The Immunoglobulin Allotypes (Gm and Km) of Twelve Indian Tribes of Central and South America

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ABSTRACT   The Gm and Km immunoglobulin allotypes are presented, for the first time, for six South American Indian tribes (Baniwa, Kanamari, Kraho, Makiritare, Panoa, and Ticuna) and one Central American tribe (Guaymi). Additional allotype information is presented for five previously reported South American tribes (Cayapo, Piaroa, Trio, Xavante and Yanomama). The distributions of the Gm and Km allotypes among all the tribal populations tested to date are reviewed and evidence is presented for the presence of a north(high)-south(low) cline in *Km* frequency. The wave theory of the populating of the South American continent was tested by an examination of the distribution of six alleles ($Gm^{ax;g}$, $Gm^{a;b0,3,t}$, Di^a, R^z, TF^D Chi, and $6PGD^C$), absent in some populations but with polymorphic proportions in others. The present, limited, data failed to confirm the theory.

For some years we have been interested in the usefulness of the genetic approach in unraveling the biological relationships of Amerindian tribes. To this end, typings with respect to 12 genetic systems regularly characterized by genetic polymorphisms have been performed. Thus far our data for only five tribes, Ayoreo (Salzano et al., '77), Cayapo (Salzano et al., '73), Macushi and Wapishana (Neel et al., '77) and Xavante (Shreffler and Steinberg, '67) have been presented with respect to two of these systems, involving the gamma globulin allotypes, Gm and Inv (hereafter referred to as Km). This paper reports typings for additional specificities on the same Xavante specimens, on an enlarged number of Cayapo specimens, and on newly collected samples from the Piaroa, Trio and Yanomama. Immunoglobulin allotypes have been reported previously for the last three tribes; Trio, by Geerdink et al. ('74) and both Piaroa and Yanomama (Waica), by Gallango and Arends ('65a,b). In addition, we report on the results of typing 3,671 persons from seven new tribes with respect to these systems. In all, we present here the results of immunoglobulin allotype studies on 9,037 South American Indians. We will also review the present state of knowledge concerning Gm and Km types in the Amerindians of South America and will discuss the implications of the finding in the Gm system and other of our findings for the manner of origin of Amerindian tribes.

METHODS

Test procedures

The 3-drop inhibition test described by Borel et al. ('67) was used except that all dilutions were performed in saline and that the results were read after the plates were centrifuged for ten seconds at 2,000 rpm. When the study was initiated, all sera were routinely diluted 1/30 in saline for testing and those exhibiting saline agglutination were then retested after being heated at 70°C for ten minutes. The frequency of the finding of saline agglutination was so high, however, that after the first several hundred determinations, all sera were routinely heated at 70°C for ten minutes and then tested at 1/10 dilution. The change from a 1/30 to a 1/10 dilution was found to be necessary because the heat treatment caused a weakening of some of the "b complex" specificities.

All sera were tested for G1m(a, x and f) and G3m (g and b0). Sera positive for G3m (b0) were then tested for the G3m specificities (b1) and (b3) and, in some cases (c3) and (t).

TABLE 1

Test combinations used in Gm and Km typing

Specificity		Anti-allotype	Anti-Rh coat[**]
Alphameric	Numeric		
G1m a	1	Hel	Har, Spr
x	2	Gey	Har, Pet [1]
f	3	Dul	Sta
G3m g	21	Gha	Bar, Qua
		R146[*]	Bar
b0	11	R163[*]	Sut
		15783	Sut
b[1]	5	Ble	Sut
b[3]	13	Log	Sut
t	16	Ros	Puhr,[2] Vai,[3] 3068 [4]
c[3]	6	Eil [1]	Ada [2]
Km 1	Inv 1	Les[*]	Abr, Dul
		Sim [2]	Abr
3	3	Nee [1]	Abr

* Most used in screening.
** The first anti-Rh listed is, in each case, the one most often used for screening.
[1] Avid, Inc.
[2] Courtesy of Dr. M. S. Schanfield.
[3] Courtesy of Dr. L. Martensson.
[4] Courtesy of Dr. E. van Loghem.

TABLE 2

Number of individuals tested for the various Gm and Km specificities

Tribe	Gm						Km	
	a,x,f,g	b0	b1	b3	t	c3	1	3
Ayoreo*	256			1	53	—	255	102
Baniwa	377					—	377	
Cayapo*	925	915	497	5	4	—	916	
Guaymi	486				—	—	486	
Kanamari	100					—	100	
Kraho	192		6	6	6	6	192	
Macushi*	507		203	89	200	15	507	
Makiritare	718	710		413	406	—	715	404
Panoa	335					8	335	
Piaroa	146					—	146	
Ticuna	1,763					9	1,763	
Trio	95					2	95	
Wapishana*	619		151	89	149	89	619	
Xavante*	453		392	335	451	392	440	431
Yanomama	3,447	3,165	3,261		1,373**	150 +	3,447	45

Note: for all but the first columns of each system, only *changes* from entries in the first column are listed. A dash (—) indicates none tested.
*The information in this table was not presented in the original reports on these tribes.
**All the individuals in 22 villages.
· Randomly selected individuals in each of 30 villages.

