladder disease. As with NIDDM, gallbladder disease has been associated with the presence of Amerindian ancestry. For Mexican American females, by age 85 the risk is as high as 40%; also, the mean age of onset of the disease is lower in Hispanics (40 years) than in white Americans (50 years). The prevalence ratio in females compared to males is 2–3 to 1 in white Americans but 4–5 to 1 in Hispanics (Weiss et al. 1984).

Similar to what happened with NIDDM, however, a recent study by Tseng et al. (1998) did not support the Amerindian association. Tseng et al. estimated admixture rates based on *GM* and *KM* haplotypes and found no association with gallbladder disease (36% and 40% of Amerindian in cases and noncases, respectively). They suggested that the reasons for the high prevalence of gallbladder disease in Mexican Americans is mostly related to nongenetic factors (weight, diabetes, acculturation).

In Chile Miquel et al. (1998) tested the frequency of possible aboriginal cholesterol lithogenic genes and determined that those genes appeared to be widely spread in Chilean Indians and Hispanics. According to Miquel et al., this fact could be related to the formation of gallstones and to the high prevalence of gallbladder disease among some South American populations.

Another disease that has been analyzed with regard to admixture, in this case European ancestors, is cystic fibrosis. Cabello et al. (1999) found a low frequency of the *DF508* allele in Rio de Janeiro, Brazil, and also a low frequency of the disease in the population; this finding was attributed to non-European admixture. Similar results were found in Uruguay (H. Cardoso, personal communication, 1999).

A study related to drug-metabolizing enzymes underlined the influence of genetic admixture between Amerindians and European descendants that could affect the results when these individuals are treated with drugs that are inactivated through polymorphic enzymes (Martínez et al. 1998).

Finally, some recent studies have investigated the resistance to HIV1 and AIDS afforded by the *δCCR5* deletion allele. González et al. (1998) pointed out that the frequency of heterozygotes with this allele is 15% in Caucasians, 5–7% in Hispanics and US blacks, and 1% or less in Asians. Data from Brazil indicate that the allele frequency is 3.5% and that the frequency of heterozygous individuals is 7% (Passos and Picanço 1998). This value agrees with the expected value for an admixed population.

Admixture Studies in the 21st Century

To predict what will happen in the 21st century is an almost impossible task. As can be seen by looking at the futures conceived by H.G. Wells in *The Shape of Things To Come* or by George Orwell in *Nineteen Eighty Four* or, more recently, by Arthur C. Clarke in *2001: A Space Odyssey*, the risks are huge. Usually, the present is far different from the one that was predicted. However, some of the research done in the recent past can help us to think about the future, and hopefully Aldous Huxley's *A Brave New World* will not reach us very fast.

First of all, Latin America cannot be separated from what happens in other regions of the world. The spread of methods and techniques is increasingly faster, and contacts among scientists from different areas are more frequent every day. The use of computers (and the facility they give to bibliographic access) is being expanded and will simplify future research.

Some of the different studies developed in the 20th century will probably continue. People's need to know their origins will not end and, after the postulated globalization, the expectation is that this search will be intensified. Therefore admixture studies with the goal of understanding our past will remain, enriched by the use of molecular markers and the possibility of writing a more clear history considering male and female contributions.

Related to molecular anthropology, some work needs to be done. Basically, this work will be related to methods, such as the methods recently developed by Shriver et al. (1997) and Bertorelle and Excoffier (1998). Also, more data about specific markers (e.g., point mutations, RFLPs) are needed, and studies in Latin America will be connected to those made on parental populations abroad.

However, the most important field of research related to admixture studies in the 21st century will probably be related to ethnic groups and diseases. At present, there is a long list of pathological conditions that have different population frequencies. Until now, some results have been inconclusive because of the effect of nongenetic factors and the difficulty of isolating them. In the future a larger number of studies with better controls will help us to

understand complex diseases. Then ancestral identification will be an easy way to evaluate the risk of disease and its prevention. This will also have an economic effect, because screening techniques related to that risk will be applied.

