A Preliminary Study of the Population History of the Pima Indians[1]

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THE DISCOVERY THAT a large proportion of the Pima Indians of southern Arizona possess a rare auxiliary cusp (protostylid) on the anterior portion of the buccal surface of the first mandibular molars (Dahlberg, 1950) has made for increased interest in the genetics of the Pima population. The occurrence of this and similar cusps on the second or third mandibular molars is not unusual, but its occurrence on the first molar is extremely rare in modern man. A similar cusp is seen, however, in many of the pre-hominid fossil remains. It has been suggested by Dahlberg (1951) that the appearance of the protostylid in the Pima population is an ativism resulting from the introduction of modifying gene combinations by admixture with other populations. It is thus of interest to assess the relationship of the Pima to other Indian groups in the southwest and to attempt to estimate the extent to which admixture with other populations may have occurred.

The degree of relationship between populations and the amount of admixture between them may be estimated by measurement of the amount of genic exchange between them. The blood group allelic frequencies have been used by many investigators (Boyd, 1939, 1950; Wiener, 1943; Ottensooser, 1944; da Silva, 1948; de Alverez, 1951) as the basis for such estimates for various populations. In the present paper the A-B-O, M-N and Rh allelic frequencies among the Pima Indians are estimated. The A-B-O frequencies of the Pima are compared with those of other Indians of the southwest and of a Caucasoid population to estimate the amount of admixture which may have occurred between various groups during the histories of the present day Indian populations.

BLOOD GROUP FREQUENCIES OF THE PIMA

Blood samples were collected by finger puncture from members of the Pima and Maricopa Indian tribes at Sacaton, Casa Blanca, Salt River and Gila Crossing, Arizona. Several drops of blood were expressed into small tubes which, after labeling, were packed in ice and shipped by air express to Mount Sinai Hospital in Chicago, where serological examination was carried out by

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Dr. I. Davidsohn[2]. All examinations were made within four days after the blood specimens were drawn.

The Pima Indian sample includes eighty-four children of school age and thirteen adults. Most of the adults were selected because of their relationship to children in the sample, for it was hoped that the serological tests would be of value in clarifying familial relationships in the population. Thus the sample is not random, but contains family groups of different size and having different degrees of relationship. Since the same allele may be counted more than once within a family, failure to take into consideration the relationships in a sample may lead to erroneous estimates of the allelic distributions in the population. Cotterman (1947) and Finney (1948a, b) have proposed methods for obtaining efficient estimates of allelic frequencies from family data by weighting each related group according to its degree of relationship. The method proposed by Cotterman is employed in the present paper.

The serological results reported to us by Dr. Davidsohn and arranged according to family size and relationship are given in table 1. If the relationships in the sample are ignored, analysis by the method of Bernstein (1930) gives frequencies as follows:

$Ag^M = .711$
$Ag^N = .289$

$I^{A_1} = .109$
$I^B = .005$
$i = .889$

R^1 (*CDe*) $= .574$
R^2 (*cDE*) $= .337$
R^0 (*cDe*) or.
r (*cde*) $= .009$
R^z (*CDE*) $= .080$
(by difference)

Although the estimates obtained assuming randomness are consistent estimates of the population frequencies, the standard errors would be smaller than if the relationships were considered, and would indicate greater validity of the estimates than is the case.

The calculation of the M-N allelic frequencies by the method of Cotterman and the values obtained are given in table 2. The phenotypic distribution in each family is given a weight which is related to the coefficient of relationship for each group and the frequency of Ag^N is then calculated using the weighted totals. The scored sample of 97 individuals is equivalent to a random sample of 64.09 individuals.

The calculation of the A-B-O frequencies and the values obtained are given in table 3. For the determination of these frequencies the weight assigned to

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each family group is a function both of the coefficient of relationship and of the frequency (q) of the recessive allele i, for it is not possible to distinguish homozygous from heterozygous group A and B individuals in the family. Weights