Test reagents

All tests were performed with reagents listed in table 1. The table indicates the two systems of nomenclature; we have chosen to use the alphabetic system which is essentially the alphanumeric without the IgG subclass designation. All the human allotype sera (except R(abbit) sera) were SNaggs (i.e., derived from non-immunized humans); even the anti-G3m(g) Gha, although obtained from a patient with rheumatoid arthritis, did not exhibit a prozone and serum Gha did not contain G3m(g), thus testifying that the antibody was not autoimmune in origin. Unless otherwise indicated in the table, all reagents were produced in this laboratory. The number of individuals tested for the various specificities

TABLE 3

*The Km phenotypes and Km[1] gene frequencies among one Central American
and 11 South American Indian tribes*

Tribe	No. of villages	Km phenotypes							Ref.
		N	1+3−	1+3+	1−3+	1+	1−	Km[1]	
Baniwa	1*	377	52	194	131			0.395	This paper
Cayapo [1]	5	916	140	442	334			0.394	Salzano et al., '77
Guaymi	4	486	142	245	99			0.544	Tanis et al., '77
Kanamari	1	100	12	52	36			0.380	This paper
Kraho	2	192	28	86	78			0.370	Salzano et al., '77
Makiritare	13**	715	135	190	79	260	51	0.574 [3]	Gershowitz et al., '70
Panoa	4	335	50	176	109			0.412	This paper
Piaroa	1	146	120	26	—			0.911	Tanis et al., '73
Ticuna	6	1,763	462	905	396			0.519	This paper
Trio	1	95	15	53	27			0.437	Salzano et al., '74
Xavante [2]	3	431	77	240	114			0.457	Neel et al., '64 Salzano et al., '67
Yanomama	50	3,447	8	28	9	2,115	1,287	0.387	Ward, '72

*The inhabitants of several villages included in this sample.
**A "miscellaneous" group, constituted by pooling several very small village samples, is included.
[1] This report includes most of the specimens previously reported by Salzano et al., '73.
[2] This report includes all the specimens previously reported by Shreffler and Steinberg, '67.
[3] Km[1] calculated from all data, using the two phenotypes Km (1+) and Km (1−).

are indicated in table 2. Note that only very few of the Yanomama have been typed with anti-Km(3).

Genes and gene frequencies

The notation of phenotypes and haplotypes is according to the recommendation made by the W.H.O. Committee on Immunoglobulin Allotypes ('76).

Throughout this paper, we will refer to the $G1m^{a,z}$ gene as $G1m^a$ because typings have not been performed with anti-Gm(z). Similarly, our designation $G3m^{b0,3,t}$ of the Mongoloid gene, $G3m^{b0,3,s,t}$, omits the G3m(s) specificity because typings for that specificity were not performed.

Km gene frequencies were calculated by gene counting for all tribes except the Yanomama where Km^1 was calculated by the square root method. Gm haplotype frequencies were derived from the MAXLIK computer program of Reed and Schull ('68).

The tribes

The tribes for which we are presenting data are listed alphabetically in table 3, and the approximate center of each tribe's distribution shown in figure 1. Table 3 also lists the references to the locations at which the samples were collected, and the circumstances of collections. However, with respect to four of these tribes (Baniwa, Kanamari, Panoa, and Ticuna), there is as yet no primary publication

from this laboratory because of the recency of the collections. Minimal information concerning these tribes is as follows; more extended accounts will be provided later; *Baniwa* — a tribe of some 1,500 Arawak-speakers largely distributed in proximity to the Icana River, a right bank tributary to the upper Rio Negro, in the northwest of Amazonas State, Brazil; *Kanamari* — a tribe of some 800 persons speaking an isolated language, situated near the upper Jurua River, in the southwest of Amazonas State, Brazil; *Central Panoa* — a tribe of some 18,000 Panoan-speakers widely scattered throughout southwestern Amazonas State and Acre State of Brazil and northeastern Peru, in groups with many local designations (the present samples were all collected in Brazil); *Ticuna* — a tribe of perhaps as many as 15,000 persons speaking an isolated language, on both sides of the Amazon River from the mouth of the Icá River in Brazil upriver to the lower portion of the Peruvian Amazon. All our collections were in Brazil.

The tribes were in general selected for study because of prior evidence for minimal admixture with Caucasians or Negroes. As we shall see, the Gm groups provide important evidence concerning the nature and amount of whatever admixture has occurred. No tribe estimated to have more than 5% admixture with non-Indians is included in this study.