The possibility of analyzing individual admixture will have a preponderant role in the future. Some research has already been done in relation to this (Chakraborty 1986; Hanis et al. 1986; Shriver et al. 1997), but more markers, more data, and more accurate methods are needed. We should also be alert to avoid the pitfall that the knowledge may eventually be used to discriminate against individuals or groups.

The importance of admixed populations for genetic epidemiological investigations must be emphasized, especially the possibility of detecting linkage related to genes involved in complex diseases. This subject was considered in a recent paper by McKeigue (1998), and its title probably summarizes 1 of the most important subjects to be developed in the next century: "Mapping genes that underlie ethnic differences in disease risk: Methods for detecting linkage in admixed populations by conditioning on parental admixture."

Finally, some speculation is warranted. The feasibility of cloning animals has been demonstrated, and therefore the limit to do the same with humans relates more to ethics than to technology. More easily, it is now possible to choose the sex of a future baby, and probably the chance to choose a child's eye, hair, and skin color will soon become possible. How this will affect admixture studies, especially those related to individual admixture, is unpredictable, and some of the possibilities can disturb our sleep. Will the ancestor's genetic background be an essential issue when some of our future descendants select their spouses?

Literature Cited

Acquaye, C.T.A., and J.H. Oldham. 1973. Variants of hemoglobin and glucose-6-phosphate dehydrogenase. I. Distribution in southern Ghana. *Ghana Med. J.* 12/14:412–418.

Afonso, J.M., J.M. Larruga, V.M. Cabrera et al. 1989. Human enzyme polymorphism in the Canary Islands. III. Tenerife Island population. *Hum. Biol.* 61:543–549.

Arends, T. 1971. Hemoglobinopathies and enzyme deficiencies in Latin American populations. In *The Ongoing Evolution of Latin American Populations.* F.M. Salzano, ed. Springfield, IL: Charles C Thomas, 509–559.

Arpini-Sampaio, Z., M.C. Costa, A.A. Melo et al. 1999. Genetic polymorphisms and ethnic admixture in African-derived black communities of northeastern Brazil. *Hum. Biol.* 71:69–85.

Azevedo, E.S., and N.B.V.M. Freire. 1984. Nome e sobrenomes na interpretação da história do povo. *Cienc. Cult.* 36:753–758.

Barrantes, R. 1993. Diversidad genética y mezcla racial en Amerindios de Costa Rica y Panamá. *Rev. Biol. Trop.* 41:379–384.

Bean, F.D., and B.S. Bradshaw. 1970. Intermarriage between persons of Spanish and non-Spanish surname: Changes from the mid-nineteenth to the mid-twentieth century. *Soc. Sci. Q.* 51:389–395.

Bernstein, F. 1931. Die geographische verteilung der blutgruppen und ihre anthropologische bedentung. In *Comitato: Italiano per Studio dei Problemi della Populazione.* Rome, Italy: Istituto Poligrafico dello Stato, 227–243.

Bertoni, B. 1999. Aplicación de marcadores moleculares en el estudio de poblaciones híbridas humanas. Master's thesis, Universidad de la República, Montevideo, Uruguay (in preparation).

Bertorelle, G., and L. Excoffier. 1998. Inferring admixture proportions from molecular data. *Molec. Biol. Evol.* 15:1298–1311.

Beutler, E. 1991. Glucose-6-phosphate dehydrogenase deficiency. *New Engl. J. Med.* 324:169–174.

Bieber, J. 1997. Race, resistence, and regionalism: Perspectives from Brazil and Spanish America. *Lat. Am. Res. Rev.* 32:132–168.

Biondi, G., G. Battistuzzi, O. Rickards et al. 1988. Migration pattern and genetic marker distribution of the Afro-American populations of Bluefields, Nicaragua. *Ann. Hum. Biol.* 15:399–412.

Bonilla, C. 1998. Linajes amerindios en la población de Tacuarembó, Uruguay. Master's thesis, Universidad de la República, Montevideo, Uruguay.