TABLE 1. DISTRIBUTION OF BLOOD TYPES AMONG FAMILIES OF THE PIMA INDIAN SAMPLE

NUMBER OF			NUMBER OF INDIVIDUALS HAVING BLOOD OF TYPE									
Families	Parents	Sibs	M	MN	N	A_1	B	O	Rh_1Rh_2	Rh_2	$Rh_1hr'-$	Rh_1hr+'
1	2	4	3	3	0	0	0	6	4	1	1	0
1	2	3	0	4	1	0	0	5	3	1	1	0
2	2	1	2	3	1	0	0	6	4	0	2	0
1	1	5	4	2	0	4	0	2	2	0	4	0
1	1	2	0	2	1	3	0	0	2	0	1	0
3	0	4	7	4	1	3	0	9	12	0	0	0
2	0	3	5	1	0	3	0	3	1	0	5	0
10	0	2	10	10	0	1	1	18	12	3	5	0
4	Cousins		1	2	1	1	0	3	2	1	1	0
Unrelated			16	11	2	5	0	24	11	5	12	1
Totals			48	42	7	20	1	76	53	11	32	1

TABLE 2. CALCULATION OF THE FREQUENCY OF THE ALLELE Ag^N IN THE PIMA INDIAN POPULATION FROM FAMILY DATA BY THE METHOD OF COTTERMAN (1947)

NUMBER OF PARENTS	NUMBER OF SIBS	NUMBER OF COUSINS	BLOOD TYPE			WEIGHT (W)	W(b + 2c)	2W(a + b + c)
			M (a)	MN (b)	N (c)			
2	4	0	3	3	0	0.3000	0.9000	3.6000
2	3	0	0	4	1	.3571	2.1426	3.5710
2	1	0	2	3	1	.6000	3.0000	7.2000
1	5	0	4	2	0	.2857	0.5714	3.4284
1	2	0	0	2	1	.5000	2.0000	3.0000
0	4	0	7	4	1	.4000	2.4000	9.6000
0	3	0	5	1	0	.5000	0.5000	6.0000
0	2	0	10	10	0	.6667	6.6670	26.6680
0	0	4	1	2	1	.8889	3.5556	7.1112
Unrelated			16	11	2	1.0000	15.0000	58.0000
Totals			48	42	7	—	36.7366	128.1786

$$q_N = \frac{\Sigma W(b + 2c)}{\Sigma 2W(a+b+c)} = .287 \qquad \text{S.D.} = \sqrt{\frac{(p_M)(q_N)}{\Sigma 2W(a+b+c)}} = .040$$

for q values greater and smaller than the estimated population value are assigned to each family group, and the true population frequency of i is obtained by interpolation from the weighted values. The frequencies of I^{A_1} and I^B may be obtained by applying the same correction factor to determine the proportion of group A and B individuals in the weighted sample. The sample of 97 individuals is, as scored from the determination of the A-B-O frequencies, equivalent to a random sample of 65.25 individuals.

Because of the complexity of the Rh-hr allelic system, it is not possible to obtain frequency estimates by the method of Cotterman unless certain simplifying assumptions may be made. The method may be employed to obtain estimates in the Pima Indian population if it is assumed that the alleles r' (*Cde*), r'' (*cdE*), and r^y (*CdE*) are not found among the Pima. This assumption is justified in part by the fact that these alleles do not appear to have been represented among early (pure) Indians. If the allele r' (*Cde*) is assumed absent in the Pima population the individuals classed serologically as Rh_1 (hr′ −) must have genotype R^1/R^1 (*CDe/CDe*) and the single Rh_1 (hr′ +) individual may

TABLE 3. CALCULATION OF THE FREQUENCY OF THE ALLELE *i* IN THE PIMA INDIAN POPULATION FROM FAMILY DATA BY THE METHOD OF COTTERMAN

NUMBER OF PARENTS	NUMBER OF SIBS	NUMBER OF COUSINS	BLOOD GROUP		a + b = k	WEIGHT (W) at q = .85	WEIGHT (W) at q = .90
			A₁ or B (a)	O (b)			
2	4*	0	0	2	2	1.0000	1.0000
2	3*	0	0	2	2	1.0000	1.0000
2	1*	0	0	4	4	1.0000	1.0000
1	5	0	4	2	6	.2972	.2931
1	2	0	3	0	3	.5175	.5112
0	4	0	3	9	12	.4100	.4064
0	3	0	3	3	6	.5103	.5067
0	2	0	2	18	20	.6758	.6726
0	0	4	1	3	4	.8970	.8941
Unrelated			5	24	29	1.0000	1.0000
Totals			21	67	88	—	—