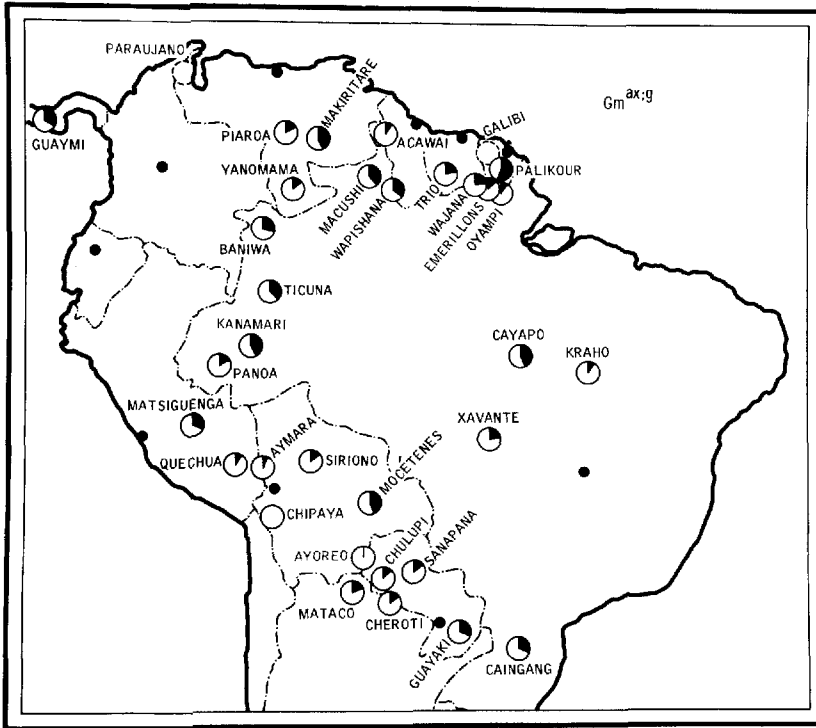The unit of sampling has been the tribal

Fig. 1 $Gm^{ax;g}$ haplotype frequencies in South American Indian tribes. ● = capital cities.

village, within which samples have been obtained from as many persons as possible. There is thus the material for determining the familial nature of genetic variants where encountered. On the other hand, the number of independent genomes is far below the sample size. In our opinion, given the high level of inbreeding in Indian villages (Spielman et al., '77) it is not feasible to select from the total sample a sub-sample of unrelated persons on whom to base estimates of allele frequencies. The use of "total village populations" as opposed to "samples" has been discussed by Neel et al ('64) and by Giles et al. ('66).

RESULTS

Km allotypes

Km allotypes and gene frequencies by tribe are given in table 3. Our studies of Indian populations have resulted in the typing of the inhabitants of 108 discrete villages; 91 are reported here, 3 each among the Ayoreo and Macushi and 11 among the Wapishana having been previously reported. For the purpose of this report, all the members of each tribe were pooled to establish tribal gene frequencies.

The Km^1 gene seems to be maintained at moderate frequencies, 0.3 to 0.6, among most South American Indian tribes. Only the Piaroa deviate significantly from this range, the frequency of 0.91 in that tribe being the highest reported for any population.

Gm groups

Phenotype and haplotype frequencies

The Gm phenotypes determined for 9,037 specimens are reported in table 4 and the haplotype frequencies established for the twelve tribes in table 5. For the purpose of exactness of reporting, the footnote to table 4 records that 8 Makiritare, 282 Yanomama and 10 Cayapo were not tested for G3m(b0). Thus, for these three tribes, although $Gm^{a;b0,3,t}$ haplotype may have existed and not have been detected among these relatively few individuals, they were, in view of the failure to detect any other evidence for the existence of that haplotype, scored as negative for G3m(b0).

Table 5 illustrates the previously recognized phenomenon (e.g., Johnson et al., '77) that the two haplotypes $Gm^{a;g}$ and $Gm^{ax;g}$ are exceedingly common among South American

Indians, accounting together for close to 99% of all the haplotypes present.

The $Gm^{a;b0,3,t}$ haplotype which occurs in Chinese, Japanese, Thais, and other Mongoloid groups in frequencies ranging from 0.003 to 0.27 (cf. Johnson et al., '77) is found in 4 of the 12 tribes. However, in two of these tribes (Kraho and Ticuna) it is very rare and presumably introduced by intertribal admixture, leaving two tribes in which it may safely be presumed the allele has been present since ancient times. This series certainly presents the largest screening of South American Indians for which the frequency of this haplotype can be confidently assessed.

We should note the detection of a single individual among the Guaymi with the unusual phenotype Gm(a,f; g). The serum of this individual was devoid of any b0, b1, b3, c3 or t activity, all members of the "b" complex. In the absence of family information, we cannot determine whether this unusual phenotype is due to the $G1m^{a,f}$ gene, suspected in some Asiatic populations (Schanfield, '71) or to a $gm^{f;g}$ haplotype as proposed in some family studies by van Loghem ('71). The mechanisms by which aberrant haplotypes may be produced have been discussed by, among others, van Loghem and Natvig ('70), Schanfield ('71 and Lefranc et al. ('77).

Evidence for admixture

In addition to the four Gm haplotypes mentioned in the preceding section, there is evidence for three other haplotypes. Since these other haplotypes are common in Caucasian and Negro populations but absent from Indian populations in which the ABO and Kell groups fail to provide independent evidence of admixture, we will presume the presence of these alleles indicates admixture.