Bortolini, M.C., W.A. Da Silva Jr., D. Castro de Guerra et al. 1999. African-derived South American populations: a history of symmetrical and asymmetrical matings according to sex revealed by bi- and uniparental genetic markers. *Am. J. Hum. Biol.* 11:551–563.

Bortolini, M.C., T.A. Weimer, M.H.L.P. Franco et al. 1995. Evolutionary relationships between black South American and African populations. *Hum. Biol.* 67:547–559.

Bortolini, M.C., T.A. Weimer, F.M. Salzano et al. 1997. Genetic structure in two urban Afro-Brazilian populations. *Int. J. Anthropol.* 12:5–16.

Bravi, C.M., M. Sans, G. Bailliet et al. 1997. Characterization of mitochondrial and Y-chromosome haplotypes in a Uruguayan population of African ancestry. *Hum. Biol.* 69:641–652.

Cabello, G.M., A.F. Moreira, D. Horovitz et al. 1999. Cystic fibrosis: Low frequency of *DF508* mutation in 2 population samples from Rio de Janeiro, Brazil. *Hum. Biol.* 71:189–196.

Carnese, F.R., A.S. Goicochea, J.A. Rey et al. 1993. Grupos sanguíneos en una población mapuche de Blancura Centro, provincia de Río Negro, Argentina. *Bol. Soc. Esp. Antropol. Biol.* 14:31–39.

Castro de Guerra, D., H. Arvelo, and J. Pinto-Cisternas. 1993. Estructura de población y factores influyentes en dos poblaciones negros venezolanas. *América Negra* 5:37–47.

Castro de Guerra, D., H. Arvelo, A. Rodríguez-Larralde et al. 1996. Genetic study in Panaquire, a Venezuelan population. *Hum. Hered.* 46:323–328.

Cavalli-Sforza, L.L., P. Menozzi, and A. Piazza. 1993. *The History and Geography of Human Genes.* Princeton, NJ: Princeton University Press.

Cerda-Flores, R.M., and R. Garza-Chapa. 1989. Variation in the gene frequencies of three generations of humans from Monterrey, Nuevo León, México. *Hum. Biol.* 61:249–261.

Chakraborty, R. 1975. Estimation of race admixture: A new method. *Am. J. Phys. Anthropol.* 42:93–102.

Chakraborty, R. 1983. Extent of between- versus within-population variation of quantitative traits: Model and data. In *Proceedings of the Indian Statistical Institute Golden Jubilee International Conference on Human Genetics and Adaptation,* K.C. Malhotra and A. Basu, eds. Calcutta, India: Indian Statistical Institute Press, v. 1, 87–102.

Chakraborty, R. 1985. Gene identity in racial hybrids and estimation of admixture rates. In *Genetic Microdifferentiation in Man and Other Animals,* J.V. Neel and Y. Ahuja, eds. Delhi, India: Indian Anthropological Association, 171–180.

Chakraborty, R. 1986. Gene admixture in human populations: Models and predictions. *Yrbk. Phys. Anthropol.* 29:1–43.

Chakraborty, R. 1990. Quantitative traits in relation to population structure: Why and how are they used and what do they imply? *Hum. Biol.* 62:147–162.

Chakraborty, R., and K.M. Weiss. 1988. Admixture as tool for finding linked genes and detecting that difference from allelic association between loci. *Proc. Natl. Acad. Sci. USA* 85:9119–9123.

Chakraborty, R., S.A. Barton, R.E. Ferrell et al. 1989. Ethnicity determination by names among the Aymara of Chile and Bolivia. *Hum. Biol.* 61:159–177.

Conceição, M., F.M. Salzano, M.H.L.P. Franco et al. 1987. Demography, genetics, and race admixture in Aracaju, Brazil. *Rev. Brazil. Genet.* 10:313–331.

Crawford, M.H. 1992. *Antropología Biológica de los Indios Americanos.* Madrid, Spain: Col. MAPFRE.

Crawford, M.H., and E.J. Devor. 1980. Population structure and admixture in transplanted Tlaxcaltecan populations. *Am. J. Phys. Anthropol.* 52:485–490.