At q = .85: ΣWb = 52.6599, ΣWk = 65.4215; ΣWb/ΣWk = .8049
At q = .90: ΣWb = 52.5530, ΣWk = 65.2376; ΣWb/ΣWk = .8056

$$q_i^2 = (.85)^2 + [(.90)^2 - (.85)^2] \frac{.8049 - (.85)^2}{[.8049 - (.85)^2] + [(.90)^2 - .8056]} = .8055$$

$$q_i = .898$$

$$\Sigma Wy = 65.4215 - (.1839) \frac{.8049 - (.85)^2}{[.8049 - (.85)^2] + [(.90)^2 - .8056]} = 65.247$$

$$\text{S. D.} = \sqrt{\frac{1 - q^2}{4\Sigma Wy}} = .027$$

* The blood groups of these children are not included, for their inclusion leads to a less efficient estimate of the population frequency.

have genotype R^1/R^0 (*CDe/cDe*) or R^1/r (*CDe/cde*). It is not possible on the basis of this sample to distinguish which of these alleles (R^0 or r) may be responsible for the production of the hr′ antigen in this one individual. The symbol R^0 will be used to designate this allele, but the possibility that r is present in the population is not excluded. The single R^0 represented in the sample might be thought to have been introduced into the population at a comparatively recent time, and thus not be widely represented in the population. However the family history of the Rh_1 (hr′ +) individual gives no indication of recent admixture, so that it is probable that this allele is carried by others in the Indian group. If the allele r'' is not represented among the Pima, those individuals classed serologically as Rh_2 may be of genotypes R^2/R^2 (*cDE/cDE*) or R^2/R^0 (*cDE/cDe*). Since only those individuals classed as Rh_1 (hr′ −) are all homozygotic, only the frequency of the allele R^1 may be determined by the method of Cotterman. The calculation of this frequency is given in table 4. The frequencies of R^2 and R^0 are obtained from the proportions of Rh_2 and Rh_1 (hr′ +) individuals in the weighted sample. The sample of 97 individuals is, as scored for the determination of the Rh frequencies, equivalent to a random sample of 66.86 individuals.

TABLE 4. CALCULATION OF THE FREQUENCY OF THE ALLELE R^1 IN THE PIMA POPULATION FROM FAMILY DATA BY THE METHOD OF COTTERMAN

NUMBER OF PARENTS	NUMBER OF SIBS	NUMBER OF COUSINS	BLOOD TYPE				k	WEIGHT (W) at q = .55	WEIGHT (W) at q = .60
			Rh_1Rh_2 (a)	Rh_2 (b)	Rh_1hr − (c)	Rh_1hr + (d)			
2	4	0	4	1	1	0	6	0.3570	0.3478
2	3	0	3	1	1	0	5	.4229	.4124
2	1	0	4	0	2	0	6	.6788	.6667
1	5	0	2	0	4	0	6	.3316	.3243
1	2	0	2	0	1	0	3	.5688	.5581
0	4	0	12	0	0	0	12	.4382	.4324
0	3	0	1	0	5	0	6	.5391	.5333
0	2	0	12	3	5	0	20	.7006	.6957
0	0	4	2	1	1	0	4	.9185	.9143
Unrelated			11	5	12	1	29	1.0000	1.0000
Totals			53	11	32	1	97	—	—

At q = .55; $\Sigma Wc = 23.1497$, $\Sigma Wk = 67.2043$

At q = .60; $\Sigma Wc = 23.0082$, $\Sigma Wk = 66.7289$

$(q_{R^1})^2 = .3398$, q = .583

$\Sigma Wy = 66.8553$

S. D. = .050

The sum of the estimated frequencies of R^1, R^2 and R^0 is 0.954 rather than unity. This deviation suggests that there may be additional alleles in the population with a frequency of approximately 0.046. In a sample of 67 individuals an allele having this frequency might not be expressed phenotypically. Such an allele could be expressed phenotypically only as Rh_1Rh_2 in the Pima sample. If the alleles R^1 and R^2 are the only alleles present in the population which produce the phenotype Rh_1Rh_2, then this serological type should comprise approximately 42 per cent of the group, or 28 individuals in the weighted sample. Since 34.04 individuals in the weighted sample are of type Rh_1Rh_2, it is probable that more than one genotype is represented in this group. Only R^1/R^2 (*CDe*/*cDE*) and genotypes containing R^z (*CDE*) are capable of producing this serological type. If the distribution of types expected assuming R^z present in the population with a frequency of 0.046 is compared with the calculated distribution of the scored sample, a value of $\chi^2_{(2)} = 0.028$ is obtained. This value indicates a probability of greater than 0.8 that the two distributions are the same. The presence of R^z in this Indian group is in agreement with the results of Wiener, Zapeda, Sonn and Polivka (1945), who reported the presence of R^z in Mexican Indians, and of Ottensooser and Pasqualin (1949) who found R^z in Indian populations in Brazil.