The three other haplotypes are racially distinctive markers; $Gm^{f;b}$, found in all Caucasian populations, is generally absent from Amerindian and Negro populations which do not give independent evidence of admixture, and the two $Gm^{a;b}$ haplotypes, found in all African Negro populations, are generally absent from unadmixed Amerindian and Caucasian populations. We will refer to $Gm^{a;b}$ as the Negro racial marker; it is not relevant for the detection or calculation of admixture that the $Gm^{a;b}$ haplotype actually subsumes within it several different $Gm^{a;b}$ haplotypes differentiated by the presence or absence of members of the "b-complex" of specificities (Schanfield,

TABLE 4

The distribution of Gm phenotypes among one Central American and 11 South American Indian tribes

Phenotype G1m / G3m → Tribe	a / g	ax / g	a / g,b0,1,3	ax / g,b0,1,3	a / g,b0,3,t	ax / g,b0,3,t	a / g,b0,3,c3	ax / g,b0,1,c3	a,f / g,b0,1,3	ax,f / g,b0,1,3	a / b0,3,t	a / b0,1,3,c3,t	a,f / g	Total
Baniwa	178	163	1		22	14			11					377
Cayapo [1]	323	600							4					925
Guaymi	218	252	6	2						3			1	486
Kanamari	31	69												100
Kraho	145	41						1		4				192
Makiritare	228	486		1			3		1			1		718
Panoa	209	124			3		1							335
Piaroa	90	56			3									146
Ticuna	726	1,005	3	3		1	1		16	6	1	1		1,763
Trio	51	38												95
Xavante [2]	262	190							1					453
Yanomama	2,507	940												3,447
														9,037

Note: The following non-b types were not tested for G3m(b0):

	a;g	ax;g
Cayapo	8	2
Makiritare	4	4
Yanomama	198	84

[1] This report includes retests of most of the specimens previously reported by Salzano and Steinberg, '73.

[2] This report includes retests of most of the same specimens previously reported by Shreffler and Steinberg, '67.

TABLE 5

Gm haplotype frequencies in one Central American and 11 South American Indian tribes

Tribe	a;g	ax;g	a;b0,3,t	Gm Haplotypes a;b0,1,3	a;b0,1,c3	f;b	f·*
Baniwa	0.682	0.270	0.048				
Cayapo	0.592	0.407		0.0005		0.0005	
Guaymi	0.670	0.314		0.008		0.007	0.001
Kanamari	0.557	0.443					
Kraho	0.868	0.116	0.003		0.010	0.003	
Makiritare	0.562	0.435				0.003	
Panoa	0.789	0.208		0.001	0.002		
Piaroa	0.785	0.215					
Ticuna	0.642	0.349	0.001	0.002		0.006	
Trio	0.732	0.225	0.032		0.011		
Xavante	0.761	0.238				0.001	
Yanomama	0.852	0.148					

*Gm^f in this haplotype is not associated with Gm^b. Its association with either Gm^a or Gm^g is unknown here.

'76). $Gm^{f;b}$ has a frequency averaging 0.7 for most Caucasian populations and $Gm^{a;b}$ is usually greater than 0.95 in African Negro populations (Johnson et al., '77). These two markers, then, readily permit the calculation of admixture of these tribes with Caucasians and Negroes (cf. Bernstein, '31). By this approach none of these 12 tribes has experienced more than 5% admixture. However, the considerable error inherent in these estimates is illustrated by a consideration of the familial distribution of these "marker alleles." Thus, for example, in the Macushi, four Gm (ax,f;b,g) were sibs in the Wapishana, three of nine Gm (a,f;b,g) were a mother and her two children. The number of persons contributing "outside" genes to the gene pool is thus probably relatively small, again illustrating the problem in applying a number of standard statistics to data of this type.

DISCUSSION

1. The distribution of Gm haplotypes in South American Indians

Table 6 presents a summary of all the available data on Gm haplotypes in South American Indians. Several points about the table merit explanation.

(a) Among the total of 15 tribes on which we have reported in this and previous papers, similar studies have been carried out by others on seven. For four of the seven, Makiritare, Piaroa, Wapishana and Yanomama, our villages of collection overlap with those of other investigators. Since the present data are more numerous and/or based on a more exten-

sive battery of typing antisera, we do not include their data in the table. For the remaining three of these seven, Ayoreo, Macushi and Trio, the description of the place of collection makes it clear there should be little or no overlap, and we have combined these results with our own.

(b) There are data in the literature on 19 other tribes for whom the sample number is greater than 50, and these are included in the table. However, on the basis of insufficient sample size to provide a satisfactory picture of the tribal frequency, we exclude from the tabulation the 34 Guarani of Brazil reported by Salzano and Steinberg ('65) and the 42 Toba, the 45 Lengua, the 14 Guarayu, and 19 Tapiete, all of Paraguay, reported by Brown et al. ('74).

Section A of table 6 presents the $Gm^{a;g}$, $Gm^{ax;g}$ and $Gm^{a;b0,3,t}$ haplotype frequencies for the 34 tribes included in the table. Section B presents data on the occurrence of the Gm haplotypes of Caucasian or Negroid origin. As noted earlier, the $Gm^{f;b}$ haplotype is a marker of Caucasian ancestry and the $Gm^{a;b}$ of Negro ancestry. Since neither anti-Glm(f) nor anti-G3m(g) were available for the studies of the Caingang, Galibi, Mocétènes, or Palikour, the total Gm^b frequency as given in the table represents *total* admixture, both Caucasian and Negro. Two of the 19 tribes studied by other investigators (the Paraujana of Venezuela and the Galibi of French Guiana) show evidence of non-Indian admixture in excess of 5%. The locations and the $Gm^{ax;g}$ frequencies of all 34 tribes (15 reported by us and 19 reported by