Crawford, M.H., N.L. González, M.S. Schanfield et al. 1981. The Black Caribs (Garifuna) of Livingston, Guatemala: Genetic markers and admixture estimates. *Hum. Biol.* 53:87–103.

Crawford M.H., P.L. Workman, C. McLean et al. 1976. Admixture estimates and selection in Tlaxcala. In *The Tlaxcaltecans: Prehistory, Demography, Morphology, and Genetics,* M.H. Crawford, ed. Publications in Anthropology 7. Lawrence, KS: University of Kansas, 161–168.

Curtin, P.D. 1969. *The Atlantic Slave Trade: A Consensus.* Madison, WI: University of Wisconsin Press.

de Díaz Ungría, A.G. 1987. The North: Colombia. Venezuela, the Guayanas. In *Amerika II: Mittel und Südamerika.* I. Schwidetzky, ed. Munich, Germany: R. Oldenbourg Verlag, 105–135.

Dipierri, J.E., E. Alfaro, V.L. Martinez-Marignac et al. 1998. Paternal directional mating in two Amerindian subpopulations located at different altitudes in northwestern Argentina. *Hum. Biol.* 70:1001–1010.

Dobyns, H.F. 1966. Estimating aboriginal American populations: An appraisal of techniques with a new hemispheric estimate. *Curr. Anthropol.* 7:395–416.

Elston, R. 1971. The estimation of admixture in racial hybrids. *Ann. Hum. Genet.* 35:9–17.

Encuesta: Desde el origen. *El País,* November 22, 1998, sec. 3, 4–5.

Esteban, E., J.M. Dugoujon, N. Valveny et al. 1998. Spanish and African contribution to the genetic pool of the Canary Islanders: Data from *GM* and *KM* haplotypes and RFLPs in the immunoglobulin *IGHG* loci. *Ann. Hum. Genet.* 62:33–45.

Franco, M.H.L.P., T.A. Weimer, and F.M. Salzano. 1982. Blood polymorphisms and racial admixture in two Brazilian populations. *Am. J. Phys. Anthropol.* 58:127–132.

Gardner, L.I., Jr., M.P. Stern, S.M. Haffner et al. 1984. Prevalence of diabetes in Mexican Americans. *Diabetes* 33:86–92.

González, S., G. Tirado, G. Revuelta et al. 1998. *CCR5* chemokine receptor genotype frequencies among Puerto Rican HIV1-seropositive individuals. *Bol. Asoc. Med. Puerto Rico* 90:12–15.

Gottlieb, K. 1983. Genetic demography of Denver, Colorado: Spanish surname as a marker of Mexican ancestry. *Hum. Biol.* 55:227–234.

Guerrero Romero, J.F., M. Rodríguez Morán, F. Sandoval Romero. 1997. Low prevalence of non-insulin-dependent diabetes mellitus in indigenous communities of Durango, Mexico. *Arch. Med. Res.* 28:137–140.

Hanis, C.L., R. Chakraborty, R.E. Ferrell et al. 1986. Individual admixture estimates: Disease associations and risk of diabetes and gallbladder disease among Mexican Americans of Starr County, Texas. *Am. J. Phys. Anthropol.* 70:433–441.

Harb. Z., E. Llop, R. Moreno et al. 1998. Poblaciones costeras chilenas: Marcadores genéticos en cuatro localidades. *Rev. Med. Chile* 126:753–760.

Harris, M. 1964. *Patterns of Race in the Americas.* New York: Walker.

Krieger, H., N.E. Morton, M.P. Miet al. 1965. Racial admixture in northeastern Brazil. *Ann. Hum. Genet.* 29:113–125.

Lisker, R., and V. Babinsky. 1986. Admixture estimates in nine Mexican Indian groups and five East Coast localities. *Rev. Invest. Clin.* 38:145–149.

Lisker, R., E. Ramírez, and V. Babinsky. 1996. Genetic structure of autochthonous populations of Meso-America: Mexico. *Hum. Biol.* 385–404.