The allelic frequencies obtained by analyzing the Pima sample of 97 individuals by the method of Cotterman are as follows:

$Ag^N = .287 \pm .040$	$i = .898 \pm .027$	R^1 (*CDe*) $= .583 \pm .050$
$Ag^M = .713 \pm .040$	$I^{A_1} = .097 \pm .062$	R^2 (*cDE*) $= .358 \pm .057$
	$I^B = .006$	R^0 (*cDe*) or r (*cde*) $= .013$
		R^z (*CDE*) $= .046$

HISTORY OF THE PIMA INDIANS

The histories of the Indians of the southwestern United States, as determined from archeological and ethnological studies, have been reviewed by Wormington (1947). The Pima Indians are believed to be descended from Indians of the Hohokam culture (*Pima: those who have vanished*) who lived in and near the Salt and Gila River valleys from the early part of the Christian era. Other Hohokam groups that lived in the desert region south of the Gila River are believed to have been ancestral to the Papago Indians now living in the same area. The Hohokam peoples are believed to have been descended from groups of the ancient Cochise culture which disappeared from this general region about 500 A.D. (Haury, 1943).

During the late thirteenth century Pueblo groups, probably originally from northern Arizona, moved into the area occupied by the Hohokam peoples. These groups, known as the Salado, remained in the same area as the River Hohokam for some time. Although in some areas the two peoples lived together in the same 'compounds', both maintained their cultures to a great extent. The Desert Hohokam to the south appear to have had little contact with the Pueblo peoples, for they actively resisted the settlement of their land by the Salado (Haury, 1945). About 1400 A.D. the Salado moved from this area and apparently became dispersed among other populations of the southwest.

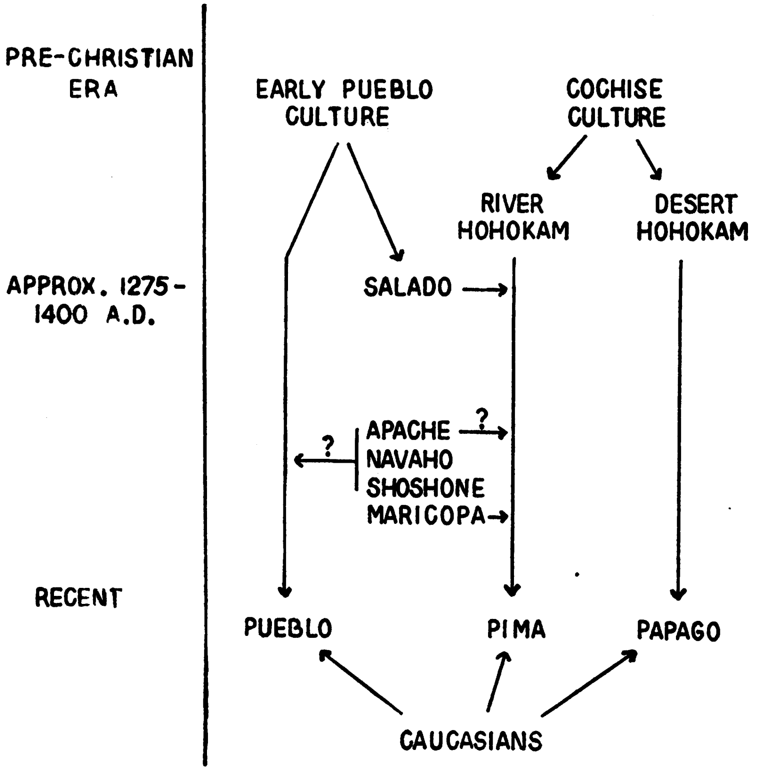

FIG. 1. The historical relationships among Indian populations of Arizona, as based upon archeological studies. Questionable relationships (based upon linguistic similarities and tribal lore) are indicated.