TABLE 6

Gm-haplotype and Km-gene frequencies in South American Indians

Tribe	N	A.			B.		C.	References (see key footnoted)
		a;g	a,x;g	a;b0,3,t	f;b	a;b	Km^1	
Acawai	84	0.82	0.12	n.t.	n.t.	n.t.	n.t.	1.
Aymara	283	0.91	0.05	0.004	0.029	0.002	0.35(281)	1. Insuf. data in 3 and 4.
Ayoreo $^+$ (Moro)	322	0.99	0.002	0	0.002	0(251)	0.38	A,C = 5 + 6. B = 6
Baniwa	377	0.68	0.27	0.05	0	0	0.39	7.
Caingang	110	0.71	0.27	n.t.	(Gm^b = 0.02)		n.t.	8. Aweikoma included.
Cayapo	941	0.59	0.41	0*	0.001	0.001	0.39(916)	7. Includes samples of 2, 5 and 9.
Cheroti	167	0.81	0.19	$^+$	0	0	0.29(161)	2 + 5.
Chipaya	196	1.00	0	0	0	0	0.60	2.
Chulupi	121	0.84	0.16	$^+$	0	0	0.20	5.
Emerillons	78	0.64	0.17	0.16	0	0.03 (38)	n.t.	A = 10 + 11. B = 11.
Galibi	191	0.64	0.30	n.t.	(Gm^b = 0.06)		n.t.	11. Frequencies reported were incorrect.
Guayaki	61	0.69	0.31	$^+$	0	0	0.14	5.
Guami	486	0.67	0.31	0	0.007	0.008	0.54	7.
Kanamari	100	0.56	0.44	0	0	0	0.38	7.
Kraho	192	0.87	0.12	0.003	0.003	0.010	0.37	7.
Macushi	623	0.58	0.38	0.022	0.014	0(507)	0.50(507)	A = 1 + 12. B,C = 12.
Makiritare	718	0.67	0.43	0	0.003	0	0.57(715)	7. Specimens from same area as reported in 1 and 13.
Mataco	196	0.79	0.20	0	0.013	0	0.38(118)	2.
Matsiguenga	205	0.71	0.28	0	0.01	0	0.51	2.
Mocétènes	76	0.52	0.47	0	(Gm^b = 0.007)		n.t.	4.
Oyampi	195	0.78	0.16	0.061	0	0	0.61(99)	A,B = 10 + 11. C = 10.
Palikour	75	0.44	0.53	n.t.	(Gm^b = 0.03)		n.t.	11.
Panoa	335	0.79	0.21	0	0	0.003	0.41	7.
Paraujano	114	0.51	0.17	n.t.	(non-a = 0.32) n.t.		0.35(112)	A,B = 13. C = 14, 15.
Piaroa	146	0.79	0.21	0	0	0	0.91	7. Specimens from same village as reported in 14 and 15.
Quechua	759	0.87	0.08	0.012	0.030	0.005	0.32(364)	2.
Sanapana	97	0.84	0.16	$^+$	0	0	0.59	5.
Siriono	110	0.83	0.16	0	0.005	0	0.15	2.
Ticuna	1,763	0.64	0.35	0.001	0.006	0.002	0.52	7.
Trio (Tiriyo)	471	0.73	0.23	0.34	0	0.002	0.41	7 + 16.
Wajana (Wayana Oyana)	357	0.74	0.24	0.018	0	0	0.35	10 + 16. Data in 11 insufficient.
Wapishana	619	0.57	0.34	0.049	0.017	0.020	0.46	12. Specimens from same area as reported in 1.
Xavante	453	0.76	0.24	0	0.001	0	0.46(431)	7. Retests of same specimens reported in 17.
Yanomama	3,401	0.85	0.15	0	0	0	0.38(3,402)	7. Specimens from same area as reported in 13, 14 and 15.

*Salzano et al., (9) report one Gm (a;b0,3) individual among the Txukahame Cayapo. We did not detect this type among our retests.
$^+$ Johnson et al. ('77) report Gm (a;b0,3) frequency among "pooled" Paraguayans, originally reported by Brown et al. (5), of 0.024.

Key to references

1. Gallango and Arends, '64
2. Quilici, '75
3. Carles-Trochain, '68
4. Ruffie et al., '66
5. Brown et al., '74
6. Salzano et al., '77
7. This paper
8. Salzano and Steinberg, '65
9. Salzano et al., '73
10. Daveau et al., '75
11. Fernet et al., '64
12. Neel et al., '77
13. Gallango and Arends, '63
14. Gallango and Arends, '65a
15. Gallango and Arends, '65b
16. Geerdink et al., '74
17. Shreffler and Steinberg, '67

others) are shown in figure 1, but the two admixed tribes (Paraujano and Galibi) are indicated by broken circles in the figure.

Reference citations for the table are appended to the table. Where pertinent, citations are given for individual sections of the table. The presence of a plus (+) sign between references indicates that the data in the section were derived by pooling the data of the indicated references.