Lisker, R., R. Pérez Briceño, J. Granados et al. 1986. Gene frequencies and admixture estimates in Mexico City population. *Am. J. Phys. Anthropol.* 71:203–207.

Lisker, R., R. Pérez Briceño, J. Granados et al. 1988. Gene frequencies and admixture estimates in the state of Puebla, Mexico. *Am. J. Phys. Anthropol.* 76:331–335.

Lisker, R., E. Ramírez, R. Pérez Briceño et al. 1990. Genetic frequencies and admixture estimates in four Mexican urban centers. *Hum. Biol.* 62:791–801.

Livingstone, F.B. 1984. The Duffy blood groups, *vivax* malaria, and malaria selection in human populations: A review. *Hum. Biol.* 56:413–425.

Livingstone, F.B. 1989. Who gave whom hemoglobin S: The use of restriction site haplotype variation for the interpretation of the evolution of the beta S-globin genes. *Am. J. Hum. Biol.* 1:289–302.

Long, J.C. 1991. The genetic structure of admixed populations. *Genetics* 127:417–428.

Long, J.C., R.C. Williams, J.E. McAuley et al. 1991. Genetic variation in Arizona Mexican Americans: Estimation and interpretation of admixture proportions. *Am. J. Phys. Anthropol.* 84:141–157.

López-Camelo, J.S., P.H. Cabello, and M.G. Dutra. 1996. A simple model for the estimation of congenital malformation frequencies in racially mixed populations. *Braz. J. Genet.* 19:659–663.

MacLean, C.J., and P.L. Workman. 1973a. Genetic studies on hybrid populations. I. Individual estimates of ancestry and their relation to quantitative traits. *Ann. Hum. Genet.* 36:341–351.

MacLean, C.J., and P.L. Workman. 1973b. Genetic studies on hybrid populations. II. Estimation of the distribution of ancestry. *Ann. Hum. Genet.* 36:459–465.

Markie, M. 1991. Los que hicieron la Argentina. *Noticias,* September 8, 72–81.

Martínez, C., J.A. Agúndez, M. Olivera et al. 1998. Influence of genetic admixture on polymorphisms of drug-metabolizing enzymes: Analyses of mutations on *NAT2* and C gamma *P2E1* genes in mixed Hispanic population. *Clin. Pharmacol. Ther.* 63:623–628.

McKeigue, P.M. 1998. Mapping genes that underlie ethnic differences in disease risk: Methods for detecting linkage in admixed populations by conditioning on parental admixture. *Am. J. Hum. Genet.* 63:241–251.

Merriwether, D.A., S. Huston, S. Iyengar et al. 1997. Mitochondrial versus nuclear admixture estimates demonstrate a past history of directional mating. *Am. J. Phys. Anthropol.* 102:153–159.

Miquel, J.F., C. Covarrubias, L. Villarroel et al. 1998. Genetic epidemiology of cholesterol cholelithiasis among Chilean Hispanics, Amerindians, and Maoris. *Gastroenterology* 115:937–946.

Morilla, J.M., J.M. Afonso, M. Hernández et al. 1988. Human enzyme polymorphism in the Canary Islands. II. African influence. *Hum. Hered.* 38:101–105.

Morner, M. 1967. *Race Mixture in the History of Latin America.* Boston, MA: Little, Brown.

Murguia, E., and W.P. Frisbie. 1977. Trends in the Mexican American intermarriage: Recent findings in perspective. *Soc. Sci. Q.* 58:374–389.

Ottensooser, F. 1944. Cálculo do grau de mistura racial através dos grupos sangüíneos. *Rev. Bras. Biol.* 4:531–537.

Ottensooser, F. 1962. Analysis of trihybrid populations. *Am. J. Hum. Genet.* 14:278–280.

Passos, G.A., Jr., and V.P. Picanco. 1998. Frequency of the delta ccr5 deletion allele in the urban Brazilian populations. *Immunol. Lett.* 61:205–207.