Ethno-archeological studies suggest that the Pima Indians may have a fairly recent biological relationship with the Papago and perhaps with some groups among the Pueblo Indians of the present time, and that the Papago have little or no relationship with the Pueblo Indians. All three Indian groups have probably exchanged genes with Caucasoid groups and with other Indian populations in the southwest. A very general, though incomplete, picture of the history of these Arizona Indians may be examined to estimate relationships among the populations. The relationships are represented graphically in figure 1.

ADMIXTURE DURING THE HISTORY OF THE PIMA

The proportion of admixture of two populations in producing a third may be easily estimated if the A-B-O blood group frequencies of the three populations are known. To estimate the amount of admixture during the history of the Pima, it is necessary to know the frequencies among the Hohokam and Salado. These frequencies must be estimated from examination of the frequencies among the present day descendents of these tribes. To do this, it is necessary to assume that the Salado tribes were a homogeneous population having the same allelic frequencies as the contemporary population from which the present day Pueblo Indians are descended. It is also necessary, because of limited knowledge of the allelic frequencies among different Indian populations, to disregard the immigration of other Indians into the Pima, Papago and Pueblo groups.

TABLE 5. THE A-B-O BLOOD GROUP FREQUENCIES OF INDIAN TRIBES OF THE SOUTHWESTERN UNITED STATES AND OF A REPRESENTATIVE CAUCASOID POPULATION

POPULATION	REPORTED BY	SIZE OF SAMPLE	ALLELIC FREQUENCIES		
			I^A	I^B	i
Papago	Breazeale et al. (1947)	600	.031	0	.969
Pueblo	Boyd (1950)	310	.105	.007	.888
Pima	Present study	65	.097	.005	.898
Spaniards	de Hoyos Sainz (1947)	50,791	.305	.076	.618

The A-B-O blood group frequencies among 600 Papago Indians have been reported by Breazeale, Greene and Kantor (1941) and among 310 Pueblo Indians by Boyd (1950). The frequencies in the Pima, Papago and Pueblo Indians and in a Caucasoid population are given in table 5. The Spanish population reported by de Hoyos Sainz (1947) has been chosen because the Caucasoid population of the southwestern United States has been predominantly Spanish until fairly recently. Boyd (1939) has noted that the blood group allelic frequencies of western European populations do not differ strikingly, and that in calculating the amount of admixture of Caucasians with Indian populations, substitution of one European group for another will not materially alter the results obtained. Breazeale et al. and Boyd have not distinguished the subgroups of A in their analyses of the Indian populations. It will be assumed for our purposes that all of the reported group A individuals are of sub-group A_1.

Let U, W and Y represent the percentage contribution of the Caucasoid population to the Pueblo, Pima and Papago Indians respectively, S and Z the contributions of the Hohokam to the Pima and Papago Indians and T and V

the contributions of the Salado to the Pima and Pueblo Indians. Then $Y + Z = 1$, $U + V = 1$ and $W + S + T = 1$. The unknown blood group frequencies of the Hohokam and Salado groups and the percentage contribution of each population to the Pima, Papago and Pueblo populations may be estimated from formulae of the following form:

$$\begin{array}{l} W(p_C) + S(p_H) + T(p_S) = p_P \\ Y(q_C) + Z(q_H) = q_{Pa} \\ U(r_C) + V(r_S) = r_{Pu} \end{array}$$

p, q and r being respectively the frequencies of the alleles I^{A_1}, I^B and i and the subscript symbols indicating the population in which this frequency is found as follows: C = Caucasoid, H = Hohokam, S = Salado, P = Pima, Pa = Papago and Pu = Pueblo.

Since no group B or AB individuals are found among the Papago, the frequency of these phenotypes in the population is less than 1/600 (.00167). The frequency of I^B among the Papago is then less than .001, which suggests (1) that the proportion of admixture with Caucasians has been low and (2) that I^B may not have been represented among the Hohokam. Since the allele I^B is believed to have been absent among Indians before admixture with other groups (Wiener, 1943; Boyd, 1950) we will assume that I^B did not occur among either the Hohokam or Salado Indians. If this is assumed, then by substitution into the equations the following values are obtained:

$$\begin{array}{llll} Y \leq .011 & p_H = .028 & U = .092 & p_S = .085 \\ Z \geq .989 & q_H = 0 & V = .908 & q_S = 0 \\ & r_H = .973 & & r_S = .915 \end{array}$$

The Salado and Hohokam frequencies may be substituted into equations for the determination of W, S and T. The value $W = .066$ is obtained either by solution of the equation in q or by the simultaneous solution of the equations in r and p and the equation $W + S + T$ = unity. Substitution of this value of W into the equations in r and p gives values of $S = .042$ and $T = .892$ when the equations are solved simultaneously.