As has been noted previously only two Gm haplotypes, $Gm^{a;g}$ and $Gm^{ax;g}$, are common in South American Indians. Although considerable variation is found in the frequencies of the two genes, the frequency of $Gm^{ax;g}$ exceeds $Gm^{a;g}$ in only one tribe, the Palikour of French Guiana. $Gm^{ax;g}$ is totally absent from the Chipaya and while a single Gm (ax) person, presumably Gm (ax;g), was reported among 71 Ayoreo by Brown et al. ('74), we found none among 251. One can conclude that $Gm^{a;g}$ has been fixed among the Chipaya and Ayoreo, both of Bolivia. It is noteworthy that other tribes in this region (Bolivia) have low frequencies of $Gm^{ax;g}$; they are the Aymara, also of Bolivia, and the Quechua, on both sides of Lake Titicaca. In fact, inspection of figure 1 reveals that a region of comparatively low levels of $Gm^{ax;g}$ extends from Southeast Peru to Northwest Paraguay. Other widely separated tribes may however, also be characterized by low levels of $Gm^{ax;g}$, e.g. the Kraho of Brazil, (0.12), the Yanomama of Venezuela-Brazil (0.15), and the Acawai of British Guiana (0.12).

Two Gm haplotypes ($Gm^{a,f;b}$ and $Gm^{a;b0,3,t}$) are known to be restricted to the Mongoloid peoples. We have not observed the $Gm^{a,f;b}$ haplotype in these studies of South American Indians. Johnson et al. ('77) state that the haplotype is found in Brazil and Bolivia. An examination of the alleged finding in Brazil (Salzano and Steinberg, '65) reveals only the presence of the phenotype Gm(a;b), in a population where Gm(f) was not tested; 36 of the Gm(a;b) were among known Mestizos and seven were among supposedly pure Indians. The finding of two individuals (both Mestizos) with the phenotype Gm(a − b +) certainly suggests the presence of $Gm^{f;b}$ in this admittedly admixed population; it is most probable that the Gm(a;b) phenotypes are in reality Gm (a,f;b,g), Caucasian admixed, if not Gm (a;b,g), Negro admixed. We have not been able to examine the report (Carles-Trochain, '68)

cited by Johnson et al. ('77) as evidence for the existence of $Gm^{a,f;b}$ among the Aymara of Bolivia. Since Quilici ('75) found no evidence that $Gm^{a,f;b}$ exists among any of the 283 Aymara, we conclude that this haplotype is also absent from unmixed South American Indians. This haplotype is also absent from the peoples of Northern Asia (Schanfield and Gershowitz, '73), a finding supportive of the hypothesis of a commonality of origin of the Amerindian and the Mongoloid inhabitants of northwestern Siberia.

The other "Mongoloid" haplotype, $Gm^{a;b0,3,t}$, reaches polymorphic proportions (>0.01) in eight of the 25 tribes for whom data are available, is found in lesser frequency in only three others, and has not been found in 14. Of the eight tribes characterized by significant frequencies of this Mongoloid marker, seven are found in the northeastern part of the continent (Baniwa, Macushi, Wapishana, Trio, Wajana, Emerillons and Oyampi). The presence of the haplotype in the Macushi may well be due to admixture with the Wapishana. We note, too, that the Emerillons, with the highest frequency of this haplotype are in close contact with the Trio, Wajana, and Oyampi, who also have high frequencies. The remaining tribe with a significant frequency of $Gm^{a;b0,3,t}$ is the Quechua. Johnson et al. ('77) report finding a pooled frequency of 0.024 among the sample of Paraguayan Indians originally described by Brown et al. ('74).

2. Distribution of Km genotypes among South American Indians

The Km^1 frequencies are presented in Section C of table 6 and mapped in figure 2. Clearly, the Km^1 frequencies vary from quite low (0.15 in the Siriono) to near fixation (0.91 in the Piaroa), although the majority of tribes seem to be characterized by moderate frequencies (0.3-0.6) of the gene. A casual reading of the review by Johnson et al. ('77) might lead the reader to believe that Salzano et al. ('73) reported a Km^1 frequency of 0.95 in some South American Indians. However, only the Km^1 frequency of the Piaroa, not studied by Salzano, attains such an unusually high frequency.

3. Differences between tribes in the frequency of the Gm and Km alleles

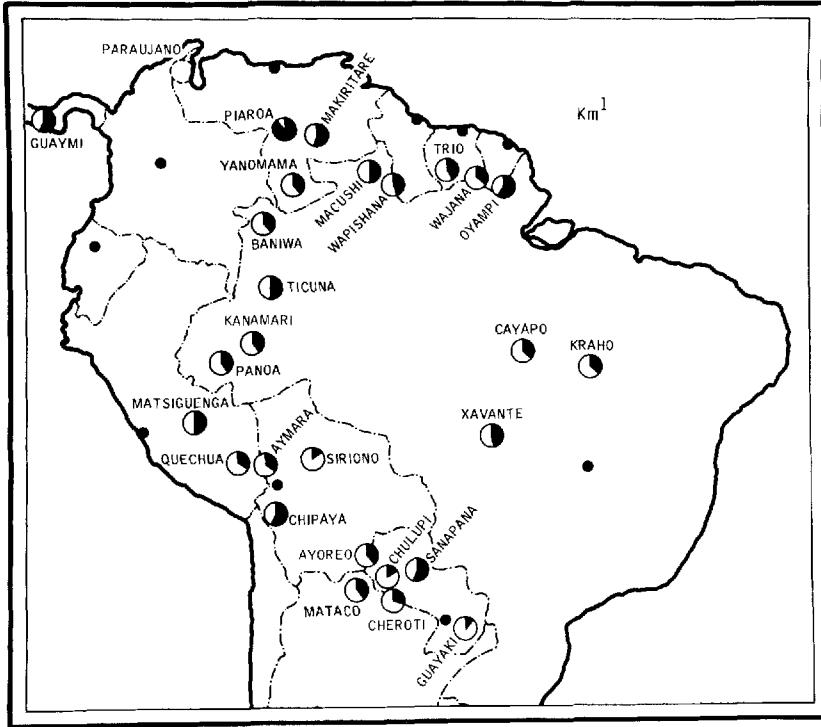The magnitudes of the observed differences between tribes in the frequencies of alleles of