Pinto, F, A.M. González, M. Hernández et al. 1996. Genetic relationship between the Canary Islanders and the African Spanish ancestors inferred from mitochondrial DNA sequences. *Ann. Hum. Genet.* 60:321–330.

Politizer, W.S., and R.C. Elston. 1973. Racial admixture. In *Physical Anthropology and Its Extending Horizons—S.S. Sarkar Memorial Volume*. A. Basu, A.K. Gosh, and S.K. Biswas, eds. Calcutta, India: Orient Longman, 163–173.

Ramos, A. 1939. *The Negro in Brazil*, R. Pattee, trans. Washington DC: Associated Publishers.

Restrepo, M., W. Rojas, F. Montoya et al. 1988. *HLA* and malaria in four Colombian ethnic groups. *Rev. Inst. Med. Trop. São Paulo* 30:323–331.

Reuter, M.B. 1934. Introduction. In *Race and Culture Contacts*, E.B. Reuter, ed. New York: McGraw-Hill, 1–18.

Ribeiro, D. 1969. *Las Americas y la Civilización*. Buenos Aires: Centro Editor de América Latina.

Rodriguez-Delfin, L., V.E. Rubín-de-Celis, and M.A. Zago. 1998. Estimativa da miscigenação andina do Peru com base em marcadores de DNAmt e cromossomo Y. *Genet. Molec. Biol.* 21(suppl):354.

Rojas Posada, P. 1992. 12 genes negros + 62 genes blancos + 26 genes indígenas = un colombiano. *El Espectador*. September 20, sec. C.

Rosenblat, A. 1954. *La Población Indígena y el Mestizaje en América*, v. 1, *La Población Indígena*. Buenos Aires, Argentina: Editorial Nova.

Rothhammer, F. 1987. Biological history of continental Chile. In *Amerika II: Mittel und Südamerika*, I. Schwidetzky, ed. Munich, Germany: R. Oldenbourg Verlag, 219–236.

Rothhammer, F. 1993. Mestizagción en Chile. In *Resúmenes, XXIV Congreso Argentino de Genética*. Posadas, Argentina: Sociedad Argentina de Genética, 22.

Rout, L.B. 1976. *The African Experience in Spanish America: 1502 to the Present Days*. Cambridge, England: Cambridge University Press.

Ruiz-Reyes, G. 1998. Hemoglobinas anormales y thalassemias en México. *Rev. Invest. Clin.* 50:163–170.

Saldanha, P.H. 1962. Race mixture among northeastern Brazilian populations. *Am. Anthropol.* 64:751–759.

Salzano, F.M. 1985. Incidence, effects, and management of sickle cell disease in Brazil. *Am. J. Pediatr. Hematol. Oncol.* 7:240–244.

Salzano, F.M. 1997. Human races: Myth, invention, or reality? *Interciencia* 22:221–227.

Salzano, F.M., and S.M. Callegari-Jacques. 1988. *South American Indians: A Case Study in Evolution*. Oxford, England: Clarendon Press.

Salzano, F.M., and C.V. Tondo. 1982. Hemoglobin types of Brazilian populations. *Hemoglobin* 6:85–97.

Salzano, F.M., T.A. Weimer, M.H.L.P. Franco et al. 1988. Protein genetic studies on the Tupi-Mondé Indians of the Brazilian Amazonia. *Am. J. Hum. Biol.* 10:711–722.

Sans, M., F. Mañé-Garzón, and R. Kolski. 1986. Presencia de mancha mongólica en recién nacidos de Montevideo. *Arch. Pediatr. Uruguay* 57:149–156.

Sans, M., F.M. Salzano, and R. Kolski. 1991. Utilización de marcadores genéticos para el estudio del mestizaje en la población uruguaya. *Antropol. Biol.* 1:72–85.

Sans, M., F.M. Salzano, and R. Chakraborty. 1997. Historical genetics in Uruguay: Estimates of biological origins and their problems. *Hum. Biol.* 69:161–170.