Although these values of W, S and T give consistent results when substituted in the equations for p_P, q_P and r_P, they are not consistent with the hypothesis that the Pima are more closely related to the Papago than to the Pueblo Indians. If the interpretation of the cultural evidence is correct, then we should expect S to be greater than T. If the interpretation is taken to be correct, then the only alternative hypothesis is that other Indian populations, which were not taken into account in this analysis, contributed materially to the genic make-up of the present day Pima and Pueblo populations. Although the identity of these contributors may be suspect, it is not possible, because of lack of knowledge of their allelic frequencies, to determine the amount of admixture which may have taken place with the Pima and Pueblo populations.

The earliest recorded contact of the Pima with Caucasians occurred in 1530. Thus genic exchange between the two groups may have been taking place over a period of four centuries. The Salado Indians are believed to have dwelt among the Hohokam for a little over 100 years. Thus if there have been no cultural or racial factors affecting the rate of admixture, T should be approximately $W/4$. It may be argued that the proximity of the Salado and Hohokam peoples during the fourteenth century might lead to a greater proportion of admixture between them than between the Pima and Caucasoid populations. It is also possible that social barriers to admixture existed in these extinct groups, for both maintained their ways of life during the period. If it is assumed that $T = .25\ W$ (approximately), it is then possible to estimate the allelic frequencies of the population, or group of populations, which have contributed to the Pima. The values of p and r which are obtained, assuming that the rate of Hohokam-Salado genic exchange was from ½ to 2 times as great as the rate of Pima-Caucasian exchange, are similar, and indicate that the unaccounted-for population has a frequency of I^A greater (greater than .13) and a frequency of i somewhat smaller (less than .87) than the Pima population studied. From 35 to 45 per cent of the allelic distribution in the Pima population may have resulted from admixture with this population, from 47 to 57 per cent may be derived from the Hohokam, approximately 1 to 3 per cent from the Salado, and the remainder, totaling approximately 6 to 7 per cent, from Caucasoid groups.

It is hoped that further study of the blood group frequencies, as well as of other population characteristics, will clarify the relationships among the tribes of this area and make possible conclusions regarding the source of genetically determined traits among the Pima.

SUMMARY

1. A-B-O, M-N and Rh blood group allelic frequencies have been estimated in a sample of 97 Pima Indians from southern Arizona.

2. The frequencies estimated by the method of Cotterman (1947) are as follows:

$$\begin{array}{lll}
Ag^M = .713 \pm .040 & I^{A_1} = .097 \pm .062 & R^1\ (CDe) = .583 \pm .050 \\
Ag^N = .287 \pm .040 & I^B = .006 & R^2\ (cDE) = .358 \pm .057 \\
 & i = .898 \pm .027 & R^0\ (cDe) \text{ or} \\
 & & r\ (cde) = .013 \\
 & & R^z\ (CDE) = .046
\end{array}$$

3. The population histories of the Indians of the southwestern United States, as determined by archeological and ethnological studies, are presented briefly.

The relationship of the Pima to other Indians of the area has been studied by comparing the A-B-O allelic frequencies of these groups to estimate the amounts of admixture occurring during the population histories of the Indians.

4. The allelic distribution of the Papago Indian population is estimated to be derived largely from their assumed Hohokam ancestors (approximately 99 per cent) and in small part by admixture with Caucasoid populations (approximately 1 per cent).

5. Approximately 91 per cent of the distribution among the Pueblo Indian population is derived from extinct Pueblo groups contemporary with the Salado Indians of the early fourteenth century A.D. The remaining 9 per cent of the distribution is the result of admixture with Caucasoid populations.

6. From 47 to 57 per cent of the distribution in the Pima Indian population may be derived from their Hohokam ancestors. Approximately 1 to 3 per cent may be the result of admixture of the Salado Indians with the Hohokam of the Gila and Salt River valleys and approximately 6 to 7 per cent the result of admixture of Caucasoid populations with the Pima. From 35 to 45 per cent of the allelic distribution in the Pima population may have resulted from admixture with another, or other Indian populations of the area having a frequency of I^{A_1} greater and a frequency of i smaller than the present day Pima population. The identity of this group is not known.

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