Fig. 2 Km^1 frequencies in South American Indian tribes. ● = capital cities.

these two systems is conveniently expressed by Wright's F_{ST} defined as

$$\frac{\sigma^2}{\overline{p}(1-\overline{p})}$$

where

$\overline{p}$ = allele frequency in the total sample, and

$$\sigma^2 = \sum_{i=1}^{N} w_1(p_i - \overline{p})^2$$

In the calculation of F_{ST} we have omitted the Paraujano and Galibi tribes. F_{ST} for the $Gm^{ax;g}$ and Km^1 alleles in the remaining 32 tribes of table 6 is 0.094 for both $Gm^{ax;g}$ and Km^1. Salzano ('75) has presented the F_{ST} values for a series of 29 tribes meeting the above restrictions with regard to non-admixture (but not numbers), with respect to 11 alleles of six genetic systems, namely, MNSs, Rh, Duffy, Diego, Kidd, and haptoglobin. The values range from 0.039 for the L^{Ns} allele to 0.074 with respect to Fy^a, with a mean of 0.057. Thus the values for the Gm and Km systems appear on the high side. However, a more appropriate comparison would be restricted to tribes typed for all eight of the systems under discussion and also meeting the numerical requirements

mentioned above. There are 14 such tribes (Acawai, Aymara, Cayapo, Cheroti, Chulupi, Macushi, Makiritare, Mataco, Piaroa, Ticuna, Wajana, Wapishana, Xavante, and Yanomama). F_{ST} for this group of 14 tribes ranges from 0.025 for L^{NS} to 0.126 for Km^1 with a mean of 0.057. The value for $Gm^{ax;g}$ is 0.063.

One indirect approach to detecting the action of genetic selection in man is a search for heterogeneity among the F_{ST} values obtained for a series of alleles in a series of tribes. Uniformity of frequency for a particular allele with reference to the others could indicate the action of stabilizing selection, whereas wide variability in frequency could indicate a response to localized selective forces. Unfortunately, in our opinion both the highly stochastic element we have postulated in the determination of the gene frequencies of a new tribe (Neel, '67) and the high level of inbreeding within a tribe, which lessens effective sample size (Spielman et al., '77), preclude the application of standard statistical tests to the normality of the distribution of tribal gene frequencies in Amerindians. In the

present situation, inspection of the data reveals that the high F_{ST} value for Km^1 is due to a single outlier value, the gene frequency of 0.91 in the Piaroa. With the elimination of that value F_{ST} becomes 0.058. We suggest that the unusually high Km^1 value observed in the Piaroa is much more likely to be due to the operation of chance than a reflection of unusual selective pressure on this tribe.

Another traditional approach to the search for indices of selection is the quest for clines in allele frequencies. This type of evidence is often compromised by the role admixture may play in creating a cline (not a problem with the Amerindian) and the role of chance (perhaps greater than realized, cf. Ward and Neel, '76). Inspection of figures 1 and 2 reveals no obvious pattern. There is, however, a modest North-South gradient, better defined for Km^1 than $Gm^{ax;g}$. Thus, if the data are grouped by 10° changes in latitude, we observe the following changes in (unweighted) allele frequencies:

Latitude	$Gm^{ax;g}$	Km^1
0 - 10°N	0.272	0.512
0 - 10°S	0.306	0.412
10° - 20°S	0.183	0.398
20° - 30°S	0.187	0.330

We simply note the Km^1 cline at this time, with no attempt to attach significance to it. We do note, however, that this is the second report on a cline in Km^1 frequencies, the first being the finding, among the villages of Bougainville, Solomon Island, of a cline ranging from 0.83 in the north to 0.41 in the south (Friedlaender and Steinberg, '70) and its apparent southerly extension to the island of Malaita (Steinberg et al., '72).

4. *The problem of Amerindian subtypes*

The date of the first arrival of the Amerindian in the New World remains highly conjectural. Uncertain, too, is the question of whether there was only one influx of migrants, possibly over an extended period, or whether there were several migratory waves, either by way of the Bering Land Bridge or, much less likely, via other portals of entry. Anthropologists have repeatedly attempted to identify, on the basis of physical traits, types reflecting these postulated waves. The number of such types has varied from two to six (Imbelloni, '38; Birdsell, '51; Rivet, '58). More recently, on the basis of a genetic distance

analysis utilizing the frequencies of alleles at six different loci for the 20 different tribes of Central and South America for whom data were available, we have pointed to an apparent dichotomy between the Yanomama, Guaymi, and Yupa, on the one hand, and the remaining 17 tribes, on the other hand (Ward et al., '75).