Sans, M., C. Bonilla, I. Barreto et al. 1999. The hidden contribution: Genetic and demographic evidence of Amerindian admixture in Uruguayan populations. *Am. J. Phys. Anthropol.* 28(suppl.):239.

Sans, M., F. Mañé-Garzón, R. Kolski et al. 1993. Análisis del grado de mestizaje en una muestra de la población de Montevideo, Uruguay. *Bol. Soc. Esp. Antropol. Biol.* 14:43–51.

Sans, M., M. Sosa, I. Alvarez et al. 1993. Blood group frequencies and the question of race admixture in Uruguay. *Interciencia* 18:29–32.

Sans, M., T.A. Weimer, S.C. Franczak et al. 1999. Unequal contributions of male and female gene pools from parental populations in the African descendants of the city of Melo, Uruguay. Unpublished.

Santos, S.E.B., J.F. Guerreiro, F.M. Salzano et al. 1987. Mobility, blood genetic traits, and race mixture in the Amazonian population of Oriximiná. *Rev. Bras. Genet.* 10:745–759.

Santos, S.E.B., F.M. Salzano, M.H.L.P. Franco et al. 1983. Mobility, genetic markers, susceptibility to malaria, and race mixture in Manaus, Brazil. *J. Hum. Evol.* 12:373–381.

Schanfield, M.S., R. Brown, and H.W. Crawford. 1984. Immunoglobulin allotypes in the Black Caribs and Creoles of Belize and St. Vincent. In *Current Developments in Anthropological Genetics*, v. 3, *Black Caribs: A Case Study in Biocultural Adaptation*, M.H. Crawford, ed. New York: Plenum Press, 345–363.

Schneider, H., and F.M. Salzano. 1979. *Gm* allotypes and racial admixture in two Brazilian populations. *Hum. Genet.* 53:101–105.

Schneider, H., J.F. Guerreiro, S.E.B. Santos et al. 1987. Isolate breakdown in Amazonia: The Blacks of the Trombetas River. *Braz. J. Genet.* 10:565–574.

Schüler, L, F.M. Salzano, M.H.L.P. Franco et al. 1982. Demographic and blood genetic characteristics in an Amazonian population. *J. Hum. Evol.* 11:549–558.

Shriver, M.D., M.W. Smith, L. Jin et al. 1997. Ethnic affiliation by use of population-specific DNA markers. *Am. J. Hum. Genet.* 60:957–964.

Stepan, N.L. 1991. *The Hour of Eugenics: Race, Gender, and Nation in Latin America*. Ithaca, NY: Cornell University Press.

Szathmary, E.J.E., and T.E. Reed. 1978. Calculation of the maximum amount of gene admixture in a hybrid population. *Am. J. Phys. Anthropol.* 48:29–33.

Tseng, M., R.C. Williams, K.R. Maurer et al. 1998. Genetic admixture and gallbladder disease in Mexican Americans. *Am. J. Phys. Anthropol.* 106:361–371.

Ubelaker, D.H. 1976. Prehistoric New World population size: Historical review and current appraisal of North American estimates. *Am. J. Phys. Anthropol.* 45:661–666.

Wagley, C. 1968. *The Latin American Tradition: Essays on the Unity and the Diversity of Latin American Culture*. New York: Columbia University Press.

Wagley, C. 1971. The formation of the American people. In *The Ongoing Evolution of Latin American Populations*, F.M. Salzano, ed. Springfield, IL: Charles C Thomas, 19–39.

Weiss, K.M., R.E. Ferrell, C.L. Hanis et al. 1984. Genetics and epidemiology of gallbladder disease in New World native peoples. *Am. J. Hum. Genet.* 36:1259–1278.

Weiss, K.M., H.S. Ulbrecht, P.R. Cavanagh et al. 1989. Diabetes mellitus in American Indians: Characteristics, origins, and preventive health care implications. *Med. Anthropol.* 11:283–304.

Zago, M.A., and F.F. Costa. 1985. Hereditary hemoglobin disorders in Brazil. *Trans. R. Soc. Trop. Med. Hyg.* 79:385–388.