On the assumption that the founding populations were small in numbers, it has been a recurrent hope among geneticists to identify "marker genes" with respect to these hypothetical waves. The first possible example of this is due to Layrisse and Wilbert ('61), who, observing that some Amerindian tribes lacked Di^a, suggested that those tribes with and those tribes without the allele reflected different waves of migration. The observations of the present paper with respect to the $Gm^{ax;g}$ and $Gm^{a;b0,3,t}$ haplotypes obviously lend themselves to this type of speculation.

Given the opportunities for genetic exchange across tribal boundaries, it is scarcely to be expected that any original "presence-absence" differences would persist, but on a "successive wave" hypothesis one might reasonably postulate a bimodality in the frequencies of certain alleles. One might also reasonably expect that the immigrants of the later wave might be found on the coastal regions or on the major water-ways systems. Unfortunately, these are the very populations most subject to gene flux. Nonetheless, a suitable body of data for a systematic (rather than episodic) search for this type of evidence is beginning to become available. For 11 of the tribes whose Gm and Km groups we have reported, data are available on allele frequencies for 37 genetic systems (complete data are not yet available for the Panoa, Baniwa, Ticuna and Kanamari). In tables 7 and 8, we have undertaken such a search in connection with alleles of wide-spread distribution *attaining substantial frequencies in some tribes but known to be absent in at least one of these 11 tribes* (excluding private polymorphisms).

Elsewhere (Neel, '78) we have suggested that among the tribes listed in table 7 in which very low frequencies (<0.01) of the $6PGD^C$ allele are encountered, the presence of the allele can be explained by admixture with Caucasians or Negroes, so that only one tribe in this series, the Guaymi, has a substantial "native" frequency of this gene. We have also attributed the presence of the Di^a allele in the Yanomama to recent admixture with the

TABLE 7

Some characteristics of Amerindian tribes

Tribe	Linguistic Affiliation	Gma;b0,3,t	Gmax;g	Dia	Rz	TFDChi	6PGDC
1. Ayoreo (Moro)	Zamuco	0.000	0.000	0.000	0.000	0.000	0.000
2. Cayapo	Ge	0.000	0.407	0.229	0.026	0.000	0.003
3. Guaymi	Macro-Chibchan	0.000	0.314	0.000	0.000	0.068	0.085
4. Kraho	Ge	0.003	0.116	0.110	0.000	0.000	0.000
5. Macushi	Carib	0.022	0.393	0.117	0.020	0.000	0.002
6. Makiritare	Carib	0.000	0.435	0.196	0.017	0.000	0.004
7. Piaroa	Saliban	0.000	0.215	0.120	0.000	0.092	0.000
8. Trio	Carib	0.032	0.225	0.090	0.120	0.000	0.000
9. Wapishana	Arawak	0.048	0.340	0.162	0.044	0.000	0.010
10. Xavante	Ge	0.000	0.238	0.168	0.045	0.000	0.000
11. Yanomama	Isol.	0.000	0.147	0.004	0.094	0.000	0.000

TABLE 8

An attempt to demonstrate pattern on the basis of six alleles present in some tribes but missing in others, based on the data of table 7. Further explanation in text

Tribe	Linguistic affiliation	Allele					
		6PGDC	TFDChi	GMa;b0,3,t	Dia	Rz	Gmax;g
Ayoreo	Zamuco	0	0	0	0	0	0
Guaymi	Chibchan	+	+	0	0	0	+
Yanomama	Isolated	0	0	0	0	+	+
Piaroa	Saliva	0	+	0	+	0	+
Kraho	Ge	0	0	0	+	0	+
Xavante	Ge	0	0	0	+	+	+
Cayapo	Ge	0	0	0	+	+	+
Makiritare	Carib	0	0	0	+	+	+
Macushi	Carib	0	0	+	+	+	+
Trio	Carib	0	0	+	+	+	+
Wapishana	Arawak	0	0	+	+	+	+

Makiritare and Awake (Ward et al., '75), and believe the same explanation (admixture) to apply to the presence of $Gm^{a;b0,3,t}$ in the Kraho. Accordingly, the situation in pre-Columbian tribes might be presented as shown in table 8, in which the tribes are arranged to emphasize such pattern as is present. It is apparent that an effort to define major dichotomies on the basis of any one system quickly runs into conflicts on the basis of other systems. Furthermore there is as yet no suggestion of bimodalities of allele frequencies for any of the alleles that are present. Even within linguistic groups where there is no reason to suspect recent linguistic borrowing, one of these six alleles may be present in some tribes and absent in another.

As of now, the lack of pattern in these data is suggestive of random loss of alleles from small populations, to such an extent as to obscure any simple di- or trichotomy which might ever have existed in the past. It seems clear that the next major step in the effort to develop rational genetic groupings of Amerindians is the application of a variety of multiple variable techniques to data on a much expanded number of Indian tribes, perhaps 50, and this we propose to do. However, it is already apparent that this approach must be applied with discrimination. One product of such techniques is a genetic dendrogram; earlier we referred to the clustering of Yanomama and Guaymi in one such dendrogram (Ward et al., '75). The current analysis certainly gives no support to that clustering; other, additional observations further weaken the case for a relatively close genetic relationship between these two tribes (Spielman et al., '78), and we are now inclined to discount any special genetic relationship between those two tribes relative to an early dichotomization of Amerindian tribes. Thus far the genetic approach has failed to supply supporting evidence for the existence of distinct sub-groups

of Amerindians such as could be traced to successive waves of immigration.

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